

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 10:18:04 ; Search time 450.333 Seconds  
(without alignments)  
8620.743 Million cell updates/sec

Title: US-09-451-739H-4  
Perfect score: 857  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 2941586 seqs, 2264995651 residues

Total number of hits satisfying chosen parameters: 5883172

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:  
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2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
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5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*  
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19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	616.4	71.9	2886	13 US-09-874-347-1	Sequence 1, Appli
2	616	71.9	2897	13 US-09-874-347-3	Sequence 3, Appli
3	616	71.9	8487	9 US-09-764-877-3454	Sequence 3454, Ap
4	616	71.9	8487	16 US-10-242-515-3454	Sequence 3454, Ap
5	606.4	70.8	873	10 US-09-968-853A-4	Sequence 4, Appli
6	604	70.5	2061	10 US-09-968-853A-2	Sequence 2, Appli
7	534.4	62.4	633	10 US-09-968-853A-6	Sequence 6, Appli
8	355	41.4	451	9 US-09-738-973-146	Sequence 146, App
9	355	41.4	451	9 US-09-854-133-146	Sequence 146, App
10	355	41.4	451	15 US-10-144-649A-146	Sequence 146, App
11	156.8	18.3	8370	13 US-10-221-714A-437	Sequence 437, App
12	142.6	16.6	840	14 US-10-115-899-6	Sequence 6, Appli
13	142.6	16.6	1078	14 US-10-115-899-7	Sequence 7, Appli
14	142.6	16.6	1080	13 US-10-203-532-7	Sequence 7, Appli

C 15	141	16.5	1890	13	US-10-027-632-261924	Sequence 261924,
C 16	141	16.5	1890	13	US-10-027-632-261925	Sequence 261925,
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C 18	141	16.5	1890	16	US-10-027-632-261925	Sequence 261925,
C 19	131.4	15.3	8370	13	US-10-221-714A-438	Sequence 438, App
C 20	110.2	12.9	421	10	US-09-918-995-37033	Sequence 37033, A
C 21	96.8	11.3	693	13	US-10-276-774-709	Sequence 709, App
C 22	96.8	11.3	1300	13	US-10-302-172-403	Sequence 403, App
C 23	84	9.8	1611	13	US-10-276-774-951	Sequence 951, App
C 24	77.6	9.1	667	13	US-10-425-114-36447	Sequence 36447, A
C 25	66.6	7.8	1336	16	US-10-264-049-545	Sequence 545, Appl
C 26	66.6	7.8	1807	13	US-10-203-532-2	Sequence 2, Appli
C 27	66.6	7.8	1864	15	US-10-037-270-435	Sequence 435, App
C 28	66.6	7.8	1864	16	US-10-117-722-435	Sequence 435, App
C 29	63.2	7.4	1254	13	US-10-424-599-73616	Sequence 73616, A
C 30	61.6	7.2	657	13	US-10-424-599-73612	Sequence 73612, A
C 31	61.2	7.1	669	13	US-10-425-114-17679	Sequence 17679, A
C 32	61.2	7.1	1200	13	US-10-424-599-19419	Sequence 19419, A
C 33	60.2	7.0	435	13	US-09-770-423-37	Sequence 37, Appl
C 34	60.2	7.0	813	9	US-09-938-842A-1178	Sequence 1178, Ap
C 35	60.2	7.0	813	11	US-09-938-842A-1178	Sequence 1178, Ap
C 36	59.6	7.0	1926	15	US-10-294-804-3	Sequence 3, Appli
C 37	59.6	7.0	8705	15	US-10-291-230-14	Sequence 14, Appl
C 38	59.6	7.0	8705	15	US-10-231-249-14	Sequence 14, Appl
C 39	59.6	7.0	8705	17	US-10-273-678-16	Sequence 16, Appl
C 40	59.6	7.0	9600	15	US-10-278-751-1	Sequence 1, Appli
C 41	59.6	7.0	10233	15	US-10-050-898-283	Sequence 283, App
C 42	59.6	7.0	10285	15	US-10-050-902-283	Sequence 283, App
C 43	58	6.8	919	13	US-10-425-114-22481	Sequence 22481, A
C 44	57.8	6.7	993	9	US-09-801-368-257	Sequence 257, App
C 45	57.8	6.7	14800	9	US-09-954-456-1601	Sequence 1601, Ap

## ALIGNMENTS

RESULT 1  
US-09-874-347-1  
; Sequence 1, Application US/09874347  
; Publication No. US20020039735A1  
; GENERAL INFORMATION:  
; APPLICANT: RIABOWOL, Karl T.  
; APPLICANT: BOLAND, Donna  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO INGI ISOFORMS  
; FILE REFERENCE: 028722-296  
; CURRENT APPLICATION NUMBER: US/09/874,347  
; CURRENT FILING DATE: 2001-06-04  
; PRIOR APPLICATION NUMBER: US 60/208,829  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: US 09/532,868  
; PRIOR FILING DATE: 2000-03-22  
; PRIOR APPLICATION NUMBER: US 09/258,372  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: US 08/751,230  
; PRIOR FILING DATE: 1996-11-15  
; PRIOR APPLICATION NUMBER: US 08/569,721  
; PRIOR FILING DATE: 1995-12-08  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 2886  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (433)..(1701)  
US-09-874-347-1

Query Match 71.9%; Score 616.4; DB 13; Length 2886;  
Best Local Similarity 85.5%; Pred. No. 3.6e-148;  
Matches 686; Conservative 0; Mismatches 116; Indels 0; Gaps 0;  
QY 56 CGCCCTCGGGCTATCCACCTCTTCTGGGCTCGCACTAGACGACCTTCCCTCTCA 115

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Db 811 CTCTCCCGCTCAGCCCGGCACTTTCCGGCGGGATTTATAGCAGTAGCAGTGATCCCG 870
Qy 116 GGCCCTTTGCTCCAAAGCGTTCCAACTGAGTACCGGAGACACACAAAGGGAGGC 175
Db 871 GGCTGTGGCTCGGGCGCGGGCTGAGTTCGACCGCTCCCGGACCCCGGGGCG 930
Qy 176 GGTGACGATGCGCCAGCGCGGGAGCCGCTGAGTGTGCGAGTGTGTGTCGGCGCG 235
Db 931 GCTCGGAGACAGTTTTCAGGCGCATCTTTGCTGACCCAGGGTGGGGCCGCGTGGCG 990
Qy 236 GGAATGAGATCTTGAAGGAGTAGACGAGTGTACGAGCGCTTCACTGCGGAGACAGAC 295
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Qy 296 GGGCGGAGAAAGCGCGGATGCTGCACTGTGTGAGCGCGCGCTGTATCCGACCGAGAG 355
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Qy 836 AATCATAAACCCAGGCAAGT 857
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RESULT 2

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US-09-874-347-3
; Sequence 3, Application US/09874347
; Publication No. US20020039735A1
; GENERAL INFORMATION:
; APPLICANT: RIABOWOL, Karl T.
; APPLICANT: BOLAND, Donna
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO INGI ISOFORMS
; FILE REFERENCE: 028722-296
; CURRENT FILING DATE: US/09/874,347
; PRIOR APPLICATION NUMBER: US 60/208,829
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 09/532,868
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: US 09/258,372
; PRIOR FILING DATE: 1999-02-26

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; PRIOR APPLICATION NUMBER: US 08/751,230
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: US 08/569,721
; PRIOR FILING DATE: 1995-12-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2897
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (873)..(1712)
; US-09-874-347-3

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Query Match

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Best Local Similarity 71.9%; Score 616; DB 13; Length 2897;
Matches 616; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 242 GAGATCCTGAAGGAGCTAGACGAGTGTTCAGAGCGCTTCACTGCGGAGACAGACGGGCG 301
Db 1008 GAGATCCTGAAGGAGCTAGACGAGTGTTCAGAGCGCTTCACTGCGGAGACAGACGGGCG 1067
Qy 302 CAGAACCGCGGATGCTGCACTGTGTGAGCGCGCGCTGATCCCGACCGAGGCTGGC 361
Db 1068 CAGAACCGCGGATGCTGCACTGTGTGAGCGCGCGCTGATCCCGACCGAGGCTGGC 1127
Qy 362 GACGAGAGATCCAGATCGTGAGCCAGATGTGTGAGTGTGTGAGAACCGCACCGGCGAG 421
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Db 1308 AACACAAAGCGCTACGCGCGACGCGCAACCAACGAGAACCGTGAGAACCGCTCCAGCAAC 1367
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Db 1368 CACGACCCAGAGCGCGGCGCTCCGCGCACACCCAGGAGAGAGAGGCGCAAGACCTCCAG 1427
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Db 1428 AAGAAAGAGCGCTCCAAAGGCCAAGCGGAGCGAGAGCGTCCCTGCGGACCTCCCATC 1487
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Db 1488 GACCCCAAGACCCAGCTACTGTGTGCAACAGGCTCTCTATGGGAGATGATCGGC 1547
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RESULT 3

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US-09-764-877-3454
; Sequence 3454, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877

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; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 4031  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3454  
; LENGTH: 8487  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-764-877-3454

Query Match 71.9%; Score 616; DB 9; Length 8487;  
Best Local Similarity 100.0%; Pred. No. 5e-148;  
Matches 616; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 242 GAGATCTGAGGAGCTAGAGAGTCTACGAGCGCTTCAGTCGGAGACAGCGGGCG 301  
DB 6232 GAGATCTGAGGAGCTAGAGAGTCTACGAGCGCTTCAGTCGGAGACAGCGGGCG 6291  
QY 302 CAGAGCGCGGATGCTGCACTGTGTGAGCGCGCTGATCCGAGCCAGGAGCTGGGC 361  
DB 6292 CAGAGCGCGGATGCTGCACTGTGTGAGCGCGCTGATCCGAGCCAGGAGCTGGGC 6351  
QY 362 GACGAGAGATCCAGATCGTAGCGAGATGTTGGAGCTGTGGAGACCGCACGGCGAG 421  
DB 6352 GACGAGAGATCCAGATCGTAGCGAGATGTTGGAGCTGTGGAGACCGCACGGCGAG 6411  
QY 422 GTGACAGCCAGCTGGAGCTGTTGAGGCGCAGCAGAGGCTGGGCGACACAGCGGCAAC 481  
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QY 482 AGCGGAGGCTGGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 541  
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QY 542 AACAGCAAGCGCTCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 601  
DB 6532 AACAGCAAGCGCTCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 6591  
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DB 6592 CAGGACCGAGCGGCGGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 6651  
QY 662 AAGAGAGCGCTCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 721  
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US-10-242-515-3454  
; Sequence 3454, Application US/10242515  
; Publication No. US20040009488A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC005C1  
; CURRENT APPLICATION NUMBER: US/10/242,515  
; PRIOR FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: 09/764,877  
; PRIOR FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: 60/179,065  
; PRIOR FILING DATE: 2000-01-31

; PRIOR APPLICATION NUMBER: 60/180,628  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: 60/214,886  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/217,487  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/225,758  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/220,963  
; PRIOR FILING DATE: 2000-07-26  
; PRIOR APPLICATION NUMBER: 60/217,496  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/225,447  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/218,290  
; PRIOR FILING DATE: 2000-07-14  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 4031  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3454  
; LENGTH: 8487  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-242-515-3454

Query Match 71.9%; Score 616; DB 16; Length 8487;  
Best Local Similarity 100.0%; Pred. No. 5e-148;  
Matches 616; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 242 GAGATCTGAGGAGCTAGAGAGTCTACGAGCGCTTCAGTCGGAGACAGCGGGCG 301  
DB 6232 GAGATCTGAGGAGCTAGAGAGTCTACGAGCGCTTCAGTCGGAGACAGCGGGCG 6291  
QY 302 CAGAGCGGCGATGCTGCACTGTGTGAGCGCGCTGATCCGAGCCAGGAGCTGGGC 361  
DB 6292 CAGAGCGGCGATGCTGCACTGTGTGAGCGCGCTGATCCGAGCCAGGAGCTGGGC 6351  
QY 362 GACGAGAGATCCAGATCGTAGCGAGATGTTGGAGCTGTGGAGAACCGCACGGCGAG 421  
DB 6352 GACGAGAGATCCAGATCGTAGCGAGATGTTGGAGCTGTGGAGAACCGCACGGCGAG 6411  
QY 422 GTGACAGCCAGCTGGAGCTGTTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 481  
DB 6412 GTGACAGCCAGCTGGAGCTGTTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 6471  
QY 482 AGCGGAGGCTGGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 541  
DB 6472 AGCGGAGGCTGGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 6531  
QY 542 AACAGCAAGCGCTCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 601  
DB 6532 AACAGCAAGCGCTCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 6591  
QY 602 CAGGACCGAGCGGCGGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 661  
DB 6592 CAGGACCGAGCGGCGGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 6651  
QY 662 AAGAGAGCGCTCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 721  
DB 6652 AAGAGAGCGCTCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 6711  
QY 722 GACCCCAAGCGGCGGCTGCTGTGTCACCGAGGCTCTCTATGGGAGATGATCGGC 781  
DB 6712 GACCCCAAGCGGCGGCTGCTGTGTCACCGAGGCTCTCTATGGGAGATGATCGGC 6771  
QY 782 TCGGACACGAGGTCGCCATCGAGTGTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 841  
DB 6772 TCGGACACGAGGTCGCCATCGAGTGTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 6831  
QY 842 AAACCCAAAGGCAAGT 857  
DB 6832 AAACCCAAAGGCAAGT 6847



LOCATION: 16...897  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-968-653A-2

Query Match 70.5%; Score 604; DB 10; Length 2061;  
Best Local Similarity 95.4%; Pred. No. 5.3e-145;  
Matches 622; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 206 CTAGGCTGCTGGAGTGTGTGCTCCGGCCCGGGAATGGAGATCTCTGAAGAGCTAGACGAG 265  
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DB 280 GTGACGCGCGCTGATCCGACGACGAGGCTGGGCGACGAGAAATCCAGATCTGTGAC 339  
QY 386 CAGATGCTGAGCTGTGTGAGAACCGACGCGCGAGGTGGACAGCCAGCTGGAGCTGTC 445  
DB 340 CAGATGCTGAGCTGTGTGAGAACCGACGCGCGAGGTGGACAGCCAGCTGGAGCTGTC 399  
QY 446 GAGGCGACGAGCTGGGCGACACAGCGGGCAACAGCGGCAAGGCTGGCGCGACAGG 505  
DB 400 GAGGCGACGAGCTGGGCGACACAGTGCGGCAACAGCGGCAAGGTTGGCGCGACAGG 459  
QY 506 CCCAAGGCGAGCGCGACGCGAGCTGACAGCCCAACAGCAAGGCTCAGCGGCGAG 565  
DB 460 CCCAATGGCGATGCGGTAGCGAGTCTGACAGCCCAACAGCAAGGCTCAGCGGCGAG 519  
QY 566 CGCAACCAACGAGAACCGTCCAGCAACCGCTCCAGCAACCGACGACGAGCGCGCTCG 625  
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DB 580 GGCACACCAAGAGAAAGGCGACCTCCAGAGAAAGAGGCTCCAGGCGAG 639  
QY 686 GCGGAGCGAGAGCGCTCCCTGCGGACCTCCCATCGACCCCAACGAAACCGACGACTGT 745  
DB 640 GCGGAGCGAGAGCGCTCCCTGCGGACCTCCCATCGACCCCAACGAAACCGACGACTGT 699  
QY 746 CTGTGCAACAGGCTTCCTATGGGAGATGATCGGCTCGGACAAAGAGTGCCCATC 805  
DB 700 CTGTGCAACAGGCTTCCTATGGGAGATGATCGGCTCGGACAAAGAGTGCCCATC 759  
QY 806 GAGTGCTTCCACTTCTCGTGGGCTCAATCATAAACCAAGGCAAGT 857  
DB 760 GAGTGCTTCCACTTCTCGTGGGCTCAATCATAAACCAAGGCAAGT 811

RESULT 7  
US-09-968-653A-6  
Sequence 6, Application US/09968653A  
Publication No. US20030073084A1  
GENERAL INFORMATION:  
APPLICANT: Gudkov, Andrey V  
Garkavstev, Igor  
Riabowol, Karl  
TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
STREET: 300 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/968,653A  
FILING DATE: 01-Oct-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/006,783A  
FILING DATE: 15-JAN-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: No. US20030073084Ainan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 97,837  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-913-0001  
TELEFAX: 312-913-0002  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 633 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..630  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-968-653A-6

Query Match 62.4%; Score 534.4; DB 10; Length 633;  
Best Local Similarity 98.9%; Pred. No. 3.2e-127;  
Matches 538; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 314 ATGCTGACCTGTGTGACGCGCGCTGATCCGACGAGGCTGGCGACGAGAGATC 373  
DB 1 ATGCTGACCTGTGTGACGCGCGCTGATCCGACGAGGCTGGCGACGAGAGATC 60  
QY 374 CAGATCTGAGCCAGATGTGTGAGCTGTGTGAGAACCGACGCGGAGGTGTGACGCCAC 433  
DB 61 CAGATCTGAGCCAGATGTGTGAGCTGTGTGAGAACCGACGCGGAGGTGTGACGCCAC 120  
QY 434 GTGAGCTGTTTCGAGGCGGACGAGGAGCTGGGCGACACAGCGGCGCAAGGCT 493  
DB 121 GTGAGCTGTTTCGAGGCGGACGAGGAGCTGGGCGACACAGTGGGCGACAGCGCAGGTT 180  
QY 494 GGCCTGACGAGCGCCCAAGGCGGAGCGGAGCGGAGCTGACAGCCCAACAGCAAGCGC 553  
DB 181 GGCCTGACGAGCGCCCAATGCGATGCGGTAGCGAGTCTGACAAAGGCCCAACAGCAAGCGC 240  
QY 554 TCACGCGGCGACGCAACACGAGGAGCCGTGAGAACCGCTCCAGACACGACGACGAC 613  
DB 241 TCACGCGGCGACGCAACACGAGGAGCCGTGAGAACCGCTCCAGACACGACGACGAC 300  
QY 614 GACGCGCTCTCGGCGACACCCCAAGGAGAGAGCCCAAGACCTCCCAAGAGAGAGAGCGC 673  
DB 301 GACGCGCTCTCGGCGACACCCCAAGGAGAGAGAGCCCAAGACCTCCCAAGAGAGAGAGCGC 360  
QY 674 TCCAGGCGGAGCGGAGGAGGCGTCCCTGCGGAGCTCCCATCGACGCGGAGAGAG 733  
DB 361 TCCAGGCGGAGCGGAGGAGGCGTCCCTGCGGAGCTCCCATCGACGCGGAGAGAG 420  
QY 734 CCCACGCTACTGTCTGTGCAACCGAGTCTCTATGGGAGATGATCGGCTCGGACCAAGC 793  
DB 421 CCCACGCTACTGTCTGTGCAACCGAGTCTCTATGGGAGATGATCGGCTCGGACCAAGC 480  
QY 794 GAGTGCCCGGATCGAGTGTTCCTCTCTGCGGTGGGCTCAATCATAAACCAAGGCG 853  
DB 481 GAGTGCCCGGATCGAGTGTTCCTCTCTGCGGTGGGCTCAATCATAAACCAAGGCG 540  
QY 854 AAGT 857  
DB 541 AAGT 544

APPLICANT: Benson, Darin R.  
APPLICANT: Secrist, Heather  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR  
FILE REFERENCE: 210121.475C10  
CURRENT APPLICATION NUMBER: US/09/854,133  
CURRENT FILING DATE: 2001-05-11  
NUMBER OF SEQ ID NOS: 735  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 146  
LENGTH: 451  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-854-133-146

Query Match 41.4%; Score 355; DB 9; Length 451;  
Best Local Similarity 99.7%; Pred. No. 2.7e-81;  
Matches 366; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 242 GAGATCCTGAAGAGCTAGACGAGTGTACGAGCGCTTCAGTCGCGAGACAGACGCGGCG 301  
DB 86 GAGATCCTGAAGAGCTAGACGAGTGTACGAGCGCTTCAGTCGCGAGACAGACGCGGCG 145  
QY 302 CAGAAAGCGCGGATCTGCTGCTGTCAGCGCGGCTGATCCGAGCCAGGAGCTGGGC 361  
DB 146 CAGAAAGCGCGGATCTGCTGCTGTCAGCGCGGCTGATCCGCA-CCAGGAGCTGGGC 204  
QY 362 GACGAGAGATCCAGATCGTGAGCCAGATGTTGGAGTGTGGAGAACCGCACGCGGCG 421  
DB 205 GACGAGAGATCCAGATCGTGAGCCAGATGTTGGAGTGTGGAGAACCGCACGCGGCG 264  
QY 422 GTGGACAGCCAGTGGAGCTGTTGAGCGGAGGAGGCTGGGCGGAGCAGCGGCGCAAC 481  
DB 265 GTGGACAGCCAGTGGAGCTGTTGAGCGGAGGAGGCTGGGCGGAGCAGCGGCGCAAC 324  
QY 482 AGCGGCAAGGCTGGCGGAGCAGGCGGCGGAGGCGGCGGAGGCGGCGGAGGCGGCGG 541  
DB 325 AGCGGCAAGGCTGGCGGAGCAGGCGGCGGAGGCGGCGGAGGCGGCGGAGGCGGCG 384  
QY 542 AACAGCAAGGCTGACGCGGCGGAGGCGGCGGAGGCGGCGGAGGCGGCGGAGGCGGCG 601  
DB 385 AACAGCAAGGCTGACGCGGCGGAGGCGGCGGAGGCGGCGGAGGCGGCGGAGGCGGCG 444  
QY 602 CACGACC 608  
DB 445 CACGACC 451

RESULT 10  
US-10-144-649A-146  
Sequence 145, Application US/10144649A  
Publication No. US2003011859A1  
GENERAL INFORMATION:  
APPLICANT: Lodes, Michael J.  
APPLICANT: Wang, Tongtong  
APPLICANT: Fan, Liqun  
APPLICANT: Algate, Paul A.  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR  
FILE REFERENCE: 210121.475C11  
CURRENT APPLICATION NUMBER: US/10/144,649A  
CURRENT FILING DATE: 2002-08-21  
NUMBER OF SEQ ID NOS: 749  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 146  
LENGTH: 451  
TYPE: DNA  
ORGANISM: Homo sapien  
US-10-144-649A-146

Query Match 41.4%; Score 355; DB 15; Length 451;  
Best Local Similarity 99.7%; Pred. No. 2.7e-81;

APPLICANT: Benson, Darin R.  
APPLICANT: Secrist, Heather  
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.475C9  
CURRENT APPLICATION NUMBER: US/09/738,973  
CURRENT FILING DATE: 2000-12-14  
NUMBER OF SEQ ID NOS: 587  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 146  
LENGTH: 451  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-738-973-146

Query Match 41.4%; Score 355; DB 9; Length 451;  
Best Local Similarity 99.7%; Pred. No. 2.7e-81;  
Matches 366; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 242 GAGATCCTGAAGAGCTAGACGAGTGTACGAGCGCTTCAGTCGCGAGACAGACGCGGCG 301  
DB 86 GAGATCCTGAAGAGCTAGACGAGTGTACGAGCGCTTCAGTCGCGAGACAGACGCGGCG 145  
QY 302 CAGAAAGCGCGGATCTGCTGCTGTCAGCGCGGCTGATCCGAGCCAGGAGCTGGGC 361  
DB 146 CAGAAAGCGCGGATCTGCTGCTGTCAGCGCGGCTGATCCGCA-CCAGGAGCTGGGC 204  
QY 362 GACGAGAGATCCAGATCGTGAGCCAGATGTTGGAGTGTGGAGAACCGCACGCGGCG 421  
DB 205 GACGAGAGATCCAGATCGTGAGCCAGATGTTGGAGTGTGGAGAACCGCACGCGGCG 264  
QY 422 GTGGACAGCCAGTGGAGCTGTTGAGCGGAGGAGGCTGGGCGGAGCAGCGGCGCAAC 481  
DB 265 GTGGACAGCCAGTGGAGCTGTTGAGCGGAGGAGGCTGGGCGGAGCAGCGGCGCAAC 324  
QY 482 AGCGGCAAGGCTGGCGGAGCAGGCGGCGGAGGCGGCGGAGGCGGCGGAGGCGGCGG 541  
DB 325 AGCGGCAAGGCTGGCGGAGCAGGCGGCGGAGGCGGCGGAGGCGGCGGAGGCGGCGG 384  
QY 542 AACAGCAAGGCTGACGCGGCGGAGGCGGCGGAGGCGGCGGAGGCGGCGGAGGCGGCG 601  
DB 385 AACAGCAAGGCTGACGCGGCGGAGGCGGCGGAGGCGGCGGAGGCGGCGGAGGCGGCG 444  
QY 602 CACGACC 608  
DB 445 CACGACC 451

RESULT 9  
US-09-854-133-146  
Sequence 146, Application US/09854133  
Publication No. US2002018349A1  
GENERAL INFORMATION:  
APPLICANT: Lodes, Michael J.  
APPLICANT: Mohamath, Raodon  
APPLICANT: Henderson, Robert A.



```
QY 661 GAAGAGAGCGCTCCRAAGGCCAAGGGGAGAGCGCGTCCCTCCGACCTCCCAT 720
Db 561 GAAAGAGAAAGCGTCCCAAGGCCAAGAGGAAAGAGCTTCCCTTTGATTTGCAAT 620
QY 721 CGAAGAGAGCGCTCCCAAGGCCAAGGGGAGAGCGCGTCCCTCCGACCTCCCAT 780
Db 621 AGATCCTAATGAACCTACATCTCTTATGCAACCAAGTGTCTTATGGGAGATGATAG 680
QY 781 CTGGACAGAGCGTCCCAAGGCCAAGGGGAGAGCGCGTCCCTCCGACCTCCCAT 840
Db 681 ATGTGACAAATGAACAGTGTCAATTTGAATGTTTCACTTTTCACTTTTCACTT 740
QY 841 TAAACCCCAAGGGCAAGT 857
Db 741 TAAACCAAGGGCAAT 757

RESULT 13
US-10-115-899-7
; Sequence 7, Application US/10115899
; Publication No. US20020151025A1
; GENERAL INFORMATION:
; APPLICANT: Oetuka Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: Human TS403 gene and human INGL1 gene
; FILE REFERENCE: Q60193
; CURRENT APPLICATION NUMBER: US/10/115,899
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/601,478
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP H10-134679
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: JP H10-73234
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: JP H10-38133
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1078
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human embryonic brain cDNA library
; NAME/KEY: CDS
; LOCATION: (92)..(931)
US-10-115-899-7

Query Match 16.6%; Score 142.6; DB 14; Length 1078;
Best Local Similarity 55.3%; Pred. No. 6.9e-27;
Matches 341; Conservative 0; Mismatches 244; Indels 32; Gaps 2;

QY 242 GAGATCCTGAAGAGCTAGACGAGTGTCTACGAGCGTTCAGTCGGGAGACAGCGGGCG 301
Db 263 GAAACGTTAAGGAAATTGATGTCTACGAAATAATAGAAAGAGATGATTAAAC 322
QY 302 CAGAAGCGGAGTGTGCTGCTGTGTGAGCGCGGCTGATCCGAGCCAGGAGCTGGC 361
Db 323 CAGAAGAAACGCTACAGCAGCTTCTCCAGAGAGCACTAAATTAATGTCAGAAATTGGGA 382
QY 362 GAGCAGAAATCCAGATCTGAGCAGAGTGTGGAGTGTGGAGAACCGCAGCGGCGAG 421
Db 383 GATGAAAAATACAGATTGTACAAATGCTCGAATTTGGTGAATAATCGGCAAGACAA 442
QY 422 GTGGACAGCCAGTGTGAGTGTTCGAGGCGGAGCAGGAGCTGGGCGACACAGCGGGCAAC 481
Db 443 ATGGAGTTACCTCACAGTGTTCCTCAAGATC----- 473
QY 482 AGCGGAAGGCTGGCGGAGCAGGCGCCCAAGGAGGCGGAGCGGAGCTGACAGAGCCC 541
Db 474 --CTGTGAAGTGAACAGCCCTCAGATAAGCAAGATGATTTCAGCCACACCAAGAG 531
QY 542 AACAGCAAG--CGTCTACGCGGCGAGCGCAACACAGAGAACCGTGAAGACCGCTCCAGCAA 600
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Db 532 ATCTTTAAAGAGACCCCGCAGGCGAGACCGAGTGAAGCGGTGATTTATGTCAATGGC 591
QY 601 CCACGACACAGCAGCGCGCTCGGGCACACCCCAAGGAGAGAGGCGCAAGACCTCCAA 660
Db 592 AATGGGATTGAGACTGTGATGATCAGCCACCTTAAGAAAGAAATCCAAGTCAGCAA 651
QY 661 GAAGAGAGCGCTCCCAAGGCCAAGGGGAGAGCGCGTCCCTCCGACCTCCCAT 720
Db 652 GAAAAAGAAACGCTCCCAAGGCCAAGCAGAAAGGAGAGCTTCACTTGTGAGTTGGCAAT 711
QY 721 CGACCCCAAGCAACCAAGTGTCTGTGCAACAGAGTCTCTATGGGAGAGATGATCGG 780
Db 712 AGATCCTAATGAACCTACATCTGCTTATGCAACCAAGTGTCTTATGGGAGATGATAGG 771
QY 781 CTGGACAGAGCGAGTGTCCCATCGAGTGTGTTCACTTCTGTCGTCGTCGTCGTCATCA 840
Db 772 ATGTGACAAATGAACAGTGTCCAATTTGAATGTTTCACTTTTCACTTGTGTTCACCTTA 831
QY 841 TAAACCCCAAGGGCAAGT 857
Db 832 TAAACCAAGGGCAAT 848

RESULT 14
US-10-203-532-7
; Sequence 7, Application US/10203532
; Publication No. US20040058379A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Curtis C.
; APPLICANT: Nagashima, Makoto
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: New Tumor Suppressor Gene, p47ING3
; FILE REFERENCE: 015280-401100US
; CURRENT APPLICATION NUMBER: US/10/203,532
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: US 60/181,292
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: WO PCT/US01/04425
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: p33ING2
US-10-203-532-7

Query Match 16.6%; Score 142.6; DB 13; Length 1080;
Best Local Similarity 55.3%; Pred. No. 6.9e-27;
Matches 341; Conservative 0; Mismatches 244; Indels 32; Gaps 2;

QY 242 GAGATCCTGAAGAGCTAGACGAGTGTCTACGAGCGTTCAGTCGGGAGACAGCGGGCG 301
Db 239 GAAACGTTAAGGAAATTGATGTCTACGAAATAATAGAAAGAGATGATTAAAC 298
QY 302 CAGAAGCGGCGAGTGTGCACTGTGTGACGCGCGGCTGATCCGAGCCAGGAGCTGGC 361
Db 299 CAGAAGAAACGCTCTACAGCAGCTTCTCCAGAGAGCACTAAATTAATAGTCAAGATTGGGA 358
QY 362 GAGCAGAGATCCAGATCTGAGCAGATGTTGGAGTGTGGAGAACCGCAGCGGGCAG 421
Db 359 GATGAAAAATACAGATTGTACAAATGCTCGAATTTGGTGAATAATCGGCAAGACAA 418
QY 422 GTGGACAGCCAGTGTGGAGTGTTCGAGGCGGAGAGCTGGGCGACACAGCGGGCAAC 481
Db 419 ATGGAGTTACCTCACAGTGTTCCTCAAGATC----- 449
QY 482 AGCGGAAGGCTGGCGGAGCAGGCGCCCAAGGAGGCGGAGCTGACAGAGCCC 541
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Db 450 --CTGCTGAAGTGAACGAGCCTCAGATTAAGCAAAAGATGGATTCCAGCCCAACCAAGAAAG 507
Qy 542 AACAGCAAG-CGCTCAGCGCGGCGAGCGCAACAAACAGAGAACCGTGAGAAACGGGTCCAGCAA 600
Db 508 ATCTTCAAGAGAACCCGCGAGCGAGCCAGTGAAGCCGTGATTTATGTCAATGGC 567
Qy 601 CCACGACCACGAGCGCGCCTCGGCGACACCCAGGAGAGAGAGCCAGACTCCAA 660
Db 568 AATGGGATGAAGACTGTGATGATCAGCCACCTAAAGAAAGAAATCAAAGTCAGCAAA 627
Qy 661 GAAGAGAGCGCTCCAGGCGCAAGCGGAGCGAGCGAGCGGTCCCTCGCGACCTCCCAT 720
Db 628 GAAAGAAACGCTCCAGGCGCAAGCGAGAAAGGAGGCTTCACTGTGAGTTTGCAAT 687
Qy 721 CGACCCCAACGACCCAGTACTGTGTGCAACAGAGTCTCTATGCGGAGATGATCGG 780
Db 688 AGATCCTAATGAACCTACATCTGTGTATGCAACCAAGTGTCTTATGGGAGATGATAGG 747
Qy 781 CTGCGACCAACGAGTGGCCCATCGAGTGGTTCACATTTCTCGTGGTGGGCTCAATCA 840
Db 748 ATGTGACATGAACAGTGTCCAAATGAATGGTTTCACTTTTCATCTGTTTCACTTACCTA 807
Qy 841 TAAACCCCAAGGGCAAGT 857
Db 808 TAAACCAAGGGGAAT 824
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## RESULT 15

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US-10-027-632-261924/c
; Sequence 261924, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 261924
; LENGTH: 1890
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-261924
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Query Match 16.5%; Score 141; DB 13; Length 1890;
Best Local Similarity 61.6%; Pred. No. 1.8e-26;
Matches 322; Conservative 0; Mismatches 175; Indels 26; Gaps 5;

Qy 289 GACAGAGCGGGCGCAGAGCGGCGGATGCTGCACTGTGTGAGCGCGCGCTGATCCGCGAG 348
Db 1670 GAGGAGGGGTACCCAGAGAGAGGGGTGTATCCGTGCAATCCAGAGAGCCCTGACTCGGAG 1611
Qy 349 CCAGGAGCTGGGCGACAGAGATCCAGATCGTGAGCCAGATGGTGGAGCTGTGGAGAA 408
Db 1610 CCAGGAGCTGGGCGTTGAGAGATCCAGA--CTGAGTCCGACGAGGAGCTGGTGGAGAG 1553
Qy 409 CCGACGCGCGCAGGTGGACAGCCACGTTGGAGTGTTTCAGGCGCCAGCAGGAGCTGGGCGA 468
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Db 1552 CAGGACCGGACAGATGGCGGTCTCCCGAGTCTCTTGGGCGAGCCAGAGATCAGGTT 1493
Qy 469 CACAGCGGGCAACAGCGGCAAGGCTGGCGCGACAGGCCCAAGGCGAGCGCGCGCA 528
Db 1492 CCTGTAGCTGTGAGAGCGCGCCACAAATCGGGGAGAAATGATAATCACGCGAG----- 1440
Qy 529 GGCTGACAAAGCCCAACAGCAAGCGCTCACGGCGGCGAGCGCAACACAGGAAACCGTGAGAA 588
Db 1439 GGAGAAACGCGCGATACAAAGTGTCTCCGCAAGTGCACAGTGAATTCGAGAGGA 1380
Qy 589 CGGCTCCAGCAACACGACCCAGCAACGACGCGCGCTCGGCGACACCCAAAGGAGAAAGGC 648
Db 1379 TGCATCCAATGATCACGACCGACGAGATCACCAAGGAAACGCGCAAGG-CAAGAAAGC 1321
Qy 649 CAAGACTTCAAGAAAGAGAGCGCTCCAGGCGGAGGCGGAGCGGAGCGCTCCCTGC 708
Db 1320 AAAGACCTTGAAGAAAGAAAGAACCACTCCAGTGTCTACAGAGA-----GGCCCCCGC 1270
Qy 709 CGACCTCCCGCATCGACCCCAACGAAACCCAGTACTGTCTGTGCAACAGGTCCTCTATGG 768
Db 1269 AGACCTTGCCATGACCGCAAGGAGACAGACAGCGTGTGGTCA-----GGTCTACAG 1217
Qy 769 GGAGATGATCGGCTGCGACAAACGACAGTGGCCCCCATCGAGTGG 811
Db 1216 AGAAGGAGCGGCTGTGACAAACCAACGAGTGGCCCCCGGAGTGG 1174
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Search completed: May 6, 2004, 14:05:49

Job time : 452.333 secs



GenCore version 5.1.6  
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CM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 06:27:28 ; Search time 2858.77 Seconds

(without alignments)  
8952.060 Million cell updates/sec

Title: US-09-451-739H-4  
Perfect score: 857  
Sequence: 1 cctccgagacgtgtccat.....tcataacccaagggcaagt 857

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

- 1: em\_estba:\*
- 2: em\_esthu:\*
- 3: em\_estin:\*
- 4: em\_estmu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_hic:\*
- 9: gb\_est1:\*
- 10: gb\_est2:\*
- 11: gb\_est3:\*
- 12: gb\_est4:\*
- 13: gb\_est5:\*
- 14: gb\_est6:\*
- 15: em\_estfun:\*
- 16: em\_estom:\*
- 17: em\_gss\_hum:\*
- 18: em\_gss\_inv:\*
- 19: em\_gss\_pln:\*
- 20: em\_gss\_vrt:\*
- 21: em\_gss\_fun:\*
- 22: em\_gss\_mam:\*
- 23: em\_gss\_mus:\*
- 24: em\_gss\_pro:\*
- 25: em\_gss\_rod:\*
- 26: em\_gss\_phg:\*
- 27: em\_gss\_vrl:\*
- 28: gb\_gss1:\*
- 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	616	71.9	873	13	BQ430264
2	615	71.8	704	29	AY404082
3	606.8	70.8	1110	12	BM457587
4	603.8	70.5	746	9	AV726745

## ALIGNMENTS

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RESULT 1
BQ430264
LOCUS      BQ430264
DEFINITION BQ430264 873 bp mRNA linear EST 24-MAY-2002
            AGENCOURT_7761891 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:5017969
            5', mRNA sequence.
ACCESSION  BQ430264
VERSION    BQ430264.1 GI:21169340
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 873)
AUTHORS   NIH-MGC http://mgc.nhl.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapps-r@mail.nih.gov
            Tissue Procurement: ATCC
            CDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLNMI3218 row: b column: 18
            High quality sequence stop: 731.

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5	592.2	69.1	742	9	AV727365	AV727365
6	591.4	69.0	982	13	BQ883364	BQ883364
7	589.8	68.8	698	29	AY404083	AY404083
8	586.8	68.5	959	13	BU166657	BU166657
9	584.6	68.2	1006	12	BM926787	BM926787
10	579.8	67.7	1201	13	EX461522	EX461522
11	574.8	67.1	894	13	BQ883151	BQ883151
12	561.4	65.5	1155	12	BM477126	BM477126
13	557.8	65.1	722	9	AV727700	AV727700
14	557	65.0	739	9	AL043324	AL043324
15	555.4	64.8	897	13	BQ679315	BQ679315
16	528	61.6	757	12	BI523956	BI523956
17	509.8	59.5	820	12	BI819716	BI819716
18	492	56.4	651	12	BM042055	BM042055
19	466.6	54.4	1000	13	BQ677075	BQ677075
20	464.2	54.2	761	12	BM042700	BM042700
21	462.6	54.0	807	12	BI755594	BI755594
22	451.6	52.7	803	12	BQ394998	BQ394998
23	447.8	52.3	1971	11	AK035490	AK035490
24	446.4	52.1	975	13	BQ934291	BQ934291
25	445.4	52.0	704	29	AY404084	AY404084
26	445.4	52.0	802	13	BU614327	BU614327
27	444.8	51.9	664	10	BB614156	BB614156
28	444.8	51.9	1514	11	AK076482	AK076482
29	439	51.2	652	13	BY729505	BY729505
30	438.8	51.2	681	14	CB447256	CB447256
31	432.8	50.5	691	13	BY720374	BY720374
32	431.4	50.3	627	14	CF791045	CF791045
33	428	49.9	694	13	BY736023	BY736023
34	423.2	49.4	582	12	BI898813	BI898813
35	419	48.9	782	14	CK032035	CK032035
36	418.8	48.9	556	29	CC544458	CC544458
37	408.2	47.6	844	12	BG862842	BG862842
38	406.4	47.4	716	12	BI107722	BI107722
39	403.2	47.0	783	13	BU748391	BU748391
40	390.2	45.5	667	9	AI956653	AI956653
41	389.2	45.4	842	14	CF909709	CF909709
42	384.2	44.8	1041	13	BU168690	BU168690
43	380.6	44.4	1151	11	AK011594	AK011594
44	378.4	44.2	729	13	BU622930	BU622930
45	374.2	43.7	746	10	BF119420	BF119420

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        /tissue_type="epithelioid carcinoma"
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ORIGIN
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  Best Local Similarity 100.0%; Pred. No. 1.5e-88;
  Matches 616; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 242 GAGATCCTGAAGAGCTAGACGAGTGTCTACGAGCGCTTCACTCGCGAGACAGACGCGGCG 301
  Db 32 GAGATCCTGAAGAGCTAGACGAGTGTCTACGAGCGCTTCACTCGCGAGACAGACGCGGCG 91
  QY 302 CAGAGCGCGGATCTCGACTGTGTGAGCGCGGCTGATCCGAGCCAGGAGCTGGGC 361
  Db 92 CAGAGCGCGGATCTCGACTGTGTGAGCGCGGCTGATCCGAGCCAGGAGCTGGGC 151
  QY 362 GACGAGAAGATCCAGATCGTAGCCAGATGTGTGAGCTGTGTGAGAAACCGCACCGCGAG 421
  Db 152 GACGAGAAGATCCAGATCGTAGCCAGATGTGTGAGCTGTGTGAGAAACCGCACCGCGAG 211
  QY 422 GTGGACGCCAGCTGGAGCTGTTCAGGCGCAGCAGGAGCTGGGCGACACAGCGGCGAAC 481
  Db 212 GTGGACGCCAGCTGGAGCTGTTCAGGCGCAGCAGGAGCTGGGCGACACAGCGGCGAAC 271
  QY 482 AGCGGCAAGGCTGGGCGGACAGGCGCCAAAGGCGGAGCGGCGAGCGCTGACAGGCC 541
  Db 272 AGCGGCAAGGCTGGGCGGACAGGCGCCAAAGGCGGAGCGGCGAGCGCTGACAGGCC 331
  QY 542 AACAGCAGCGCTCAGCGCGGCGAGCGGCGCAACAGCAGACCGTGAAGACCGCTCCAGAAC 601
  Db 332 AACAGCAGCGCTCAGCGCGGCGAGCGGCGCAACAGCAGACCGTGAAGACCGCTCCAGAAC 391
  QY 602 CACGACACGAGCGAGCGGCGCTCGGCGCACACCCAGAGGAGAGAGGCGCAAGACCTCCAG 661
  Db 392 CACGACACGAGCGAGCGGCGCTCGGCGCACACCCAGAGGAGAGAGGCGCAAGACCTCCAG 451
  QY 662 AAGAGAGCGCTCCAGGCGCAAGCGGAGCGAGCGGCTCCCTGCGGACCTCCCGATC 721
  Db 452 AAGAGAGCGCTCCAGGCGCAAGCGGAGCGAGCGGCTCCCTGCGGACCTCCCGATC 511
  QY 722 GACCCCAAGCAACCCACGCTACTGTCTGTCAACAGGCTCTCTATGGGAGATGATCGGC 781
  Db 512 GACCCCAAGCAACCCACGCTACTGTCTGTCAACAGGCTCTCTATGGGAGATGATCGGC 571
  QY 782 TCGCAACAGCAGAGTGCCTCCATTCGAGTGGTTCACATTCCTCGTGGGGCTCAATCAT 841
  Db 572 TCGCAACAGCAGAGTGCCTCCATTCGAGTGGTTCACATTCCTCGTGGGGCTCAATCAT 631
  QY 842 AAACCCCAAGGCGAAGT 857
  Db 632 AAACCCCAAGGCGAAGT 647

RESULT 2
AY404082
LOCUS
DEFINITION
  Homo sapiens INGI1 gene, VIRTUAL TRANSCRIPT, partial sequence,
  genomic survey sequence.
ACCESSION
  AY404082
VERSION
  AY404082.1 GI:39760065
KEYWORDS
  GSS.
SOURCE
  Homo sapiens (human)
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ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 704)
  Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
  Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
  Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
  Adams, M.D. and Cargill, M.
  Inferring nonneutral evolution from human-chimp-mouse orthologous
  gene trios
  Science 302 (5652), 1960-1963 (2003)
  14671302
  2 (bases 1 to 704)
  Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
  Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
  Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
  Adams, M.D. and Cargill, M.
  Direct Submission
  Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
  Rockville, MD 20850, USA
  This sequence was made by sequencing genomic exons and ordering
  them based on alignment.
  Location/Qualifiers
    source
      1..704
        /organism="Homo sapiens"
        /mol_type="genomic DNA"
        /db_xref="taxon:9606"
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  Best Local Similarity 100.0%; Pred. No. 2e-88;
  Matches 615; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 243 AGATCTCTGAAGAGCTAGACGAGTGTCTACGAGCGCTTCACTCGCGAGACAGACGCGGCGC 302
  Db 1 AGATCTCTGAAGAGCTAGACGAGTGTCTACGAGCGCTTCACTCGCGAGACAGACGCGGCGC 60
  QY 303 AGAAGCGGCGGATCTGCTGCTGTCAGCGCGCGCTGATCCGAGCCAGGAGCTGGGCG 362
  Db 61 AGAAGCGGCGGATCTGCTGCTGTCAGCGCGCGCTGATCCGAGCCAGGAGCTGGGCG 120
  QY 363 ACAGAGAAGATCCAGATCGTGAGCCAGATCGTGAGCTGTGTGAGAACCCGACCGGCGAGG 422
  Db 121 ACAGAGAAGATCCAGATCGTGAGCCAGATCGTGAGCTGTGTGAGAACCCGACCGGCGAGG 180
  QY 423 TGGACAGCCACGCTGGAGCTGTTCGAGCGCAGCAGAGCTGGGCGCACACAGCGGCGAAC 482
  Db 181 TGGACAGCCACGCTGGAGCTGTTCGAGCGCAGCAGAGCTGGGCGCACACAGCGGCGAAC 240
  QY 483 GCGGCAAGGCTGGCGCGGAGCAGGCCCAAGAGGAGGCGCGCAGCGAGGCTGCAAGCCCA 542
  Db 241 GCGGCAAGGCTGGCGCGGAGCAGGCCCAAGAGGAGGCGCGCAGCGAGGCTGCAAGCCCA 300
  QY 543 ACAGAGAAGCGCTCAGCGCGGCGAGCGCAACACAGAGAACCGTGAGACGCTGTCAGCAACC 602
  Db 301 ACAGAGAAGCGCTCAGCGCGGCGAGCGCAACACAGAGAACCGTGAGACGCTGTCAGCAACC 360
  QY 603 ACAGACACGAGCAGCGCGCTCGGGCACACCCCAAGAGAGAGGCGCAAGACCTCCAGA 662
  Db 361 ACAGACACGAGCAGCGCGCTCGGGCACACCCCAAGAGAGAGGCGCAAGACCTCCAGA 420
  QY 663 AGAAGAAAGCGCTCAAGGCGCAAGCGGAGGAGCGCTCCCTCGGACCTCCCATCG 722
  Db 421 AGAAGAAAGCGCTCAAGGCGCAAGCGGAGGAGCGCTCCCTCGGACCTCCCATCG 480
  QY 723 ACCCAAGCAAGACCCACGCTACTGTGTGCAACACAGGCTCTCTATGGGAGATGATCGGCT 782
  Db 481 ACCCAAGCAAGACCCACGCTACTGTGTGTGCAACACAGGCTCTCTATGGGAGATGATCGGCT 540
  QY 783 GCGCAACAGCAGAGTGCCTCCATTCGAGTGGTTCACATTCCTCGTGGGCTCAATCAT 842
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Db      541 GCGACAAACGACGAGTCCCGCATCGAGTGGTTCCTTCCTCGTGGGCTCAATCATATA 600
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Qy      843 AACCCAGGGCAAGT 857
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Db      601 AACCCAGGGCAAGT 615
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RESULT 3
LOCUS   BM457587 1110 bp mRNA linear EST 05-FEB-2002
DEFINITION AGENCOURT_6407600 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5585127
5', mRNA sequence.
ACCESSION BM457587
VERSION   BM457587.1 GI:18506627
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          1 (bases 1 to 1110)
AUTHORS  NIH-MGC http://mgc.nci.nih.gov/.
          National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished (1999)
          Contact: Robert Strausberg, Ph.D.
          Email: cgabsx@mail.nih.gov
          Tissue Procurement: ATCC
          cDNA Library Preparation: Life Technologies, Inc.
          DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM12350 row: 0 column: 16
          High quality sequence stop: 510.
          Location/Qualifiers
            1..1110
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="IMAGE:5585127"
              /tissue_type="embryonal carcinoma, cell line"
              /lab_host="PH10B (phage-resistant)"
              /clone_lib="NIH MGC 92"
              /notes="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI;
              Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
              Average insert size 2.5 kb. Library enriched for
              full-length clones and constructed by Life Technologies.
              Note: this is a NIH_MGC Library."

FEATURES
          source
            1..1110
              Query Match 70.8%; Score 606.8; DB 12; Length 1110;
              Best Local Similarity 95.8%; Pred. No. 4.6e-87;
              Matches 623; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy      206 CTAGGCTGCGGAGTGGTGTCCGCGCGGGAATCGAGATCTTGAAGAGCTAGACGAG 265
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Db      67 CTGACCCGAGGGTGGGGCGCGCGTGGCGGTGGGAAACAGATCTCTGAAGAGCTAGACGAG 126
      |||
Qy      266 TGCTACGAGCGCTTCAGTCCGAGACAGACGCGGGCCAGAGCGGGGATGTGCACTGT 325
      |||
Db      127 TGCTACGAGCGCTTCAGTCCGAGACAGACGCGGGCCAGAGCGGGGATGTGCACTGT 186
      |||
Qy      326 GTCCAGCGCGCTGTATCCGACGCCAGCGAGCTGGGCGAGAGAGATCCAGATCTGTGAGC 385
      |||
Db      187 GTCCAGCGCGCTGTATCCGACGCCAGCGAGCTGGGCGAGAGATCCAGATCTGTGAGC 246
      |||
Qy      386 CAGATGTGAGCTGGTGGAGAACCCGACCGCGCAGCTGGACAGCCACGCTGGAGCTGTTC 445
      |||
Db      247 CAGATGTGAGCTGGTGGAGAACCCGACCGCGCAGCTGGACAGCCACGCTGGAGCTGTTC 306
      |||
Qy      446 GAGCGCAGCAGAGCTGGCGGACACAGCGGGCAACAGCGGGCAAGGCTGGCGGACAGG 505
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Db      307 GAGCGCGCAGCAGGAGCTGGCGGACACAGCGGGCAACAGCGGCAAGGCTGGCGGGACAG 366
      |||
Qy      506 CCCAAGCGCGAGCGCGCAGCGAGGTGACAAAGCCCAACAGCAAGCGCTCACGGCGGCGAG 565
      |||
Db      367 CCNAAGCGCGAGCGCGCAGCGAGGTGACAAAGCCCAACAGCAAGCGCTCACGGCGGCGAG 426
      |||
Qy      566 CGCAACAAACGAGAACCCGTGAGAACCGTCCAGCAACACAGCAACACAGCGCGGCTGTG 625
      |||
Db      427 CGCAACAAACGAGAACCCGTGAGAACCGTCCAGCAACACAGCAACACAGCGCGGCTGTG 486
      |||
Qy      626 GGCACACCCCAAGGAGAGAGGCGCAAGACTCCCAAGAGAGAGCGCTCCCAAGGCGCAAG 695
      |||
Db      487 GGCACACCCCAAGGAGAGAGGCGCAAGACTCCCAAGAGAGAGCGCTCCCAAGGCGCAAG 546
      |||
Qy      686 GCGGAGCGAGAGCGTCCCTCGGACCTCCCATCGACCCCAAGCAAGCAAGCGTACTGT 745
      |||
Db      547 GCGGAGCGAGAGCGTCCCTCGGACCTCCCATCGACCCCAAGCAAGCAAGCGTACTGT 606
      |||
Qy      746 CTGTGCAACACAGCTCTCTATGGGAGNATCGGTGGGACCAACAGCGAGTCCCCATC 805
      |||
Db      607 CTGTGCAACACAGCTCTCTATGGGAGATGATCGGTGGGACCAACAGCGAGTCCCCATC 666
      |||
Qy      806 GAGTGGTTTCCACTTCTCGTGGTGGGGCTCAATCATAAAACCCCAAGGGCAA 855
      |||
Db      667 GAGTGGTTTCCACTTCTCGTGGTGGGGCTCAATCATAAAACCCCAAGGGCCA 716
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RESULT 4
LOCUS   AV726745 746 bp mRNA linear EST 17-OCT-2000
DEFINITION AV726745 HTC Homo sapiens cDNA clone HTCAQD06 5', mRNA sequence.
ACCESSION AV726745
VERSION   AV726745.1 GI:10836166
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          1 (bases 1 to 746)
AUTHORS  Gu, Y., Peng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X.,
          Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L.,
          Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R.,
          Chen, J., Chen, Z. and Han, Z.
          Homo sapiens cDNA HTC clones
          Unpublished (2000)
          Contact: Zeguang Han
          Chinese National Human Genome Center at Shanghai
          351 Gao Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
          201203, P. R. China
          Tel: 86-21-50801919(ex.45)
          Fax: 86-21-50801922
          Email: hanzg@chgc.sh.cn
          This clone is available at CHGC in Shanghai.
          Location/Qualifiers
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              /organism="Homo sapiens"
              /mol_type="mRNA"
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              /clone="HTCAQD06"
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              /dev_stage="Adult"
              /lab_host="SOLR"
              /clone_lib="HTC"
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              XhoI"

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              Query Match 70.5%; Score 603.8; DB 9; Length 746;
              Best Local Similarity 95.1%; Pred. No. 1.3e-86;
              Matches 520; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy      206 CTAGGCTGCTGGAGTGGTGTGCTCGCGCGGGAATCGAGATCTTGAAGAGCTAGACGAG 265
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Db      6 CTGACCCGAGGGTGGGGCCGCGGTGGCCGTGGAAACAGATCTTGAAGGAGCTAGACGAG 65
QY      266 TGCTACGAGCGCTTCAGTCGCGAGACAGACGCGGGCGCAGAAAGCGCGGATGCTGCACTGT 325
Db      66 TGCTACGAGCGCTTCAGTCGCGAGACAGACGCGGGCGCAGAAAGCGCGGATGCTGCACTGT 125
QY      326 GTGACGCGCGGCTGATCCGAGCAGCAGAGCTGGCGACGAGAAAGATCCAGATCGTGAGC 385
Db      126 GTGACGCGCGGCTGATCCGAGCAGCAGAGCTGGCGACGAGAAAGATCCAGATCGTGAGC 185
QY      386 CAGATGGTGGAGCTGGTGGAGAACCGCAGCGCGGAGTGGAGCCAGCCAGCTGGAGCTGTTT 445
Db      186 CAGATGGTGGAGCTGGTGGAGAACCGCAGCGCGGAGTGGAGCCAGCCAGCTGGAGCTGTTT 245
QY      446 GAGGCGCAGCAGGAGCTGGCGACACAGCGGGCAGCAGCGGCAAGGCTGGCGCGCAGG 505
Db      246 GAGGCGCAGCAGGAGCTGGCGACACAGCGGGCAGCAGCGGCAAGGCTGGCGCGCAGG 305
QY      506 CCCAAGCGCAGCGGCGCAGCGCTGACAAAGCCCAAGCCGCTCCAGAGAAAGAGCGCTCCAAAGCCCAAG 565
Db      306 CCCAAGCGCAGCGGCGCAGCGCTGACAAAGCCCAAGCCGCTCCAGAGAAAGAGCGCTCCAAAGCCCAAG 365
QY      566 GGCACACAGAGAAACCGTAGAACCGCTCCAGCAACCAAGCAGCAGCGGCGGCTCG 625
Db      366 GGCACACAGAGAAACCGTAGAACCGCTCCAGCAACCAAGCAGCAGCGGCGGCTCG 425
QY      626 GGCACACAGAGAAACCGTAGAACCGCTCCAGCAACCAAGCAGCAGCGGCGGCTCG 685
Db      426 GGCACACAGAGAAACCGTAGAACCGCTCCAGCAACCAAGCAGCAGCGGCGGCTCG 485
QY      686 GCGGAGCGAGAGCGGCTCCGCGAGATGATCGGCTCGCAAGCAGCAGGTCGCCCAATC 745
Db      486 GCGGAGCGAGAGCGGCTCCGCGAGATGATCGGCTCGCAAGCAGCAGGTCGCCCAATC 545
QY      746 CTGTGCAACAGAGTCTTCATGGGAGATGATCGGCTCGCAAGCAGCAGGTCGCCCAATC 805
Db      546 CTGTGCAACAGAGTCTTCATGGGAGATGATCGGCTCGCAAGCAGCAGGTCGCCCAATC 605
QY      806 GAGTGGTCCACTTCTCGTGGGCTCAATCAATAAACCAGGCAAGT 857
Db      606 GAGTGGTTCACCTTCTCGTGGGCTCAATCAATACCAAGGCAAGT 857

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RESULT 5
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LOCUS AV727365 HTC Homo sapiens cDNA clone HTCAHQ09 5', mRNA sequence.
ACCESSION AV727365
VERSION AV727365.1 GI:10836786
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Gu, Y., Peng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X.,
Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L.,
Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R.,
Chen, J., Chen, Z., and Han, Z.
Homo sapiens cDNA HT clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
1. .742
/organism="Homo sapiens"
/mol_type="mRNA"

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TITLE
JOURNAL
COMMENT
FEATURES
source
1. .742
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/lab_host="SOLR"
/clone_lib="HTC"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

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## ORIGIN

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Query Match      69.1%; Score 592.2; DB 9; Length 742;
Best Local Similarity 93.9%; Pred. No. 8.9e-85;
Matches 612; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY      206 CTAGGCTGCTGGAGTGTGTGTCGCGCGCGGATGGAGATCTTGAAGGAGCTAGACGAG 265
Db      6 CTGACCCGAGGGTGGGGCCGCGGTGGCCGTGGAAACAGATCTTGAAGGAGCTAGACGAG 65
QY      266 TGCTACGAGCGCTTCAGTCGCGAGACAGACGCGGGCGCAGAAAGCGCGGATGCTGCACTGT 325
Db      66 TGCTACGAGCGCTTCAGTCGCGAGACAGACGCGGGCGCAGAAAGCGCGGATGCTGCACTGT 125
QY      326 GTGACGCGCGGCTGATCCGAGCAGCAGAGCTGGCGACGAGAAAGATCCAGATCGTGAGC 385
Db      126 GTGACGCGCGGCTGATCCGAGCAGCAGAGCTGGCGACGAGAAAGATCCAGATCGTGAGC 185
QY      386 CAGATGGTGGAGCTGGTGGAGAACCGCAGCGCGGAGTGGAGCCAGCCAGCTGGAGCTGTTT 445
Db      186 CAGATGGTGGAGCTGGTGGAGAACCGCAGCGCGGAGTGGAGCCAGCCAGCTGGAGCTGTTT 245
QY      446 GAGGCGCAGCAGGAGCTGGCGACACAGCGGGCAGCAGCGGCAAGGCTGGCGCGCAGG 505
Db      246 GAGGCGCAGCAGGAGCTGGCGACACAGCGGGCAGCAGCGGCAAGGCTGGCGCGCAGG 305
QY      506 CCCAAGCGCAGCGGCGCAGCGCTGACAAAGCCCAAGCCGCTCCAGAGAAAGAGCGCTCCAAAGCCCAAG 565
Db      306 CCCAAGCGCAGCGGCGCAGCGCTGACAAAGCCCAAGCCGCTCCAGAGAAAGAGCGCTCCAAAGCCCAAG 365
QY      566 GGCACACAGAGAACCGTAGAACCGCTCCAGCAACCAAGCAGCAGCGGCGGCTCG 625
Db      366 GGCACACAGAGAACCGTAGAACCGCTCCAGCAACCAAGCAGCAGCGGCGGCTCG 425
QY      626 GGCACACAGAGAACCGTAGAACCGCTCCAGCAACCAAGCAGCAGCGGCGGCTCG 685
Db      426 GGCACACAGAGAACCGTAGAACCGCTCCAGCAACCAAGCAGCAGCGGCGGCTCG 485
QY      686 GCGGAGCGAGAGCGGCTCCGCGAGATGATCGGCTCGCAAGCAGCAGGTCGCCCAATC 745
Db      486 GCGGAGCGAGAGCGGCTCCGCGAGATGATCGGCTCGCAAGCAGCAGGTCGCCCAATC 545
QY      746 CTGTGCAACAGAGTCTTCATGGGAGATGATCGGCTCGCAAGCAGCAGGTCGCCCAATC 805
Db      546 CTGTGCAACAGAGTCTTCATGGGAGATGATCGGCTCGCAAGCAGCAGGTCGCCCAATC 605
QY      806 GAGTGGTCCACTTCTCGTGGGCTCAATCAATAAACCAGGCAAGT 857
Db      606 GAGTGGTTCACCTTCTCGTGGGCTCAATCAATACCAAGGCAAGT 857

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## RESULT 6

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BQ883364 982 bp mRNA linear EST 16-AUG-2002
LOCUS AGENCOURT 8071025 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6089752
DEFINITION 5', mRNA sequence.
ACCESSION BQ883364
VERSION BQ883364.1 GI:22275372
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 982)
NIH-MGC http://mgc.nci.nih.gov/.

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TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgsbbs-remail.nih.gov  
Tissue Procurement: DCTD/DP  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLCM2330 row: a column: 17  
High quality sequence stop: 577.  
Location/Qualifiers  
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/clone="IMAGE:6089752"  
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ORIGIN

Query Match 69.0%; Score 591.4; DB 13; Length 982;  
Best Local Similarity 87.2%; Pred. No. 1.3e-84; Indels 1; Gaps 1;  
Matches 660; Conservative 0; Mismatches 96;

QY 98 GAAGCAGCTCCCTCTCAGCGCCCTTTGTCTCCAGCCCTTCCAACTCAGTACCGGAG 157  
DB 11 GCAGTAGCAGTGATCCCGGCGCTGTGGCTCGGGCGGGGTGCGAGTTCGGACCGCTC 70  
QY 158 ACACACAAAGGAGGGCGGTGACGATGCGGAGCGGGGAGCGGCTAGCTGCTGG 217  
DB 71 CCGCGACCCCGGGCGCGCTCGGAGACAGATTTCAGCGCGCATCTGTGTGACCGCGAGG 130  
QY 218 GAGTGTGTGTCGGCGCGGATGGAGATCCTGAAGGAGCTAGACGAGTGTACGAGCGC 277  
DB 131 TGSGGCGCGGTGGCGGTGGAACAGATCCTGAAGGAGCTAGACGAGTGTACGAGCGC 190  
QY 278 TTCAGTCCGAGACAGACGGGGCGCGAAGACGGCGGATGCTGCACTGTGTGAGCGCGG 337  
DB 191 TTCAGTCCGAGACAGACGGGGCGCGAAGACGGCGGATGCTGCACTGTGTGAGCGCGG 250  
QY 338 CTGATCCGAGCGAGGCTGGCGGACGAGAGATCCAGATCGTAGCCAGATGTTGGAG 397  
DB 251 CTGATCCGAGCGAGGCTGGCGGACGAGAGATCCAGATCGTAGCCAGATGTTGGAG 310  
QY 398 CTGCTGAGAACCCGACGCGGAGGTGGACAGCCAGCTGTTCAGGCGGACGAG 457  
DB 311 CTGCTGAGAACCCGACGCGGAGGTGGACAGCCAGCTGTTCAGGCGGACGAG 370  
QY 458 GAGCTGGGACACAGCGGGACACGGGCAAGGCTGGCGGACAGGCGGCAAGCGGAG 517  
DB 371 GAGCTGGGACACAGCGGGACACGGGCAAGGCTGGCGGACAGGCGGCAAGCGGAG 430  
QY 518 GCGGACGCGGAGGTGACAAAGCCCAACAGCAAGCGCTCACGGCGGAGCGCAACACGAG 577  
DB 431 GCGGACGCGGAGGTGACAAAGCCCAACAGCAAGCGCTCACGGCGGAGCGCAACACGAG 490  
QY 578 AACCTGAGAACCGGTACACACACGACGACGAGCGGCGCTTCGGGACACCCAG 637  
DB 491 AACCTGAGAACCGGTACACACACGACGACGAGCGGCGCTTCGGGACACCCAG 550  
QY 638 GAGAAAGAGCCCAAGACCTCCCAAGAGAGAGAGCGTCTCCAAAGCCCAAGCGGAGGAG 697

551 GAGAGAGAGCCCAAGACCTCCAGAGAGAGAGAGCCCTCCAGGCCAAGCGGAGGAGAG 610  
QY 698 GCCTCCCTCCCGAGCCTCCCATCGACCCCAACGACCCACCTACTGTCTGTGCAACACG 757  
DB 611 GCCTCCCTCCCGAGCCTCCCATCGACCCCAACGACCCACCTACTGTCTGTGCAACACG 670  
QY 758 GTCTCTATGGGAGATGATCGGCTCGCAACGAGAGTGCCTCCATCGAGTGTGTTCCAC 817  
DB 671 GTCTCTATGGGAGATGATCGGCTCGCAACGAGTGCCTCCATCGAGTGTGTTCCAC 730  
QY 818 TTCTCTGTGGCT-GGGGCTCAATCATTAACCCCAAGGCG 853  
DB 731 TTCTCTGTGGCTGGGGGCTCATCATTAACCCCAAGGCG 767

RESULT 7  
LOCUS AY404083 698 bp DNA linear GSS 15-DEC-2003  
DEFINITION Pan troglodytes INGI gene, VIRTUAL TRANSCRIPT, partial sequence,  
Genomic survey sequence.  
ACCESSION AY404083  
VERSION AY404083.1 GI:39760066  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
REFERENCE 1 (bases 1 to 698)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,  
Adams,M.D. and Cargill,M.  
Infering nonneutral evolution from human-chimp-mouse orthologous  
Gene trios  
Science 302 (5652), 1960-1963 (2003)  
JOURNAL PUBLISHED 14671302  
REFERENCE 2 (bases 1 to 698)  
AUTHORS Todd,M.A., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Clark,A.G., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,  
Adams,M.D. and Cargill,M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
FEATURES  
Location/Qualifiers  
source 1..698  
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/db\_xref="taxon:9598"  
gene <1..-698  
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/locus\_tag="HCM1772"

ORIGIN

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Best Local Similarity 96.1%; Pred. No. 2.1e-84;  
Matches 591; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 243 AGATCTCTGAGGAGCTAGACGAGTGTACGAGCGCTTCAGTCCGAGACAGACGCGGCGC 302  
DB 1 AGATCTCTGAGGAGCTGACGAGTGTACGAGCGCTTCAGTCCGAGACAGACGCGGCGC 60  
QY 303 AGAAGCGCGGATCTGCACTGTGTGAGCGCGCTGTATCCGAGCAGCAGAGCTGGCG 362  
DB 61 AGAAGCGCGGATCTGCACTGTGTGAGCGCGCTGTATCCGAGCAGCAGAGCTGGCG 120  
QY 363 ACAGAGATCCAGATCGTAGCCAGATGTGTGAGCTGTGTGAGAACCCGACGCGGAGG 422  
DB 121 ACAGAGATCCAGATCGTAGCCAGATGTGTGAGCTGTGTGAGAACCCGACGCGGAGG 180



Email: cgabbs@mail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: the I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM12826 row: d column: 03  
 High quality sequence stop: 659.  
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 /note="Organ: Brain; Vector: pCMV-SPORT6; Site: 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH\_MGC Library."  
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 Best Local Similarity 94.6%; Pred. No. 1.6e-83;  
 Matches 616; Conservative 0; Mismatches 34; Indels 1; Gaps 1;

QY 206 CTAGGTGCTGGAGTGGTGTCCGGCCGGGAATGGAGATCTTGAGAGTGTAGACGAG 265  
 DB 102 CTGACCCGAGGGTGGGGCCGGCGGTGGCGGAGATCTTGAAGAGTGTAGACGAG 161  
 QY 266 TGCTACGAGCGCTTACGTCCGAGACAGAGCGGGCCGAGAGCGGGAGTGTGCACTGT 325  
 DB 162 TGCTACGAGCGCTTACGTCCGAGACAGAGCGGGCCGAGAGCGGGAGTGTGCACTGT 221  
 QY 326 GTGACGCGCGCTGTATCCGACCCAGGAGTGGCGGACGAGAGATCCAGATCGTGAC 385  
 DB 222 GTGACGCGCGCTGTATCCGACCCAGGAGTGGCGGACGAGAGATCCAGATCGTGAC 281  
 QY 386 CAGATGTTGAGTGTGGAGAACCCGACGCGGAGTGGACAGCCACGTGGAGCTGTC 445  
 DB 282 CAGATGTTGAGTGTGGAGAACCCGACGCGGAGTGGACAGCCACGTGGAGCTGTC 341  
 QY 446 GAGCGCAGCAGAGTGGCGGACACAGCGGGCAACAGCGGCAAGGCTGGCGGACAGG 505  
 DB 342 GAGCGCAGCAGAGTGGCGGACACAGCGGGCAACAGCGGCAAGGCTGGCGGACAGG 401  
 QY 506 CCCAAGCGAGCGGAGCGGAGTGTGACAGCCGACAGAGCGGCTTACGCGGCGAG 565  
 DB 402 CCCAAGCGAGCGGAGCGGAGTGTGACAGCCGACAGAGCGGCTTACGCGGCGAG 461  
 QY 566 CGCAACACAGAGAACCGTGTAGAGACCGTCCAGCAACACAGCAGCAGCGGCTGTG 625  
 DB 462 CGCAACACAGAGAACCGTGTAGAGACCGTCCAGCAACACAGCAGCAGCGGCTGTG 521  
 QY 626 GGCAACACAGAGAGAGGCGCAAGCTTCCAGAGAGAGAGGCTTCCAGAGGCGAG 685  
 DB 522 GGCAACACAGAGAGAGGCGCAAGCTTCCAGAGAGAGAGGCTTCCAGAGGCGAG 581  
 QY 686 GCGGAGCGAGGCGCTCCCTGCGGACCTCCCATCGACCCCAAGCAACCCAGTACTGT 745  
 DB 582 GCGGAGCGAGGCGCTCCCTGCGGACCTCCCATCGACCCCAAGCAACCCAGTACTGT 641  
 QY 746 CTGTGCAACAGAGTCTCTTATGGGAGATGATCGGTGCGACACAGAGAGTCCCGCATC 805  
 DB 642 CTGTGCAACAGAGTCTCTTATGGGAGATGATCGGTGCGAC-ACGACAGTCCCGCATC 700

QY 806 GAGTGGTTCACATCTCTGTCGTCGGGCTCAATCATATAAACCCAGGCGAAG 856  
 DB 701 GAGTGGATCCCTTCTCGTGGCGGGGTTCCACGTTAAACCCAGGCGCAG 751  
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 BX461522 1201 bp mRNA linear EST 22-MAY-2003  
 LOCUS BX461522  
 DEFINITION BX461522 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone  
 CS0DF028YP07 5-PRIME, mRNA sequence.  
 ACCESSION BX461522  
 VERSION BX461522.1 GI:31037156  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1201)  
 Li, W.B., Gruber, C., Jesse, J. and Polaves, D.  
 Full-length cDNA libraries and normalization  
 Unpublished (2001)  
 JOURNAL CONTACT: Genoscope  
 COMMENT Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 was not normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 7164.f For more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cgi-bin/cluster.cgi?seq=CS0DF028CH04QP1&cluster=7164.f. Contact :  
 Feng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
 Faraday Avenue Genoscope, sequence ID : CS0DF028CH04QP1.  
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 /note="Organ: Brain; Vector: pCMVSPORT 6; 1st strand cDNA  
 was primed with a NotI-oligo(dT) primer. Five prime end  
 enriched, double-strand cDNA was digested with Not I and  
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6  
 vector. Library was not normalized."

FEATURES  
 source  
 Query Match 67.7%; Score 579.8; DB 13; Length 1201;  
 Best Local Similarity 84.7%; Pred. No. 9.6e-83;  
 Matches 683; Conservative 1; Mismatches 119; Indels 3; Gaps 3;  
 QY 52 AAGCGCCCTTCGGGCTATCCACCTCTTCTGGGGCTCGGCACTAGGAAGCAGCTTCCT 111  
 DB 33 AAGCAGGCTGNGTACCGGTCGGGAATTCGGGGATCGGATTTATAGCAGTAGCAGTAT 92  
 QY 112 CTCAGGCCCTTTGTCTTCCAGCGGTTCCAAACTGAGTACCGGGAGACGACACAAAGGA 171  
 DB 93 CCGCGGCTGTGGGTGGGGCGGGGTCGAGTTCGAGCCGCTCCCGGACCGCGGG 152  
 QY 172 GGGCGGTGACGATGGCGCAGCGCGGAGCGCGCTAGGCTGCTGGGAGTGGTGGTGG 231  
 DB 153 GCGCGCTCGGAGACAGTTCAGGCGCGCATCTCTGTGACCCGAGGGTGGGCGCGGTG 212  
 QY 232 CCGCGGAATGGAGATCTCTGAAGAGGAGTAGACGAGTGTCTACGAGCGCTTCAGTCCGAGAC 291  
 DB 213 GCGGTGGAAACAGATCCTTGAGAGGAGTAGACGAGTGTCTACGAGCGCTTCAGTCCGAGAC 272  
 QY 292 AGACGGGCGGACAGAGCGCGGATGTGCACTGTGTCAGCGCGCGCTGTGTCGCGAGCA 351  
 DB 273 AGACGGGCGGACAGAGCGCGGATGTGCACTGTGTCGCA-CGCGCGCTGTGTCGCGAGCA 331



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352 GGAGCTGGGCGACGAGAGATCCAGATCGTGAGCCAGATGTTGGAGTGGTGGAGAACCG 411
332 GGAGCTGGGCGACGAGAGATCCAGATCGTGAGCCAGATGTTGGAGTGGTGGAGAACCG 391
412 CACGGGCGAGTGGGACGAGCAGTGGAGTGTTCAGGCGGAGCAGAGAGTGGGCGACAC 471
392 CACGGGCGAGTGGGACGAGCAGTGGAGTGTTCAGGCGGAGCAGAGAGTGGGCGACAC 450
472 AGCGGGCAACAGCGGCGAGGCTGGGCGGAGCAGAGGCGGAGGCGGAGGCGAGGCG 531
451 AGCGGGCAACAGCGGCGAGGCTGGGCGGAGCAGAGGCGGAGGCGGAGGCGAGGCG 510
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511 TGACAGCCCAACAGAGCGTCCAGCGGCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 570
592 GTCCAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 651
571 GTCCAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 630
652 GACCTCCAGAGAGAGAGCGTCCAGGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 711
631 GACCTCCAGAGAGAGAGCGTCCAGGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 690
712 CTTCCCTCATCGACCCCAACGAGCAGTGTGTGTGCAACAGTGTCTCTATGGGGA 771
691 CTTCCCTCATCGACCCCAACGAGCAGTGTGTGTGCAACAGTGTCTCTATGGGGA 749
772 GATGATCGGCTGCGACCAACGAGAGTGCCTCATGAGTGTGTGTGCAACAGTGTCTCT 831
750 GATGATCGGCTGCGACCAACGAGAGTGCCTCATGAGTGTGTGTGCAACAGTGTCTCT 809
832 GCTCAATCATAAACCAAGGCGAAGT 857
810 GCTCAATCATAAACCAAGGCGAAGT 835

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RESULT 11
LOCUS BM683151
DEFINITION AGENCOURT_8185663 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6262978
5', mRNA sequence.
ACCESSION BM683151
VERSION BM683151.1 GI:21795830
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 894)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: L1CM2426 row: c column: 11
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Location/Qualifiers
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FEATURES

source

RESULT 12  
LOCUS BM477126

DEFINITION AGENCOURT\_6484647 NIH\_MGC\_85 Homo sapiens cDNA clone IMAGE:5553778  
5', mRNA sequence.

ORIGIN

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Query Match 67.1%; Score 574.8; DB 13; Length 894;
Best Local Similarity 86.9%; Pred. No. 5.6e-82;
Matches 655; Conservative 0; Mismatches 97; Indels 2; Gaps 2;

QY 98 GAAGAGCTTCCCTCTCAGGCCCTTGTCTCCAGCCGTTCCAACTGAGTACCGGGAG 157
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QY 158 ACACACAAAGGAGGAGGCGGTGACGAGTGGCGCAGGCGCGGAGCGGCTAGCTGTCTGG 217
DB 71 CCGGACCCCGCGGGCGGCTCGGAGACAGTTTCAGGCGCATCTCTGCTGACCCGAGG 130
QY 218 GAGTGTGTTCGCGCGCGGATGGAGATCTTGAGGAGCTAGACGAGTCTTACGAGCGC 277
DB 131 TGGGGCGCGCGCTGGCGGCTGGAACAGATCCTGAAGGAGCTAGACGAGTCTACGAGCG 190
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QY 638 GAGAGAGGCGCAGACCTCCAGAGAGAGAGCGGCTCCAGGCGCAGGCGGAGCGGAGGAG 697
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QY 698 GCGTCCCTGTGCGGACCTCCCGCATCGACCCCAACGAAACCCACGTAAGTGTGTGTGCAACCAG 757
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QY 758 GTCTCTATGAGGAGATGATCGGCTGCGACAGCAGAGTG-CCCCATCGAGTGTGTCCA 816
DB 671 GTCTCTATGAGGAGATGATCGGCTGCGACAGCAGAGTG-CCCCATCGAGTGTGTCCA 730
QY 817 CTCTCT-GGTGCGTGGGCTCAATCAATAAACCCCA 849
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VERSION     BM477126.1  GI:18526157
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ORGANISM    Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1155)
            NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgaabs-remail.nih.gov
            Tissue Procurement: Lou Staudt
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12271 row: e column: 11
            High quality sequence stop: 644.
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     Average insert size 1.867 kb. Library enriched for
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     Note: this is a NIH_MGC Library."
ORIGIN
Query Match      65.5%; Score 561.4; DB 12; Length 1155;
Best Local Similarity 98.4%; Pred. No. 8.2e-80;
Matches 609; Conservative 0; Mismatches 6; Indels 4; Gaps 4;

QY 242 GAGATCCTGAGAGCTAGACAGTGTCTGACGAGCGCTTCAGTCGGAGACAGACGGGGCG 301
DB 211 GAGATCCTGAGAGCTAGACAGTGTCTGACGAGCGCTTCAGTCGGAGACAGACGGGGCG 270
QY 302 CAGAAGCGGGATGCTGCTGCTGTGACGCGCGCTGATCCGAGCGAGCGAGCTGGGC 361
DB 271 CAGAAGCGGGATGCTGCTGCTGTGACGCGCGCTGATCCGAGCGAGCGAGCTGGGC 330
QY 362 GACGAGAAGATCAGATCCTGAGCCAGATGTTGGAGCTGTTGGAGAACCGCGACCGGGCAG 421
DB 331 GACGAGAAGATCAGATCCTGAGCCAGATGTTGGAGCTGTTGGAGAACCGCGACCGGGCAG 390
QY 422 GTGGACAGCCAGCTGAGCTGTTGAGGGCGAGCAGAGCTGGGCGACACAGCGGGCAAC 481
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QY 482 AGCGCAAGGCTGGCGCGAGCAGCGCCCAAGGCGAGCGCGGCGAGCTGACAGGCC 541
DB 451 AGCGCAAGGCTGGCGCGAGCAGCGCCCAAGGCGAGCGCGGCGAGCTGACAGGCC 510
QY 542 AACAGCAAGGCTCAGCGGGGAGCGGCAACAGCAAGAACCGTGAGAACCGCTCCAGCAAC 601
DB 511 AACAGCAAGGCTCAGCGGGGAGCGGCAACAGCAAGAACCGTGAGAACCGCTCCAGCAAC 570
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722 GACCCCAAGAACCCAGCTACTGTCTGTCACCAAGGTCTCTAT-GGGGAGATGAT-CG 779
691 GACCCCAAGAACCCAGCTACTGTCTGTCACCAAGGTCTCTATGGGGAGATGATCG 750
QY 780 GCTGCGACACAGCAGAGTGCCTCA-TCGAGTGGTTCACACTTCTCGTGGCGGC-TCAA 837
DB 751 GCTGCGACACAGCAGAGTGCCTCAATTCGAGTGGTTCACACTTCTCGGCGGTGGGCTTCCA 810
QY 838 TCATAAACCCAGAGGGCAAG 856
DB 811 TCATAAACCCAGAGGGCAAG 829

RESULT 13
AV727700
LOCUS       AV727700 HTC Homo sapiens cDNA clone HTCHO4 5', mRNA linear EST 17-OCT-2000
DEFINITION AV727700
ACCESSION   AV727700
VERSION     AV727700.1 GI:10837121
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 722)
            Gu, Y., Peng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X.,
            Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L.,
            Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R.,
            Chen, J., Chen, Z., and Han, Z.
            Homo sapiens cDNA HTC clones
            Unpublished (2000)
            Contact: Zeguang Han
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
            201203, P. R. China
            Tel: 86-21-50801919 (ex. 45)
            Fax: 86-21-50801922
            Email: hanzg@chgc.sh.cn
            This clone is available at CHGC in Shanghai.
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Query Match      65.1%; Score 557.8; DB 9; Length 722;
Best Local Similarity 95.1%; Pred. No. 2.7e-79;
Matches 585; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

QY 243 AGATCTGAGAGCTAGACAGTGTCTGACGAGCGCTTCAGTCGGAGACAGACGGGGCGC 302
DB 44 AGATCTGAGAGCTAGACAGTGTCTGACGAGCGCTTCAGTCGGAGACAGACGGGGCGC 103
QY 303 AGAAGCGGGGATGCTCTGCTGCTGTGACGCGCGCTGTATCCGACGACGAGAGCTGGCG 362
DB 104 AGAAGCGGGGATGCTCTGCTGCTGTGACGCGCGCTGTATCCGACGACGAGAGCTGGCG 163
QY 363 ACAGAGAGATCCAGATGCTGAGCCAGATGTTGGAGCTGTTGGAGAACCGCACCGGCGAG 422
DB 164 ACAGAGAGATCCAGATGCTGAGCCAGATGTTGGAGCTGTTGGAGAACCGCACCGGCGAG 223
QY 423 TGGACAGCAGCTGGAGCTGTTGGAGCGCAGCAGAGCTGGGCGACACACGCGGGCAACA 482
DB 224 TGGACAGCAGCTGGAGCTGTTGGAGCGCAGCAGAGCTGGGCGACACACGCGGGCAACA 283

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Search completed: May 6, 2004, 11:48:46  
Job time : 2864.77 secs

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1. .897
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6273458"
/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 112"
/notes="organ: skin; Vector: pOTB7; Site1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

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ORIGIN

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Query Match          64.8%; Score 555.4; DB 13; Length 897;
Best Local Similarity 86.6%; Pred. No. 7e-79;
Matches 658; Conservative 0; Mismatches 97; Indels 5; Gaps 4;

QY 98 GAAGCAGCTTCCTCTCAGCGCCCTTGTCTCAAGCGTTTCCAACTGAGTACCGGGAG 157
DB 98 GAGTGTGTTCCTCTCAGCGCCCTTGTCTCAAGCGTTTCCAACTGAGTACCGGGAG 157
QY 158 ACACACAAAGGAGGCGGTGACGGATGCGCAGCGCGGGAGCGCCCTAGGCTGTCTGG 217
DB 98 CCGCGACCCCGGGCGCGGTGCGGACAGATTTCAGGCGCATCTCTGTGACCCGAGGG 157
QY 218 GAGTGTGTTCCTCTCAGCGCCCTTGTCTCAAGCGTTTCCAACTGAGTACCGGGAG 277
DB 158 TGGGGCCCGCGGTGCGGCGGAAACAGATCTCTGAAGGAGCTAGCAGAGTGTCTACGAGCGC 217
QY 278 TTTCAGTCGCGGACACAGACGCGGGCGCAGAGCGCGGATGCTGCATCTGTGCGAGCGCGG 337
DB 218 TTTCAGTCGCGGACACAGACGCGGGCGCAGAGCGCGGATGCTGCATCTGTGCGAGCGCGG 277
QY 338 CTGATCCGCGAGCAGAGCTGGGCGACGAGAGATCCAGATCTGTGAGCCAGATGTGGAG 397
DB 278 CTGATCCGCGAGCAGAGCTGGGCGACGAGAGATCCAGATCTGTGAGCCAGATGTGGAG 337
QY 398 CTGCTGGAGAACCGCAGCGCGGAGTGGACAGCCAGCTGGAGCTTTCAGGCGCAGCAG 457
DB 338 CTGCTGGAGAACCGCAGCGCGGAGTGGACAGCCAGCTGGAGCTTTCAGGCGCAGCAG 397
QY 458 GAGCTGGGCGACACAGCGGCGCAACAGCGCAAGGTTGGCGCGGACAGGCCCAAGCGGAG 517
DB 398 GAGCTGGGCGACACAGCGGCGCAACAGCGCAAGGTTGGCGCGGACAGGCCCAAGCGGAG 457
QY 518 GCGGCGAGCGGCTGACAGCCACAGCCAGCGCTCAGCGCGGCGGCGGACGACGAG 577
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QY 578 AACCGTGAGAACCGTGCCAGCAACCGACCGACCGCGCGCTTCGGGCGACACCCCAAG 637
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QY 757 -GGTCTCTCTAT -GGGAGAGATGATCGGCTGGGACAGCAGAGTGGCCCATCGAGTGGTTC 814
DB 698 GGGTCTCTCTATGCGGCGGAGATGATCGGCTGGGACAGCAGAGTGGCCCATCGAGTGGTTC 757
QY 815 CACTTCTCTGTG --CGTGGGCTCAATCATATAAACCAGGG 852
DB 758 CACTTCTCTGTGCGGCTCAATCATATAAACCAGGG 797

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:      May 6, 2004, 10:18:04 ; Search time 405.667 Seconds
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Perfect score: 772
Sequence:    1 aaagcgtctcggcgagc.....cagagcgagactccatctta 772

Scoring table:  IDENTITY NUC
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Searched:     2941586 seqs, 2264995651 residues

Total number of hits satisfying chosen parameters: 5893172

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query #			DB	ID	Description
	Score	Match	Length			
1	277.6	36.0	8487	9	US-09-764-877-3454	Sequence 3454, Ap
2	277.6	36.0	8487	16	US-10-242-515-3454	Sequence 3454, Ap
3	276	35.8	2861	10	US-09-968-653A-2	Sequence 2, Appl1
4	276	35.8	2886	13	US-09-874-347-1	Sequence 1, Appl1
5	276	35.8	2897	13	US-09-874-347-3	Sequence 3, Appl1
6	261.6	33.9	5159	9	US-09-764-877-3707	Sequence 3707, Ap
7	261.6	33.9	5159	16	US-10-242-515-3707	Sequence 3707, Ap
8	260	33.7	657	13	US-10-037-632-130764	Sequence 130764, Ap
9	260	33.7	657	16	US-10-037-632-130764	Sequence 130764, Ap
C 10	289	33.5	10953	9	US-09-764-846-313	Sequence 313, App
C 11	259	33.3	10953	15	US-10-091-483-313	Sequence 313, App
C 12	256.8	33.3	6264	16	US-10-074-024-660	Sequence 660, App
C	256.8	33.3	96597	16	US-10-085-117-112	Sequence 112, App
13	255.6	33.1	97247	13	US-10-087-192-688	Sequence 688, App

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RESULT 1
US-09-764-877-3454
; Sequence 3454, Application US/09764877
; Patent No. US2002014740A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3454
; LENGTH: 8487
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3454

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	Best Local Similarity	81.0%;	Pred. No. 6.3e-75;		
	Matches 423;	Conservative 0;	Mismatches 59;	Indels 40;	Gaps 7;
QY	2	AAGCGTTCTCGGGCAGCGCCAAACTAGAACCGTGAGAACCGCTCCAGCAACCGCGAC	61		
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QY	62	CCACGACGAGGTCACTCTGGGCGACGCCACGAGGAGAGAGCCACAGACCTCTTAAGAGAA	121		
Db	6597	CCACGACGACGGCGCCTTCGGGCHACACCAAGGAGACAGGCCACAGACCTCCACGAGAA	6656		
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 QY 275 AAAGCGCAAGTGGTACTGCTCCAGATCGCGGGGAAGAACG-----ATGGGCAAGC 326  
 Db 6837 CAAGGCGCAAGTGGTACTGCTCCAGTCCGCGGGGAGAACGAGAACCATGGAACAGC 6896  
 QY 327 CTTGAGAGTCCAGAAAAAACAAGGCTTATAACAGGTAGTTTGGGGACATCGCTTA 386  
 Db 6897 CTTGAGAGTCCCA---AAAAGAGAGGCTTACACAGGTAGTTTGTGGACAGCGCTG 6954  
 QY 387 ATAGTGAAGGAGAACCAATAGCCAGTGTGATTACATGGCCACCTTCTCAGGTGC 446  
 Db 6955 GT-GTGAGAGAGAACCAATAAAC--GTGTATTTATTACATGCTGCTTTGTGAGGTGC 7012  
 QY 447 AGGAAGTGTAAATGTATATTTTAAAGAAATGTTTGTAGAG 488  
 Db 7013 AAGGAGTGTAAATGTATATTTTAAAGAAATGTTTGTAGTAAAG 7054

## RESULT 2

US-10-242-515-3454  
 ; Sequence 3454, Application US/10242515  
 ; Publication No. US20040009488A1

## GENERAL INFORMATION:

; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

## FILE REFERENCE: PC005C1

; CURRENT APPLICATION NUMBER: US/10/242,515

; CURRENT FILING DATE: 2002-09-13

; PRIOR APPLICATION NUMBER: 09/764,877

; PRIOR FILING DATE: 2001-01-17

; PRIOR APPLICATION NUMBER: 60/179,065

; PRIOR FILING DATE: 2000-01-31

; PRIOR APPLICATION NUMBER: 60/180,628

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: 60/214,886

; PRIOR FILING DATE: 2000-06-28

; PRIOR APPLICATION NUMBER: 60/217,487

; PRIOR FILING DATE: 2000-07-11

; PRIOR APPLICATION NUMBER: 60/225,758

; PRIOR FILING DATE: 2000-08-14

; PRIOR APPLICATION NUMBER: 60/220,963

; PRIOR FILING DATE: 2000-07-26

; PRIOR APPLICATION NUMBER: 60/217,496

; PRIOR FILING DATE: 2000-07-11

; PRIOR APPLICATION NUMBER: 60/225,447

; PRIOR FILING DATE: 2000-08-14

; PRIOR APPLICATION NUMBER: 60/218,290

; PRIOR FILING DATE: 2000-07-14

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 4031

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3454

; LENGTH: 8487

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-242-515-3454

Query Match 36.0%; Score 277.6; DB 16; Length 8487;

Best Local Similarity 81.0%; Pred. No. 6.3e-75;

Matches 423; Conservative 0; Mismatches 59; Indels 40; Gaps 7;

QY 2 AAGCGTCTCGCGGAGCGGCACTAGACCGGTGAGAACGCGTCAGCAACCGCAC 61

Db 6538 AAGCGTCTCGCGGAGCGGCACTAGACCGGTGAGAACGCGTCAGCAACCGCAC 6596

QY 62 CCACGACGAGTCACTCGGCGACGCCCAAGGAGAGAAAGCCAGACCTCTAAGAGAA 121

Db 6597 CCACGACGAGTCACTCGGCGACGCCCAAGGAGAGAGGCGCAAGACCTCTAAGAGAA 6656

QY 122 GCAGGGCTCCATGGCCAAAGGGTAGCGCAGCGGTCCCGCCGACAGCCTCCCATCGACCC 181  
 Db 6657 GAAGGCGCTCCAAAGGCCAAAGGGTAGCGCAGCGGTCCCGCCGACAGCCTCCCATCGACCC 6716  
 QY 182 CAGCGAGCC-----CTCCTACTGGGAGATGATCCGCTGGGA 217  
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 QY 218 CA---ACGATGCCCATCGAGTGGTTCGGCTTCTCGTGTGTGAGTCTCAACCAATAAAC 274  
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 QY 327 CTTGAGAGTCCAGAAAAAACAAGGCTTATAACAGGTAGTTTGGGGACATCGCTTA 386  
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 QY 387 ATAGTGAAGGAGAACCAATAAGCCAGTGTGTTGATTACATTGCCACCTTTGCTAGGTGC 446  
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 QY 447 AGGAAGTGTAAATGTATATTTTAAAGAAATGTTTGTAGAG 488  
 Db 7013 AAGGAGTGTAAATGTATATTTTAAAGAAATGTTTGTAGTAAAG 7054

## RESULT 3

US-09-968-653A-2

; Sequence 2, Application US/09968653A

; Publication No. US20030073084A1

## GENERAL INFORMATION:

; APPLICANT: Gudkov, Andrey V

; Riabowol, Karl

; TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff

STREET: 300 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/09/968,653A

FILING DATE: 01-Oct-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/006,783A

FILING DATE: 15-JAN-1998

ATTORNEY/AGENT INFORMATION:

NAME: NO. US20030073084Ainan, Kevin E

REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 97,837

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-913-0001

TELEFAX: 312-913-0002

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 2061 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

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; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..897
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-968-633A-2

Query Match      35.8%; Score 276; DB 10; Length 2061;
Best Local Similarity 80.8%; Pred. No. 1e-74;
Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;

QY  2 AAGCGTTCTCGCGCGCAGCGCAACCACTAGAACCGTGAGAGCGGTCCAGCAACCGGAC 61
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QY  62 CCACGACGAGCTCACTCGGCGCACCCCAAGGAGAGAAAGCCAGACCTCTAAGAGAA 121
DB  561 CCACGACGAGCGGCGCTCGGCGCACCCCAAGGAGAGAAAGCCAGACCTCTAAGAGAA 620
QY  122 GCAGGGCTCCATGGCCAAAGCGTAGCGGCGAGCGCTCCCGCGAGACCTCCCGCATCGACCC 181
DB  621 GAAGCGCTCCAAAGGCCAAGCGGAGAGAGCGGTCCCGCGACCTCCCGCATCGACCC 680
QY  182 CAGCGAGCC-----CTCCTACTGGGAGATGATCCGCTGCGA 217
DB  681 CAACGAACCCACGTACTGTCGCAACCCAGGTCTCTATGGGAGATGATCGGCTGCGA 740
QY  218 CA---ACGATGCCCATCGAGTGTTCGGCTTCTGCTGTGTGAGTCTCAACCATAAACC 274
DB  741 CAACGACGAGTCCCGCATCGAGTGTTCACCTTCCTGCGTGGGCTCAATCAATAACC 800
QY  275 AAAGCGCAAGTGTACTGTTCCAGATGCCGGGGAAGAACG-----ATGGGCAAAAGC 326
DB  801 CAAGGCAAGTGTACTGTTCCCAAGTCCCGGGGAGAGACGAGAACCATGGACAAAGC 860
QY  327 CTTGAGAGAGTCCAGAAAAAAGCGCTTATAACAGGTAGTTTGGGACATGCGTCTA 386
DB  861 CTTGAGAGAAATCCA--AAAAAGAGAGGGCTTACAACAGGTAGTTTGTGGACAGCGCGCTG 918
QY  387 ATAGTGAGAGAACAAATAAGCCAGTGTGTGATTACATTGCCACCTTTGCTGAGGTGC 446
DB  919 GT-GTGAGAGAGCAAAATAAAC--GTGTATTATTATACATTGCTGCTTTGTTGAGGTGC 976
QY  447 AGGAAGTGTAAATGTATATTTTAAAGAAATGTTGTAGAGG 488
DB  977 AAGGAGTGTAAATGTATATTTTAAAGAAATGTTAGAAAAG 1018

RESULT 4
US-09-874-347-1
; Sequence 1, Application US/09874347
; Publication No. US20020039735A1
; GENERAL INFORMATION:
; APPLICANT: RIABOWOL, Karl T.
; APPLICANT: BOLAND, Donna
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO INGI ISOFORMS
; FILE REFERENCE: 028722-296
; CURRENT APPLICATION NUMBER: US/09/874,347
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 60/208,829
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 09/532,868
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: US 09/258,372
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: US 08/751,230
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: US 08/569,721
; PRIOR FILING DATE: 1995-12-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2886

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (433)...(1701)
US-09-874-347-1

Query Match      35.8%; Score 276; DB 13; Length 2886;
Best Local Similarity 80.8%; Pred. No. 1.2e-74;
Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;

QY  2 AAGCGTTCTCGCGCGCAGCGCAACCACTAGAACCGTGAGAGCGGTCCAGCAACCGGAC 61
DB  1303 AAGCGCTACGCGCGCAGCGCAACCACTAGAACCGGTGAGAACCGGTCCAGCAACCGA- 1361
QY  62 CCACGACGAGCTCACTCGGCGCACCCCAAGGAGAGAAAGCCAGACCTCTAAGAGAA 121
DB  1362 CCACGACGAGCGGCGCTCGGCGCACCCCAAGGAGAGAAAGCCAGACCTCTAAGAGAA 1421
QY  122 GCAGGGCTCCATGGCCAAAGCGTAGCGGCGAGCGCTCCCGCGAGACCTCCCGCATCGACCC 181
DB  1422 GAAGCGCTCCAAAGGCCAAGCGGAGAGAGCGGTCCCGCGACCTCCCGCATCGACCC 1481
QY  182 CAGCGAGCC-----CTCCTACTGGGAGATGATCCGCTGCGA 217
DB  1482 CAACGAACCCACGTACTGTCGCAACCCAGGTCTCTATGGGAGATGATCGGCTGCGA 1541
QY  218 CA---ACGATGCCCATCGAGTGTTCGGCTTCTGCTGTGTGAGTCTCAACCATAAACC 274
DB  1542 CAACGACGAGTCCCGCATCGAGTGTTCACCTTCCTGCGTGGGCTCAATCAATAACC 1601
QY  275 AAAGCGCAAGTGTACTGTTCCAGATGCCGGGGAAGAACG-----ATGGGCAAAAGC 326
DB  1602 CAAGGCAAGTGTACTGTTCCCAAGTCCCGGGGAGAGACGAGAACCATGGACAAAGC 1661
QY  327 CTTGAGAGAGTCCAGAAAAAAGCGCTTATAACAGGTAGTTTGGGACATGCGTCTA 386
DB  1662 CTTGAGAGAAATCCA--AAAAAGAGAGGGCTTACAACAGGTAGTTTGTGGACAGCGCGCTG 1719
QY  387 ATAGTGAGAGAACAAATAAGCCAGTGTGTGATTACATTGCCACCTTTGCTGAGGTGC 446
DB  1720 GT-GTGAGAGAGCAAAATAAAC--GTGTATTATTATACATTGCTGCTTTGTTGAGGTGC 1777
QY  447 AGGAAGTGTAAATGTATATTTTAAAGAAATGTTGTAGAGG 488
DB  1778 AAGGAGTGTAAATGTATATTTTAAAGAAATGTTAGAAAAG 1819

RESULT 5
US-09-874-347-3
; Sequence 3, Application US/09874347
; Publication No. US20020039735A1
; GENERAL INFORMATION:
; APPLICANT: RIABOWOL, Karl T.
; APPLICANT: BOLAND, Donna
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO INGI ISOFORMS
; FILE REFERENCE: 028722-296
; CURRENT APPLICATION NUMBER: US/09/874,347
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 60/208,829
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 09/532,868
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: US 09/258,372
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: US 08/751,230
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: US 08/569,721
; PRIOR FILING DATE: 1995-12-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2897
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Db 134 AGGTTTCTTACCTCTTGGACCTGTTAAGAGCGTGACAGGTGGCGGGCGGTGGCTCAC 193  
QY 507 GCCTGTAATCCAGCACCTTTGGAGCGCGAGCGGTGCGATCAGAGGTGAGGAGATCGA 566  
Db 194 GCCTGTAGTCCAGCACCTTTGGAGCGCGAGCGGTGCGATCAGAGGTGAGGAGATCGA 253  
QY 567 GACCATCTCTGGCTAACACCGGTGAACCCCGTCTCTACTAAATAATCAAAAAAATAATTAG 626  
Db 254 GACCATCTCTGGCTAACACCGGTGAACCCCGTCTCTACTGAAATACAAAAACAAATAATTAG 313  
QY 627 CTGGGCGTGTGGCGGGCGCTGTAGTCCAGCTATTCGGAGGCTGAGGAGGAGATG 686  
Db 314 CCGGGCGTGTGGCGGGCTCTGTAGTCCAGCTACTCGGAGGCTGAGGAGGAGATG 373  
QY 687 GCTGAGACCTGGAGGTGGAGCTTCANTGAGCAAGGTGCGGCCACTGCATCTCCAGGCT 746  
Db 374 GCTGAGACCTGGAGGCGGAGCTTTCAGTGAGCCCGATCGCACCCTGCATCTCCAGGCT 433  
QY 747 GGCGGACAGAGCGAGACTCCATCTTA 772  
Db 434 GGAGAGACAGCGAGACTCCGACTCA 459

RESULT 7

US-10-242-515-3707  
; Sequence 3707, Application US/10242515  
; Publication No. US2004009488A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC005C1  
; CURRENT APPLICATION NUMBER: US/10/242,515  
; CURRENT FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: 09/764,877  
; PRIOR FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: 60/179,065  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: 60/180,628  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: 60/214,886  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/217,487  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/225,758  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/220,963  
; PRIOR FILING DATE: 2000-07-26  
; PRIOR APPLICATION NUMBER: 60/217,496  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/225,447  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/218,290  
; PRIOR FILING DATE: 2000-07-14  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 4031  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3707  
; LENGTH: 5159  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-242-515-3707

Query Match 33.9%; Score 261.6; DB 16; Length 5159;  
Best Local Similarity 87.4%; Pred. No. 4.6e-70;  
Matches 285; Conservative 0; Mismatches 41; Indels 0; Gaps 0;  
QY 447 AGGAAGTGTAAATGTATATTTTAAAGATGTTTAAAGAGCGCGGCGGTGGCTCAC 506  
Db 134 AGGTTTCTTACCTCTTGGACCTGTTAAGAGCGTGACAGGTGGCGGGCGGTGGCTCAC 193  
QY 507 GCCTGTAATCCAGCACCTTTGGAGCGCGAGCGGTGCGATCAGAGGTGAGGAGATCGA 566  
Db 194 GCCTGTAGTCCAGCACCTTTGGAGCGCGAGCGGTGCGATCAGAGGTGAGGAGATCGA 253

; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (873)..(1712)  
US-09-874-347-3  
Query Match 35.8%; Score 276; DB 13; Length 2897;  
Best Local Similarity 80.8%; Pred. No. 1.2e-74;  
Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;  
QY 2 AAGGCTTCTCGGCGCGAGCGCAACCTAGAACCGTGAGAGCGGTGCCAGCAACCGGAC 61  
Db 1314 AAGGCTTCTCGGCGCGAGCGCAACCTAGAACCGGTGAGAGCGGTGCCAGCAACCGA- 1372  
QY 62 CCACGACGACGTCACCTCGGCGCACCCCAAGGAGAGAAAGCCAGACCTTTAAGAAGAA 121  
Db 1373 CCACGACGACGTCGCTCGGCGCACCCCAAGGAGAGAAAGCCAGACCTTTAAGAAGAA 1432  
QY 122 CGAGGCTCCATGGCCAGGCGTAGCGGAGCGCTCCCGCCAGACCTCCCGCATCGACCC 181  
Db 1433 GAAGGCTCCAAAGGCGCAAGCGGAGAGAGCGGTCCTCGGACCTCCCGCATCGACCC 1492  
QY 182 CAGCGAGCC-----CTCTACTGGGAGATGATCCGCTGCGA 217  
Db 1493 CAACGAACCCAGCTACTGTCTGTGCAACCCAGGTCTCTATGGGAGATGATCGGCTGCGA 1552  
QY 218 CA---ACGATCCCGCATCGAGTGTCTCGTCTCTGTTGAGTCTCACCATAAACC 274  
Db 1553 CAACGACGAGTCCCGCATCGAGTGTCTCGTCTCTGTTGAGTGTCTCACCATAAACC 1612  
QY 275 AAAGCGCAAGTGTACTGTTCAGATGCCGGGGAAGAACG-----ATGGGCAAGC 326  
Db 1613 CAAGGCAAGTGTACTGTCTCCCAAGTGGCGGGGAGAACGAGAACCATGGACAAAGC 1672  
QY 327 CTTGAGAGTCCAGAAACAGGCTTATACAGTAGTTTGGGACATCGTCTA 386  
Db 1673 CTTGAGAAATCCA--AAAAGAGAGGCGCTTACACAGTAGTTTGTGGACAGGCGCTG 1730  
QY 387 ATAGTGAGGAGAACAAATAAGCAGTGTGTTGATTACATTCACCTCCCTTTGTGAGGTGC 446  
Db 1731 GT-GTGGAGGAGCAAAATTAACC-GTGTATTATTATACCTCTGCCITTTGTGAGGTGC 1788  
QY 447 AGGAAGTGTAAATGTATATTTTAAAGATGTTTGTAGAG 488  
Db 1789 AAGGAGTGTAAATGTATATTTTAAAGATGTTTAAAGAAATGTTAGAAAGG 1830

RESULT 6

US-09-764-877-3707  
; Sequence 3707, Application US/09764877  
; Patent No. US20020147140A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC005  
; CURRENT APPLICATION NUMBER: US/09/764,877  
; CURRENT FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: 60/179,065  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: 60/180,628  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: 60/214,886  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/217,487  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/225,758  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/220,963  
; PRIOR FILING DATE: 2000-07-26  
; PRIOR APPLICATION NUMBER: 60/217,496  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/225,447  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/218,290  
; PRIOR FILING DATE: 2000-07-14  
; Remaining Prior Application data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 4031  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3707  
; LENGTH: 5159  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-764-877-3707

Query Match 33.9%; Score 261.6; DB 9; Length 5159;  
Best Local Similarity 87.4%; Pred. No. 4.6e-70;  
Matches 285; Conservative 0; Mismatches 41; Indels 0; Gaps 0;  
QY 447 AGGAAGTGTAAATGTATATTTTAAAGATGTTTAAAGAGCGCGGCGGTGGCTCAC 506

QY 567 GACATCTGCTGCTAACACGGTGAACCCCGTCTCTCTACTATAAAATTCAAAAAATTAG 626  
 Db 254 GACATCTGCTGCTAACACGGTGAACCCCGTCTCTCTACTATAAAATTCAAAAAATTAG 313  
 QY 627 CTGGCGGTGGTGGCGGGCGCTGTAGTCCAGCTATTTCGGAGGCTCAGGCGAGAGATG 686  
 Db 314 CCGGCGGTGGTGGCGGGCGCTGTAGTCCAGCTATTTCGGAGGCTCAGGCGAGAGATG 373  
 QY 697 GCGTAACTCGGAGGTGGAGTTCGANTAGCCAGGTCGCGGCTCAGCTCCAGCCT 746  
 Db 374 GCGTAACTCGGAGGTGGAGTTCGANTAGCCAGGTCGCGGCTCAGCTCCAGCCT 433  
 QY 747 GGGGACAGAGCGAGACTCCATCTTA 772  
 Db 434 GGGGACAGAGCGAGACTCCGACTCA 459

RESULT 8  
 US-10-027-632-130764  
 ; Sequence 130764, Application US/10027632  
 ; Publication No. US20020198371A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
 ; FILE OF INVENTION: Polymorphisms in the Human Genome  
 ; FILE REFERENCE: 108827.129  
 ; CURRENT APPLICATION NUMBER: US/10/027,632  
 ; CURRENT FILING DATE: 2002-04-30  
 ; PRIOR APPLICATION NUMBER: US 60/218,006  
 ; PRIOR FILING DATE: 2000-07-12  
 ; PRIOR APPLICATION NUMBER: US 60/198,676  
 ; PRIOR FILING DATE: 2000-04-20  
 ; PRIOR APPLICATION NUMBER: US 60/193,483  
 ; PRIOR FILING DATE: 2000-03-29  
 ; PRIOR APPLICATION NUMBER: US 60/185,218  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: US 60/167,363  
 ; PRIOR FILING DATE: 1999-11-23  
 ; PRIOR APPLICATION NUMBER: US 60/156,358  
 ; PRIOR FILING DATE: 1999-09-28  
 ; PRIOR APPLICATION NUMBER: US 60/146,002  
 ; NUMBER OF SEQ ID NOS: 325720  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 130764  
 ; LENGTH: 657  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-10-027-632-130764

Query Match 33.7%; Score 260; DB 13; Length 657;  
 Best Local Similarity 88.4%; Pred. No. 5.6e-70;  
 Matches 281; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 455 TAAATGTATATTTTAAAGATGTTGTTAGAGCGCGGGCGGTGCTCAGCGCTGTAA 514  
 Db 72 TAACTATTTCAGTTAAACAAACAAAGAGCGCGGTGCTCAGCGCTGTAA 131  
 QY 515 TCCAGCATTTCGGAGGCGGAGCGGTTCGATTCAGAGGTTCAGAGATTCGAGCATCC 574  
 Db 132 TCCAGCATTTCGGAGGCGGAGCGGTTCGATTCAGAGGTTCAGAGATTCGAGCATCC 191  
 QY 575 TGGCTAACACGTTGAACCCCGTCTCTACTATAAAATTCAAAAAATTAGCTGGCGGT 634  
 Db 192 TGGCTAACACGTTGAACCCCGTCTCTACTATAAAATTCAAAAAATTAGCTGGCGGT 251  
 QY 635 GGTGGCGGGCGCTGTAGTCCAGCTATTTCGGAGGCTCAGGCGAGAGATTCGNTGAAC 694  
 Db 252 GGTGGCGGGCGCTGTAGTCCAGCTATTTCGGAGGCTCAGGCGAGAGATTCGNTGAAC 311  
 QY 695 CTGGCGGGCGCTGTAGTCCAGCTATTTCGGAGGCTCAGGCGAGAGATTCGNTGAAC 754  
 Db 252 GGTGGCGGGCGCTGTAGTCCAGCTATTTCGGAGGCTCAGGCGAGAGATTCGNTGAAC 311  
 QY 695 CTGGAGGTGGAGTTCGANTAGCCAGGTCGCGGCTCAGCTCCAGCCTGGCGGACA 754

Db 312 CCGGAGGCGGAGCTTGCAGTGAGCGGAGATGCGGCCACTGCACTCCAGCCTGGCGGACA 371  
 QY 755 GAGCGAGACTCCATCTTA 772  
 Db 372 GAGCGAGACTCCGCTCTCA 389

RESULT 9  
 US-10-027-632-130764  
 ; Sequence 130764, Application US/10027632  
 ; Publication No. US20030204075A9  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
 ; FILE OF INVENTION: Polymorphisms in the Human Genome  
 ; FILE REFERENCE: 108827.129  
 ; CURRENT APPLICATION NUMBER: US/10/027,632  
 ; CURRENT FILING DATE: 2002-04-30  
 ; PRIOR APPLICATION NUMBER: US 60/218,006  
 ; PRIOR FILING DATE: 2000-07-12  
 ; PRIOR APPLICATION NUMBER: US 60/198,676  
 ; PRIOR FILING DATE: 2000-04-20  
 ; PRIOR APPLICATION NUMBER: US 60/193,483  
 ; PRIOR FILING DATE: 2000-03-29  
 ; PRIOR APPLICATION NUMBER: US 60/185,218  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: US 60/167,363  
 ; PRIOR FILING DATE: 1999-11-23  
 ; PRIOR APPLICATION NUMBER: US 60/156,358  
 ; PRIOR FILING DATE: 1999-09-28  
 ; PRIOR APPLICATION NUMBER: US 60/146,002  
 ; NUMBER OF SEQ ID NOS: 325720  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 130764  
 ; LENGTH: 657  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-10-027-632-130764

Query Match 33.7%; Score 260; DB 16; Length 657;  
 Best Local Similarity 88.4%; Pred. No. 5.6e-70;  
 Matches 281; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 455 TAAATGTATATTTTAAAGATGTTGTTAGAGCGCGGGCGGTGCTCAGCGCTGTAA 514  
 Db 72 TAACTATTTCAGTTAAACAAACAAAGAGCGCGGTGCTCAGCGCTGTAA 131  
 QY 515 TCCAGCATTTCGGAGGCGGAGCGGTTCGATTCAGAGGTTCAGAGATTCGAGCATCC 574  
 Db 132 TCCAGCATTTCGGAGGCGGAGCGGTTCGATTCAGAGGTTCAGAGATTCGAGCATCC 191  
 QY 575 TGGCTAACACGTTGAACCCCGTCTCTACTATAAAATTCAAAAAATTAGCTGGCGGT 634  
 Db 192 TGGCTAACACGTTGAACCCCGTCTCTACTATAAAATTCAAAAAATTAGCTGGCGGT 251  
 QY 635 GGTGGCGGGCGCTGTAGTCCAGCTATTTCGGAGGCTCAGGCGAGAGATTCGNTGAAC 694  
 Db 252 GGTGGCGGGCGCTGTAGTCCAGCTATTTCGGAGGCTCAGGCGAGAGATTCGNTGAAC 311  
 QY 695 CTGGAGGTGGAGTTCGANTAGCCAGGTCGCGGCTCAGCTCCAGCCTGGCGGACA 754  
 Db 312 CCGGAGGCGGAGCTTGCAGTGAGCGGAGATTCGCGGCTCAGCTCCAGCCTGGCGGACA 371  
 QY 755 GAGCGAGACTCCATCTTA 772  
 Db 372 GAGCGAGACTCCGCTCTCA 389

RESULT 10  
 US-09-764-846-313/c  
 ; Sequence 313, Application US/09764846  
 ; Patent No. US20020102638A1

GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT212  
; CURRENT APPLICATION NUMBER: US/09/764,846  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 348  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 313  
; LENGTH: 10953  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-764-846-313

Query Match 33.5%; Score 259; DB 9; Length 10953;  
Best Local Similarity 91.0%; Pred. No. 4.2e-69;  
Matches 274; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 469 TTAAGAATGTTGTAGAGCGCGCGGTGGCTCAGCGCTGTAATCCAGCAGCTTTGG 528  
DB 5346 TTTAAGAAGTAATCTGGCGCGCGGTGGCTTACGCTGTAAATCCAGCAGCTTTGG 5287  
QY 529 GAGCGCGAGCGGTGCGATCAGAGGTGAGAGATCGAGACCATCTGGCTTAACAGCGTG 588  
DB 5286 GAGCGCGAGCGGTGCGATCAGAGGTGAGAGATCGAGACCATCTGGCTTAACATGGT 5227  
QY 589 AAACCCCTCTCTACTAAAAATTCAAAAAATTTAGCTGGCGTGGTGGCGCGCT 648  
DB 5226 AAACCCCTCTCTACTAAAAATTCAAAAAATTTAGCTGGCGTGGTGGCGCGCT 5167  
QY 649 GTAGTCCAGCTATTCGGAGGCTGAGCAGAGATGGCAGAGATGGCAGAGTGGAGTGGAGC 708  
DB 5166 GTAGTCCAGCTATTCGGAGGCTGAGCAGAGATGGCAGAGATGGCAGAGTGGAGTGGAGC 5107  
QY 709 TTGCANTGAGCAGGTGCGCCACTGCATCCAGCTGGCGGAGAGAGAGACTCCAT 768  
DB 5106 TTGCAGTGGCGGAGTTCCGCCACTGCATCCAGCTGGCGGAGAGAGACTCCGT 5047  
QY 769 C 769  
DB 5046 C 5046

RESULT 11  
US-10-091-483-313/c  
; Sequence 313, Application US/10091483  
; Publication No. US20030049650A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT212C1  
; CURRENT APPLICATION NUMBER: US/10/091,483  
; CURRENT FILING DATE: 2002-03-07  
; NUMBER OF SEQ ID NOS: 348  
; Prior Application removed - See File Wrapper or Palm  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 313  
; LENGTH: 10953  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-091-483-313

Query Match 33.5%; Score 259; DB 15; Length 10953;  
Best Local Similarity 91.0%; Pred. No. 4.2e-69;  
Matches 274; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 469 TTAAGAATGTTGTAGAGCGCGCGGTGGCTCAGCGCTGTAATCCAGCAGCTTTGG 528  
DB 5346 TTTAAGAAGTAATCTGGCGCGCGGTGGCTTACGCTGTAAATCCAGCAGCTTTGG 5287  
QY 529 GAGCGCGAGCGGTGCGATCAGAGGTGAGAGATCGAGACCATCTGGCTTAACAGCGTG 588

DB 5286 GAGCCCGAGCGCGGTGATGAGTTCAGGAGATCGAGACCATCTCTGCTTAACATGGT 5227  
QY 589 AAACCCCTCTCTACTAAAAATTCAAAAAATTTAGCTGGCGTGGTGGCGCGCT 648  
DB 5226 AAACCCCTCTCTACTAAAAATTCAAAAAATTTAGCTGGCGTGGTGGCGCGCT 5167  
QY 649 GTAGTCCAGCTATTCGGAGGCTGAGCAGAGATGGCAGAGATGGCAGAGTGGAGTGGAGC 708  
DB 5166 GTAGTCCAGCTATTCGGAGGCTGAGCAGAGATGGCAGAGATGGCAGAGTGGAGTGGAGC 5107  
QY 709 TTGCANTGAGCAGGTGCGCCACTGCATCCAGCTGGCGGAGAGAGACTCCAT 768  
DB 5106 TTGCAGTGGCGGAGTTCCGCCACTGCATCCAGCTGGCGGAGAGACTCCGT 5047  
QY 769 C 769  
DB 5046 C 5046

RESULT 12  
US-10-074-024-660  
; Sequence 660, Application US/10074024  
; Publication No. US20030232975A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC001C1  
; CURRENT APPLICATION NUMBER: US/10/074,024  
; CURRENT FILING DATE: 2002-02-14  
; Prior Application removed - See file Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 879  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 660  
; LENGTH: 6264  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-074-024-660

Query Match 33.3%; Score 256.8; DB 16; Length 6264;  
Best Local Similarity 83.9%; Pred. No. 1.6e-68;  
Matches 302; Conservative 0; Mismatches 54; Indels 4; Gaps 1;

QY 413 TGTGTGATTACATTCGCCACCTTTGCTGAGGTGCGAGGATGTAATAATGTATTTTAA 472  
DB 5165 TGTTTTAAGCTAAGTGTATCATATAAAGAGTCAAAAGTTTAAAAAATTAATAATGTAT 5224  
QY 473 AGAATGTTGTTAGAGCGCGCGGTGGCTCACCGCTGTATCCAGCAGCTTTGGAGG 532  
DB 5225 AAAGTAAAAATATGCGCGCGCGGTGGCTCACCGCTGTATCCAGCAGCTTTGGAGG 5284  
QY 533 CCGAGCGGTGCGGATCAGAGGTTCAGGAGATCGAGACCATCTCTGCTAACCGTGAAC 592  
DB 5285 CCGAGCGCGCGGATCAGAGGTTCAGGAGATCGAGACCATCTCTGCTAACCGTGAAC 5344  
QY 593 CCGCTCTCTACTAAAAATTCAAAAAATTTAGCTGGCGTGGTGGCGCGCTGTAG 652  
DB 5345 CCGCTCTCTACTAAAAATTCAAAAAATTTAGCTGGCGTGGTGGCGCGCTGTAG 5400  
QY 653 TCCAGCTATTCGGAGGCTGAGCGAGAGATGGCTGAACCTGGGAGGTGGAGCTTGC 712  
DB 5401 TCCAGCTATTCGGAGGCTGAGCGAGAGATGGCTGAACCTGGGAGGTGGAGCTTGC 5460  
QY 713 ANTGAGCGAGGTGCGGCCACTGCATCCAGCTGGCGGAGAGAGACTCCATCTTA 772  
DB 5461 AGTGAGCAAGATCGCGCCACTGCATCCAGCTGGCGGAGAGAGACTCCGTTCA 5520

RESULT 13  
US-10-085-117-112/c  
; Sequence 112, Application US/10085117  
; Publication No. US2003023234A1  
; GENERAL INFORMATION:  
; APPLICANT: Morris, David W.

APPLICANT: Engelhard, Eric K.  
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER  
; FILE REFERENCE: 529452000121  
; CURRENT APPLICATION NUMBER: US/10/085,117  
; CURRENT FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: US 09/798,586  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 361  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 112  
; LENGTH: 96597  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-085-117-112

Query Match 33.3%; Score 256.8; DB 16; Length 96597;  
Best Local Similarity 90.4%; Pred. No. 5.5e-68;  
Matches 284; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

QY 460 TGTATATTTTAAAGAAATGTTTGTAGAGCCGGCGCGGTGCTCAAGCTGTAAATCCCA 519  
DB 3978 TGGGCACTGTTTCAAGTAGAGCTGAGAGCGCGCGGTGCTGCGCTGTAAATCCCA 3919

QY 520 GCACTTTGGAGCGCGGCGGTGCGATCAGAGGTTCAGGAGATCGAGACCATCTGGCT 579  
DB 3918 GCACITTTGGAGCGCGGCGGATCCAGAGTTCAGGAGATCGAGACCATCTGGCT 3859

QY 580 AACACGGTCAAAACCCCGTCTTACTTAAATTC-AAAAAAAAAATTAGTGGCGGTG 638  
DB 3858 AACACGGTCAAAACCCCGTCTTACTTAAATTC-AAAAAAAAAATTAGCAGCGGTG 3799

QY 639 GCGGGCGCTGTAGTCCAGCTATTCGGAGGCTGAGGAGGAGATGCGTGAACCTGG 698  
DB 3798 GCGGGCGCTGTAGTCCAGCTATTCGGAGGCTGAGGAGGAGATGCGTGAACCTGG 3739

QY 699 GAGGTGAGCTTGCAATGAGCAAGCTCGCGCACTGCACTCCAGCTGGGCGACAGAGC 758  
DB 3738 GAGGCGAGCTTGCAATGAGCAAGCTCATGCGCACTGCACTCCAGCTGGGCGACAGAGC 3679

QY 759 GAGACTCCATCTTA 772  
DB 3678 GAGACTCCGCTCA 3665

RESULT 14  
US-10-087-192-688  
; Sequence 688, Application US/10087192  
; Publication No. US20020182586A1  
; GENERAL INFORMATION:  
; APPLICANT: Morris, David W.  
; APPLICANT: Engelhard, Eric K.  
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR  
; FILE REFERENCE: 529452000122  
; CURRENT APPLICATION NUMBER: US/10/087,192  
; CURRENT FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: US 09/747,377  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US 09/798,586  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 2059  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 688  
; LENGTH: 97247  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(97247)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-087-192-688

Query Match 33.1%; Score 255.6; DB 13; Length 97247;

Best Local Similarity 92.7%; Pred. No. 1.3e-67;  
Matches 267; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 485 GAGCGCGCGCGGTGCTCAGCCCTGTAATCCAGCACTTTGGGAGGCGGCGGTGCG 544  
DB 33845 GGGGCTGGGCGCGGTGCTCAGCCCTGTAATCCAGCACTTTGGGAGGCGGCGGCG 33904

QY 545 GATCAGAGGTTCAGGAGATCGAGACCATCTCGCTAACACCGTGAACCCCGTCTACT 604  
DB 33905 GATCAGAGGTTCAGGAGATCGAGACCATCTCGCTAACACCGTGAACCCCGTCTACT 33964

QY 605 AAAAAATCAAAAAAATAATAGTGGCGGTGCTGGCGGCGCTGTAGTCCAGCTATTTC 664  
DB 33965 AAAAAAATAAAAAAATAATAGTGGCGGTGCTGGCGGCGCTGTAGTCCAGCTATTTC 34024

QY 665 GGGAGGCTGAGGAGGAGATGCGNTGAACTGGGAGGTGGAGCTTGCANTGAGCAAGG 724  
DB 34025 GGGAGGCTGAGGAGGAGATGCGNTGAACTGGGAGGTGGAGCTTGCANTGAGCAAGG 34084

QY 725 TCGGCGCACTGCACTCCAGCTGGGCGAGAGAGAGTCCATCTTA 772  
DB 34085 TCGGCGCACTGCACTCCAGCTGGGCGAGAGAGAGTCCATCTTA 34132

RESULT 15  
US-09-764-878-359/c  
; Sequence 359, Application US/09764878  
; Patent No. US20020090615A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PA121  
; CURRENT APPLICATION NUMBER: US/09/764,878  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 428  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 359  
; LENGTH: 2225  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-764-878-359

Query Match 33.1%; Score 255.2; DB 9; Length 2225;  
Best Local Similarity 93.0%; Pred. No. 3e-68;  
Matches 266; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 487 GCGCGCGCGCGGTGCTCAGCCCTGTAATCCAGCACTTTGGGAGGCGGCGGTGCGA 546  
DB 2219 GCGCGCGCGCGGTGCTCAGCCCTGTAATCCAGCACTTTGGGAGGCGGAGATGGCGGA 2160

QY 547 TCACGAGTTCAGGAGATCGAGACCATCTCGCTAACACCGTGAACCCCGTCTACTAA 606  
DB 2159 TCACGAGTTCAGGAGATCGAGACCATCTCGCTAACACCGTGAACCCCGTCTACTAA 2100

QY 607 AAAAAATCAAAAAAATAATAGTGGCGGTGCTGGCGGCGCTGTAGTCCAGCTATTTCGG 666  
DB 2099 AAAAAATCAAAAAAATAATAGTGGCGGTGCTGGCGGCGCTGTAGTCCAGCTATTTCGG 2040

QY 667 GAGGCTGAGGAGGAGATGCGNTGAACTGGGAGGTGGAGCTTGCANTGAGCAAGGTC 726  
DB 2039 GAGGCTGAGGAGGAGATGCGNTGAACTGGGAGGTGGAGCTTGCANTGAGCAAGGTC 1980

QY 727 GCGCACTGCACTCCAGCTGGGCGAGAGAGTCCATCTTA 772  
DB 1979 GCGCACTGCACTCCAGCTGGGCGAGAGAGTCCATCTTA 1934

Search completed: May 6, 2004, 14:05:52  
Job time : 408.667 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 07:44:53 ; Search time 72.9822 Seconds  
(without alignments)  
5870.227 Million cell updates/sec

Title: US-09-451-739H-8  
Perfect score: 772  
Sequence: 1 aaagcgtctcggcgagc.....cagagcgagactccatttta 772

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*

- 1: /cgn2\_6/prodata/2/ina/5A COMB.seq.\*
- 2: /cgn2\_6/prodata/2/ina/5B COMB.seq.\*
- 3: /cgn2\_6/prodata/2/ina/6A COMB.seq.\*
- 4: /cgn2\_6/prodata/2/ina/6B COMB.seq.\*
- 5: /cgn2\_6/prodata/2/ina/PCUS COMB.seq.\*
- 6: /cgn2\_6/prodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	276	35.8	1902	2	US-09-258-257-1 Sequence 1, Appli
2	276	35.8	1902	2	US-09-258-371-1 Sequence 1, Appli
3	276	35.8	1902	3	US-08-569-721A-1 Sequence 1, Appli
4	276	35.8	1902	3	US-08-751-230-1 Sequence 1, Appli
5	276	35.8	1902	3	US-09-499-082-1 Sequence 1, Appli
6	276	35.8	1902	3	US-09-258-372-1 Sequence 1, Appli
7	276	35.8	2061	2	US-09-258-371-9 Sequence 9, Appli
8	276	35.8	2061	3	US-08-751-230-9 Sequence 9, Appli
9	276	35.8	2061	3	US-09-499-082-9 Sequence 9, Appli
10	276	35.8	2061	3	US-09-258-373-9 Sequence 2, Appli
11	276	35.8	2061	4	US-09-006-783A-2 Sequence 1, Appli
12	272.8	35.3	2061	4	US-09-159-871-1 Sequence 6, Appli
13	249.8	32.4	14636	3	US-09-173-914-6 Sequence 6, Appli
14	248.6	32.2	15328	2	US-08-888-497-33 Sequence 33, Appli
15	248.6	32.2	15328	4	US-09-362-230-33 Sequence 33, Appli
16	248.6	32.2	15328	5	PCT-US94-07946-33 Sequence 33, Appli
17	248.4	32.2	148567	4	US-09-801-876B-3 Sequence 3, Appli
18	248.4	32.2	148567	4	US-10-254-869-3 Sequence 3, Appli
19	248	32.1	319608	4	US-09-539-333D-1 Sequence 1, Appli
20	248	32.1	319608	4	US-09-579-409-1 Sequence 1, Appli
21	247.2	32.0	1268	4	US-09-369-247-42 Sequence 42, Appli
22	246.4	31.9	1712	3	US-09-058-389A-12 Sequence 12, Appli
23	246.4	31.9	1712	4	US-09-611-781-12 Sequence 12, Appli
24	246.4	31.9	6354	3	US-09-058-389A-5 Sequence 5, Appli
25	246.4	31.9	6354	4	US-09-611-781-5 Sequence 5, Appli
26	246.4	31.9	14796	3	US-08-975-080-35 Sequence 35, Appli
27	246.4	31.9	14796	3	US-09-630-706-10 Sequence 10, Appli

28	246.4	31.9	14796	4	US-09-496-694B-3 Sequence 3, Appli
29	244.8	31.7	320	1	US-08-629-933-5 Sequence 5, Appli
30	244.8	31.7	320	1	US-08-759-873-5 Sequence 5, Appli
31	244.6	31.7	14581	4	US-08-520-373D-4 Sequence 4, Appli
32	244.6	31.7	22481	4	US-08-367-841A-43 Sequence 43, Appli
33	244.6	31.7	22481	5	PCT-US95-07201-43 Sequence 43, Appli
34	244.6	31.7	22484	4	US-09-875-223-2 Sequence 2, Appli
35	244.6	31.7	22484	4	US-09-875-114-2 Sequence 2, Appli
36	244.2	31.6	246240	2	US-08-724-394A-20 Sequence 20, Appli
37	244.2	31.6	246240	2	US-08-724-394A-21 Sequence 21, Appli
38	244.2	31.5	84495	4	US-09-797-906-3 Sequence 3, Appli
39	243.4	31.5	84495	4	US-09-797-906-3 Sequence 3, Appli
40	242.4	31.4	193303	4	US-09-497-855A-37 Sequence 37, Appli
41	242.4	31.4	193303	4	US-09-497-855A-44 Sequence 44, Appli
42	242	31.3	392000	4	US-10-027-983-11 Sequence 11, Appli
43	241.8	31.3	3742	1	US-08-694-915-5 Sequence 5, Appli
44	241.8	31.3	23187	4	US-09-499-522-1 Sequence 1, Appli
45	241.6	31.3	70000	4	US-09-851-896-3 Sequence 3, Appli

## ALIGNMENTS

RESULT 1  
US-09-258-257-1  
; Sequence 1, Application US/09258257  
; Patent No. 5965398  
; GENERAL INFORMATION:  
; APPLICANT: GARKAVTSEV, Igor  
; APPLICANT: RIAEWOL, Karl  
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A TUMOR  
; TITLE OF INVENTION: SUPPRESSOR GENE  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/09/258,257  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/569,721  
; FILING DATE: 08-DEC-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mooi, Leslie A.  
; REGISTRATION NUMBER: 37,047  
; REFERENCE/DOCKET NUMBER: 028722-128  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 854-7400  
; TELEFAX: (650) 854-8275  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1902 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 109..738  
; US-09-258-257-1  
Query Match 35.8%; Score 276; DB 2; Length 1902;  
Best Local Similarity 80.8%; Pred. No. 2.7e-68;

/	TELEPHONE:	415-854-7400
/	TELEFAX:	415-854-8275
/	INFORMATION FOR SEQ ID NO:	1:
/	SEQUENCE CHARACTERISTICS:	
/	LENGTH:	1902 base pairs
/	TYPE:	nucleic acid
/	STRANDEDNESS:	double
/	TOPOLOGY:	linear
/	MOLECULE TYPE:	CDNA
/	FEATURE:	
/	NAME/KEY:	CDS
/	LOCATION:	109..741
/	US-09-258-371-1	

  

Query Match	35.8%;	Score	276;	DB 2;	Length	1902;			
Best Local Similarity	80.8%;	Pred. No.	2.7e-58;						
Matches	422;	Conservative	0;	Mismatches	60;	Indels	40;	Gaps	7;

  

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QY	62	CCACGACGACGTCAACTCGGCACGCCCAAGGAGAAGAAAGCCAGACCTCTTAAGAAGAA	121
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QY	387	ATAGTTCGGAGACAATAATAAGCCAGGTGTGTGATTACATTGCGCACCTTTGCTGAGGTGC	446
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QY	447	AGCAAGTGTAAATGTATATTTTTTAAAGATGTTGTTAGAGG	488
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RESULT 3  
US-08-569-721A-1  
Sequence 1, Application US/08569721A  
Patent No. 6037121  
GENERAL INFORMATION:  
APPLICANT: GARKAVTSEV, Igor  
APPLICANT: RABOWOL, Karl  
TITLE OF INVENTION: DNA SEQUENCE ENCODING A TUMOR  
TITLE OF INVENTION: SUPPRESSOR GENE  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,721A
FILING DATE: 08-DEC-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Mooi, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 854-7400
TELEFAX: (650) 854-8275
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1902 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 109..738
US-08-569-721A-1

Query Match 35.8%; Score 276; DB 3; Length 1902;
Best Local Similarity 80.8%; Pred. No. 2.7e-68;
Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;

QY 2 AAGCGTTCTCGCGCGCAGCGCAACCACTAGAAACCGTGAGAAAGCGGTCCAGCAACCGCGAC 61
DB 343 AAGCGTCACTCGCGCGCAGCGCAACCAAGAGAACCGTGAGAACCGGTCCAGCAACCAAG- 401
QY 62 CCAAGCAGAGCTCACTCTCGGCGCAGCCCAAGAGAGAAAGCCAGACCTCTAAGAGAA 121
DB 402 CCACGACGACGCGCGCTCGGGCACAACCAAGAGAGAAAGGCCAAGACCTCCCAAGAGAA 461
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DB 462 GAAGCGCTCCAAGGCCAAGGCCGAGAGAGGCGTCCCTGCGGACCTCCCATCGACCC 521
QY 182 CAGCGAGCC-----CTCCTACTGGAGAGATGATCCGTGCGA 217
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QY 218 CA---ACGAATGCCCCATCGAGTGGTTCGCGTCTCGGTGTGAGTCTCAACCATATAACC 274
DB 582 CAACACAGAGTGCCCCATCGAGTGGTTCACCTTCTGTGCGTGGGCTCAATCATATAACC 641
QY 275 AAAGCGCAAGTGGTACTGTTCCAGATGCGGGGAAAGAACG-----ATGGGCAAGC 326
DB 642 CAAGGCGAAGTGGTACTGTCCCAAGTGCAGGGGGAACGAGAGACCATGGAACAAGC 701
QY 327 CTTTGAGAGATCCAGAAAAAACAAGGCTTTTAAAGGTAGTCTTGGGACATGCGTCTA 386
DB 702 CTGGAGAAATCCA-AAAAAGAGAGGGCTTACAAAGGTAGTCTTGGGACAGGGCGCGTG 759
QY 387 ATAGTGAGGAGAACAAAATAAGCCAGTGTGTGATTACATTGCCACTTTGCTGAGGTGC 446
DB 760 GT-GTGAGAGAGCAAAATRAACC-GTGATATTATTACATTGCTGCTTTGTTAGTGC 817
QY 447 AGGAAGTGTAAATGCTATATTTTAAAGATGTTGTTAGAGG 488
DB 818 AAGGAGTGTAAATGCTATATTTTAAAGATGTTGAGAAAGG 859

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1 APPLICANT: Garkavtsev Igor
2 APPLICANT: Radowo, Karl
3 TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
4 TITLE OF INVENTION: SUPPRESSOR GENE INGI
5 NUMBER OF SEQUENCES: 23
6 CORRESPONDENCE ADDRESS:
7 ADDRESSEE: Burns, Doane, Swecker & Mathis
8 STREET: 699 Prince Street
9 CITY: Alexandria
10 STATE: VA
11 COUNTRY: USA
12 ZIP: 22313-1404
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Floppy disk
15 COMPUTER: IBM PC compatible
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: PatentIn Release #1.0, Version #1.30
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/08/751,230
20 FILING DATE: 15-NOV-1996
21 CLASSIFICATION: 514
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: US 08/569721
24 FILING DATE: 08-DEC-1995
25 ATTORNEY/AGENT INFORMATION:
26 NAME: Mooi, Leslie A.
27 REGISTRATION NUMBER: 37,047
28 REFERENCE/DOCKET NUMBER: 028722-144
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: 415-854-7400
31 TELEFAX: 415-854-8275
32 INFORMATION FOR SEQ ID NO: 1:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 1902 base pairs
35 TYPE: nucleic acid
36 STRANDEDNESS: double
37 TOPOLOGY: linear
38 MOLECULE TYPE: CDNA
39 FEATURE:
40 NAME/KEY: CDS
41 LOCATION: 109..741
42 PS-08-751-230-1

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Db 760 GT-GTGAGGAGGACAAATAAACC-GTGATTTATTACATTGCTGCGCTTTGTTGAGGTGC 817  
Qy 447 AGGAAGTGTAAATGTATATTTTAAAGATGTTGTAGAGG 488  
Db 818 AAGGAGTGTAAATGTATATTTTAAAGATGTTAGAAAAGG 859

RESULT 5

US-09-499-082-1  
; Sequence 1, Application US/09499082  
; Patent No. 6143522  
; GENERAL INFORMATION:  
; APPLICANT: Helbing, Caren C.  
; APPLICANT: Riabowol, Karl  
; APPLICANT: Johnston, Randall N.  
; APPLICANT: Garkavtsev, Igor  
; TITLE OF INVENTION: METHODS OF MODULATING APOPTOSIS  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/499,082  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/828,158  
; FILING DATE: 27-MAR-1997  
; APPLICATION NUMBER: US 08/751230  
; FILING DATE: 15-NOV-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/569721  
; FILING DATE: 08-DEC-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mooi, Leslie A.  
; REGISTRATION NUMBER: 37,047  
; REFERENCE/DOCKET NUMBER: 028722-148  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-854-7400  
; TELEFAX: 650-854-8275  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1902 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 109..741  
US-09-499-082-1

Query Match 35.8%; Score 276; DB 3; Length 1902;  
Best Local Similarity 80.8%; Pred. No. 2.7e-68;  
Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;  
Qy 2 AAGCGTTCCTGGGCGGAGCGGCAACACTAGAACCGGTGAGACCGCTCCAGCAACCGGAC 61  
Db 343 AAGCGTTCAGCGGCGGAGCGGCAACACTAGAACCGGTGAGACCGCTCCAGCAACCGA 401

Qy 62 CCAGCAGACGTCACTCGGCGCGCCCAAGGAGAAAGAAAGCCAGACCTCTTAAGAGAA 121  
Db 402 CCAGCAGACCGCGCGCTCGGCGCACCCAGGAGAGAGAGCCAGACCTCCAGAGAGAA 461  
Qy 122 GCAGGGCTTCATGGCCAGGCGTAGCGGAGGCGTCCCGCGCAGACCTCCCGCATCGACCC 181  
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Qy 182 CAGCGAGCC-----CTCCTACTGGGAGATGATCCGCTCGGA 217  
Db 522 CAACGAAACCCAGTACTGTCTGTGCAACCCAGGTCTCTTATCGGGAGATGATCGGCTCGGA 581  
Qy 218 CA---ACGAATGCCCGCATCGAGTGGTTCGGCTTCTCGTGTGTAGTCTCAACCAATAAAC 274  
Db 582 CAACGACGAGTGCCCGCATCGAGTGGTTCCTTCTCGTGGGGGTCAATCATATAAAC 641  
Qy 275 AAAGCGCAAGTGTTACTGTTCCAGATGCCGGGGAAGAACG-----ATGGGCAAGC 326  
Db 642 CAAGGCGAAGTGGTACTGTCCCAAGTGCCTGGGGGAGAACGAGAACCATGGACAAAGC 701  
Qy 327 CCTTGAGAAATCCAGAAAAAAGAGGCTTTATACAGGTAGTTTGGGGACATCGGTCTA 386  
Db 702 CTGAGAAATCCA--AAAAGAGAGGCTTTACACAGGTAGTTTGTGACAGCGCGCTG 759  
Qy 387 ATAGTGAGGAGAAACAAATAGCCAGTGTGTGATTACATTGCCACCTTTGCTGAGGTGC 446  
Db 760 GT-GTGAGGAGGACAAATAAACC-GTGTATTTATTACATTGCTGCGCTTTGTTGAGGTGC 817  
Qy 447 AGGAAGTGTAAATGTATATTTTAAAGATGTTCTTTAGAGG 488  
Db 818 AAGGAGTGTAAATGTATATTTTAAAGATGTTAGAAAAGG 859

RESULT 6

US-09-258-372-1  
; Sequence 1, Application US/09258372  
; Patent No. 6238918  
; GENERAL INFORMATION:  
; APPLICANT: Garkavtsev, Igor  
; APPLICANT: Riabowol, Karl  
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR  
; TITLE OF INVENTION: SUPPRESSOR GENE INGI  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/258,372  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/751,230  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mooi, Leslie A.  
; REGISTRATION NUMBER: 37,047  
; REFERENCE/DOCKET NUMBER: 028722-144  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-854-7400  
; TELEFAX: 415-854-8275  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1902 base pairs  
; TYPE: nucleic acid

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; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 109..741
; US-09-258-372-1

Query Match      35.8%  Score 276; DB 3; Length 1902;
Best Local Similarity 80.8%; Pred. No. 2.7e-68;
Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;

QY 2 AAGCGTCTCGGGCAGCGCAACAACTAGAACCGGTGAGAACCGGTCCAGCAACCGGAC 61
Db 343 AAGCGCTCAGCGGCGAGCGCAACAACTAGAACCGGTGAGAACCGGTCCAGCAACCGGAC 401
QY 62 CCACGACGAGCTCACCTCGGCGACGCCCAAGGAGAGAAAGCCAGACCTCTAAGAGAA 121
Db 402 CCACGACGAGCGGCGCTCGGCGACACCACCAAGGAGAGAAAGCCAGACCTCTAAGAGAA 461
QY 122 GCAGGCGCTCATGGCCAAAGCGTAGCGGAGCGGTCCCGCGAGACCTCCCGCATCGACCC 181
Db 462 GAAGCGCTCAGAGCCCAAGCGGAGCGGAGCGGTCCCGCGAGACCTCCCGCATCGACCC 521
QY 182 CAGCGAGCC-----CTCTACTGGGAGATGATCGGTGCGA 217
Db 522 CAACGAAACCACTACTGTCTGTGCAACAGGTCTCTCTATGGGAGATGATCGGTGCGA 581
QY 218 CA---ACGAATGCCCATCGAGTGTTCGTCCTCTCTGTGTGAGTCTCAACCATAAACC 274
Db 582 CAACGACGAGTGCCTCATCGAGTGTTCCTCTCTGTGTGAGTCTCAACCATAAACC 641
QY 275 AAGCCCAAGTGTACTGTCTCAGATGCCGGGGAAGAGC-----ATGGGCAAGC 326
Db 642 CAAGGCAAGTGTACTGTCTCAGATGCCGGGGAAGAGC-----ATGGGCAAGC 701
QY 327 CCTTGAGAGATCCAGAAAAAAGCAGGCTTATAACAGGTAGTGTGGGACATGGGTCTA 386
Db 702 CCTGGAGAAATCCA---AAAAAGAGAGGCTTACACAGGTAGTGTGGGACATGGGTCT 759
QY 387 ATAGTGAGGAGAACAAATAAGCCAGTGTGTGATTTACATTGCGACCTTTGCTGAGGTGC 446
Db 760 GT-GTGAGGAGGACAAATAAACC-GTGATTTATTACATTGCTGCTTTGTTGAGGTGC 817
QY 447 AGGAAGTGTAAATGTATATTTTAAAGATGTTGTAGAG 488
Db 818 AAGGAGTGTAAATGTATATTTTAAAGATGTTGTAGAGG 859

RESULT 7
US-09-258-371-9
; Sequence 9, Application US/09258371
; Patent No. 5986078
; GENERAL INFORMATION:
; APPLICANT: Garkavtsev, Igor
; APPLICANT: Riabowol, Karl
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
; TITLE OF INVENTION: SUPPRESSOR GENE INGI
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/258,371

; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/751,230
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mool, Leslie A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2061 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..900
; US-09-258-371-9

Query Match      35.8%  Score 276; DB 2; Length 2061;
Best Local Similarity 80.8%; Pred. No. 2.8e-68;
Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;

QY 2 AAGCGTCTCGGGCAGCGCAACAACTAGAACCGGTGAGAACCGGTCCAGCAACCGGAC 61
Db 502 AAGCGCTCAGCGGCGAGCGCAACAACTAGAACCGGTGAGAACCGGTCCAGCAACCGGAC 560
QY 62 CCACGACGAGTCCCTCGGCGACGCCCAAGGAGAGAAAGCCAGACCTCTAAGAGAA 121
Db 561 CCACGACGAGCGGCGCTCGGCGACACCCCAAGGAGAGAAAGCCAGACCTCTAAGAGAA 620
QY 122 GCAGGCGCTCATGGCCAAAGCGTAGCGGAGCGGTCCCGCGAGACCTCCCGCATCGACCC 181
Db 621 GAACGCGTCCCAAGGCGGAGGAGCGGTCCCGCGAGACCTCCCGCATCGACCC 680
QY 182 CAGCGAGCC-----CTCTACTGGGAGATGATCGGTGCGA 217
Db 681 CAACGAAACCACTACTGTCTGTGCAACAGGTCTCTATGGGAGATGATCGGTGCGA 740
QY 218 CA---ACGAATGCCCATCGAGTGTTCGTCCTCTCTGTGTGAGTCTCAACCATAAACC 274
Db 741 CAACGACGAGTGCCTCATCGAGTGTTCCTCTCTGTGTGAGTCTCAACCATAAACC 800
QY 275 AAGCGCAAGTGTACTGTTCCTAGATGCCGGGGAAGAGC-----ATGGGCAAGC 326
Db 801 CAGGGCAAGTGTACTGTTCCTAGATGCCGGGGAAGAGC-----ATGGGCAAGC 860
QY 327 CCTTGAGAGTCCAGAAAAAAGCAGGCTTATAACAGGTAGTGTGGGACATGGGTCTA 386
Db 861 CCTGGAGAAATCCA---AAAAAGAGAGGCTTACACAGGTAGTGTGGGACATGGGTCT 918
QY 387 ATAGTGAGGAGAACAAATAAGCCAGTGTGTGATTTACATTGCGACCTTTGCTGAGGTGC 446
Db 919 GT-GTGAGGAGGACAAATAAACC-GTGATTTATTACATTGCTGCTTTGTTGAGGTGC 976
QY 447 AGGAAGTGTAAATGTATATTTTAAAGATGTTGTAGAG 488
Db 977 AAGGAGTGTAAATGTATATTTTAAAGATGTTGTAGAGG 1018

RESULT 8
US-09-751-230-9
; Sequence 9, Application US/08751230
; Patent No. 6117633
; GENERAL INFORMATION:
; APPLICANT: Garkavtsev, Igor
; APPLICANT: Riabowol, Karl
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
```



QY 122 GCAGGGCTCCATGGCCAGAGCGTAGCGGAGGCGTCCCGGAGAGCTCCCGCATCGACCC 181  
Db 621 GAAGCGCTCCAGGCGCAGGCGGAGAGGCGTCCCGTCCGACCTCCCGCATCGACCC 680  
QY 182 CAGCGAGCC-----CTCCTACTGGGAGATGATCGCGTGGGA 217  
Db 681 CAACGAACCCAGCTACTGCTGTGCAACCCAGGCTCTCTATGGGAGATGATCGCGTGGGA 740  
QY 218 CA---ACGAATGCCCATCGAGTGTTCGCTTCTCGTGTGTGAGTCTCAACCATAAACC 274  
Db 741 CAACGACGAGTGCCTCCCATCGAGTGTTCACCTTCGTCGCTGGGCTCAATCATAAACC 800  
QY 275 AAAGCGCAAGTGTACTGCTTCAGATGCGCGGGAAGAACG-----ATGGGCAAAAGC 326  
Db 801 CAAGGCAAGTGTACTGCTTCCCAAGTCCCGGGGAGAGAACGAGAACCATGGAACAAAGC 860  
QY 327 CTTGAGAGTCCAGAAAACAGGCGTTATACAGTAGTGTGGGACATCGGTCTA 386  
Db 861 CTTGGAGAATCCA--AAAAAGAGAGGCGTTTCAACAGTAGTGTGGACAGGCGCTG 918  
QY 387 ATAGTGAGGAGAACAAATAAGCCAGTGTGTGATTACATTGCCACCTTTGCTGAGGTGC 446  
Db 919 GT-GTGAGGAGCAAAATAAAC--GTGTATTATTATACATTGCTGCTTTGTTGAGGTGC 976  
QY 447 AGGAGTGTAAATGTATATTTTAAAGATGTTGTAGAGG 488  
Db 977 AGGAGTGTAAATGTATATTTTAAAGATGTTGTAGAGG 1018

## RESULT 10

US-09-258-372-9  
; Sequence 9, Application US/09258372  
; Patent No. 6238918  
; GENERAL INFORMATION:  
; APPLICANT: Garkavtsev, Igor  
; APPLICANT: Riabowol, Karl  
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR  
; TITLE OF INVENTION: SUPPRESSOR GENE INGI  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/258,372  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/751,230  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mooi, Leslie A.  
; REGISTRATION NUMBER: 37,047  
; REFERENCE/DOCKET NUMBER: 028722-144  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-854-7400  
; TELEFAX: 415-854-8275  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2061 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA

FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 16..900  
US-09-258-372-9

Query Match 35.8%; Score 276; DB 3; Length 2061;  
Best Local Similarity 80.8%; Pred. No. 2.8e-68;  
Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;  
QY 2 AAGCGTTCTCGGCGGAGGCGCAACACTAGAACCGGTGAGAACCGGTCCAGAACCGCGAC 61  
Db 502 AAGCGTCCAGCGGCGGAGCGCAACACGAGAACCGGTGAGAACCGGTCCAGAACCGACGA- 560  
QY 62 CCACGACGAGTCCATCTCGGCGGAGCGCCCAAGAGAGAAAGCCAGACCTCTAAGAGAA 121  
Db 561 CCACGACGAGCGGCGCTCGGCGCACCCCAAGAGAGAAAGCCAGACCTCTAAGAGAA 620  
QY 122 GCAGGGCTCCATGCCCAAGGCGTAGCGGAGGCGTCCCGGAGAGCTCCCGCATCGACCC 181  
Db 621 GAAGCGTCCAGGCGCAAGGCGGAGGAGGCTCCCGTCCGACCTCCCGCATCGACCC 680  
QY 182 CAGCGAGCC-----CTCCTACTGGGAGATGATCGCGTGGGA 217  
Db 681 CAACGAACCCAGCTACTGCTGTGCAACCCAGGCTCTCTATGGGAGATGATCGCGTGGGA 740  
QY 218 CA---ACGAATGCCCATCGAGTGTTCGCTTCTCGTGTGTGAGTCTCAACCATAAACC 274  
Db 741 CAACGACGAGTGCCTCCCATCGAGTGTTCACCTTCGTCGCTGGGCTCAATCATAAACC 800  
QY 275 AAAGCGCAAGTGTACTGTTCCAGATGCGCGGGAAGAACG-----ATGGGCAAAAGC 326  
Db 801 CAAGGCAAGTGTACTGTTCCCAAGTCCCGGGGAGAGAACGAGAACCATGGAACAAAGC 860  
QY 327 CTTGAGAGTCCAGAAAACAGGCGTTATACAGTAGTGTGGGACATCGGTCTA 386  
Db 861 CTTGGAGAATCCA--AAAAAGAGAGGCGTTTCAACAGTAGTGTGGACAGGCGCTG 918  
QY 387 ATAGTGAGGAGAACAAATAAGCCAGTGTGTGATTACATTGCCACCTTTGCTGAGGTGC 446  
Db 919 GT-GTGAGGAGCAAAATAAAC--GTGTATTATTATACATTGCTGCTTTGTTGAGGTGC 976  
QY 447 AGGAGTGTAAATGTATATTTTAAAGATGTTGTAGAGG 488  
Db 977 AGGAGTGTAAATGTATATTTTAAAGATGTTGTAGAGG 1018

## RESULT 11

US-09-006-783A-2  
; Sequence 2, Application US/09006783A  
; Patent No. 6297366  
; GENERAL INFORMATION:  
; APPLICANT: Gudkov, Andrey V  
; APPLICANT: Garkavtsev, Igor  
; APPLICANT: Riabowol, Karl  
; TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling  
; TITLE OF INVENTION: Pathway  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
; STREET: 300 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/006,783A  
; FILING DATE: 15-JAN-1998  
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: No. 6297366nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 97,837  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-913-0001  
TELEFAX: 312-913-0002  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2061 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 16..897  
US-09-006-783A-2

Query Match 35.8%; Score 276; DB 3; Length 2061;  
Best Local Similarity 80.8%; Pred. No. 2.8e-68;  
Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;  
QY 2 AAGCGTTCGCGCGCAGCGCAACCTAGAACCGTGAGAACCGTGCGAGCAACCGCGAC 61  
DB 502 AAGCGTTCAGCGCGCAGCGCAACCTAGAACCGTGAGAACCGTGCGAGCAACCGCGAC 560  
QY 62 CCACGACGACGTCACCTCGGCGCAGCGCAACCTAGAACCGTGAGAACCGTGCGAGCAAC 121  
DB 561 CCACGACGACGCGCTCGGCGCAGCGCAACCTAGAACCGTGAGAACCGTGCGAGCAAC 620  
QY 122 GCAGGCTCCATGCGCAAGCGGTAGCGGAGCGGTCCCGCGAGACCTCCCGCATCGACC 181  
DB 621 GAAGCGTCCAAAGCGCAAGCGGCGAGCGGTCCCGCGACCTCCCGCATCGACC 680  
QY 182 CAGCGAGCC-----CTCCTACTGGGAGATGATCCGCTCGGA 217  
DB 681 CAACGACCGACGCTACTGCTGTGCAACAGCGTCTCTTATGGGAGATGATCGGCTGCGA 740  
QY 218 CA---ACGAATGCCCATCGAGTGTTCGCTTCTCGTGTGTGAGTCTCAACCAATAAAC 274  
DB 741 CAACGACGAGTGCCTCATCGAGTGTTCACCTTCTCGTGTGTGAGTCTCAATCAATAAC 800  
QY 275 AAAGCGCAAGTGTACTGTTCCAGATGCGGCGGAAAGAACG-----ATGGCGCAAGC 326  
DB 801 CAAGGCAAGTGTACTGTTCCAGTGTCCAGTGTCCAGTGTCCAGTGTCCAGTGTCCAGT 860  
QY 327 CCTTGAGAACTCCAGAAAAAACAAGGCTTATAACAGTAGTGTGGGAGATGCGTCTA 386  
DB 861 CCTGAGAAATCCA--AAAAAGAGAGGCTTACACAGTAGTGTGGAGAGGCGCTG 918  
QY 387 ATAGTGAGAGAACAAATAAGCCAGTGTGTGATTACATTGCCACCTTGTGAGGTGC 446  
DB 919 GT-GTGAAGGAGCAAAATAAAC--GTGTATTATTATACATTGCTGCTGAGGTGC 976  
QY 447 AGGAAGTGTAAATGTATATTTTAAAGAAATGTTAGAGG 488  
DB 977 AAGGAGTGTAAATGTATATTTTAAAGAAATGTTAGAAAGG 1018

RESULT 12  
US-09-159-871-1  
Sequence 1, Application US/09159871A  
Patent No. 6420136  
GENERAL INFORMATION:  
APPLICANT: RIABOWOL, Karl T.  
TITLE OF INVENTION: METHOD OF MODULATING P53 ACTIVITY  
FILE REFERENCE: 028722-181  
CURRENT APPLICATION NUMBER: US/09/159,871A  
CURRENT FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: US 60/060,138  
PRIOR FILING DATE: 1997-09-26  
PRIOR APPLICATION NUMBER: US 09/006,783

PRIOR FILING DATE: 1998-01-14  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 1  
LENGTH: 2061  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (16)..(897)  
US-09-159-871-1

Query Match 35.3%; Score 272.8; DB 4; Length 2061;  
Best Local Similarity 80.5%; Pred. No. 2.2e-67;  
Matches 420; Conservative 0; Mismatches 62; Indels 40; Gaps 7;  
QY 2 AAGCGTTCGCGCGCAGCGCAACCTAGAACCGTGAGAACCGTGCGAGCAACCGCGAC 61  
DB 502 AAGCGTTCAGCGCGCAGCGCAACCTAGAACCGTGAGAACCGTGCGAGCAACCGCGAC 560  
QY 62 CCACGACGACGTCACCTCGGCGCAGCGCAACCTAGAACCGTGAGAACCGTGCGAGCAAC 121  
DB 561 CCACGACGACGCGGTGCGGCGCACACCCAGAGAGAAAGCCCAAGACCTCCAGAAAGAA 620  
QY 122 GCAGGCTCCATGCGCAAGCGGTAGCGGAGCGGTCCCGCGAGACCTCCCGCATCGACC 181  
DB 621 GAAGCGTCCAAAGCGCAAGCGGCGAGCGGTCCCGCGACCTCCCGCATCGACC 680  
QY 182 CAGCGAGCC-----CTCCTACTGGGAGATGATCCGCTCGGA 217  
DB 681 CAACGACCGACGCTACTGCTGTGCAACAGCGTCTCTTATGGGAGATGATCGGCTGCGA 740  
QY 218 CA---ACGAATGCCCATCGAGTGTTCGCTTCTCGTGTGTGAGTCTCAACCAATAAAC 274  
DB 741 CAACGACGAGTGCCTCATCGAGTGTTCACCTTCTCGTGTGTGAGTCTCAATCAATAAAC 800  
QY 275 AAAGCGCAAGTGTACTGTTCCAGATGCGGCGGAAAGAACG-----ATGGCGCAAGC 326  
DB 801 CAAGGCAAGTGTACTGTTCCAGTGTCCAGTGTCCAGTGTCCAGTGTCCAGTGTCCAGT 860  
QY 327 CCTTGAGAACTCCAGAAAAAACAAGGCTTATAACAGTAGTGTGGGAGATGCGTCTA 386  
DB 861 CCTGAGAAATCCA--AAAAAGAGAGGCTTACACAGTAGTGTGGAGAGGCGCTG 918  
QY 387 ATAGTGAGAGAACAAATAAGCCAGTGTGTGATTACATTGCCACCTTGTGAGGTGC 446  
DB 919 GT-GTGAAGGAGCAAAATAAAC--GTGTATTATTATACATTGCTGCTGAGGTGC 976  
QY 447 AGGAAGTGTAAATGTATATTTTAAAGAAATGTTAGAGG 488  
DB 977 AAGGAGTGTAAATGTATATTTTAAAGAAATGTTAGAAAGG 1018

RESULT 13  
US-09-173-914-6  
Sequence 6, Application US/09173914  
Patent No. 6171857  
GENERAL INFORMATION:  
APPLICANT: Hendrickson, Eric  
TITLE OF INVENTION: A No. 6171857el Leucine Zipper, KARP-1 and  
FILE REFERENCE: B0877/7017/HK  
CURRENT APPLICATION NUMBER: US/09/173,914  
CURRENT FILING DATE: 1998-10-16  
EARLIER APPLICATION NUMBER: 60/064,557  
EARLIER FILING DATE: 1997-10-17  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 6  
LENGTH: 14636  
TYPE: DNA  
ORGANISM: Homo Sapiens  
US-09-173-914-6

Query Match 32.4%; Score 249.8; DB 3; Length 14636;  
Best Local Similarity 82.8%; Pred. No. 1.6e-60;  
Matches 284; Conservative 0; Mismatches 59; Indels 0; Gaps 0;  
  
QY 430 CACCTTGTGCTGAGTGCAGGAGTCTAAATGTATATTTTAAAGAAATGTTTGTAGAGC 489  
DB 9844 CACCTTGGGTAGTGTATTTATATTAAGGCTGCTTGAACCGTTGCACTTGGC 9903  
QY 490 CGGGCGGGTGGCTCAGCGCTGTATCCAGACACTTTGGGAGCGCGGCGGTGGATCA 549  
DB 9904 CAGGCGCGGTGGCTCAGCGCTGTATCCAGACACTTTGGGAGCGCGGCGGTGATCG 9963  
QY 550 CGAGTGCAGGAGATCGAGACCATCTGGCTACAGCGTGAACCCCGCTCTACTTAAAA 609  
DB 9964 TGAGTGCAGGATCGAGACCATCTGGCTACACCGTGAACCCCGCTCTACTTAAAA 10023  
QY 610 TTTAAAAAAAATAGTGGCGGTGGTGGCGGCTGTAGTCCAGCTATTTCGGGAG 669  
DB 10024 TACAAAAAAAATAGCGGCGCATGGTGGTGGCGACCTTTAGTCCAGCTACTTGGGAG 10083  
QY 670 GCTGAGGAGGAGATGGGNTCAACTCGGAGGTGGAGCTTGCANTGAGCCAGGTGCG 729  
DB 10084 GCTGAGATAGGAGATGGGNTGAAACCGGAGCGGAGGTTCAGTGAAGCATGCG 10143  
QY 730 CCACTGCATCCAGCTGGCGGACAGAGCGAGACTCCATCTTA 772  
DB 10144 CCGTGCATCCAGCTGGCGGACAGAGCGAGACTCCATCTCA 10186

RESULT 14  
US-08-888-497-33  
; Sequence 33, Application US/08888497  
; Patent No. 5972677  
; GENERAL INFORMATION:  
; APPLICANT: Tischfield, Jay A.  
; APPLICANT: Seilhamer, Jeffrey J.  
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide  
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences  
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide  
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &  
; ADDRESSEE: Russell PA  
; STREET: 200 East Broward Boulevard  
; CITY: Fort Lauderdale  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 33301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/888,497  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/651,405  
; FILING DATE:  
; APPLICATION NUMBER: US 08/097,354  
; FILING DATE: 26-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Manso, Peter J.  
; REGISTRATION NUMBER: 32,264  
; REFERENCE/DOCKET NUMBER: IN21044-5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 305-527-2498  
; TELEFAX: 305-764-4996  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:

LENGTH: 15328 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-888-497-33  
  
Query Match 32.2%; Score 248.6; DB 2; Length 15328;  
Best Local Similarity 90.8%; Pred. No. 3.6e-60;  
Matches 275; Conservative 0; Mismatches 26; Indels 2; Gaps 1;  
  
QY 470 TAAAGAAATGTTGTAGAGCGCGGCGGTGCTACGCTGTATCCAGACACTTTGGG 529  
DB 5679 TAAAGAAATGTTGTAGAGCGCGGCGGTGCTACGCTGTATCCAGACACTTTGGG 5738  
QY 530 AGCCGAGGCGGTGCGGATCAGGAGTCAAGAGATCGAGACCATCTGGGTAAACCGGTGA 589  
DB 5739 AGCCGAGGCGGCGGATCAGGAGTCAAGAGTCAAGAGATCGAGACCATCTGGGTAAACCGGTGA 5798  
QY 590 AACCCCGTCTCTACTAAAAATCAAAAAAATAGCTGGGCGTGGTGGCGGCGCCCTG 649  
DB 5799 AACCCCGTCTCTACTAAAAAT--ACAAAAAATAGCCGCGGTGATGTTGGCGCCCTG 5856  
QY 650 TAGTCCCGCTATTCGGGAGGCTGAGGAGGAGATGGGNTGAACCTGGAGGTGGAGCT 709  
DB 5857 TAGTCCCGCTATTCGGGAGGCTGAGGAGGAGATGGGNTGAACCTGGAGGTGGAGCT 5916  
QY 710 TGCANTGAGCCAAAGGTGCGGCCACTGCATCCAGCTGGGCGGACAGGAGACTCCATC 769  
DB 5917 TGCAGTGAGCCGAGATTGGCCACTGCATCCCGCTGGGCCACAGAGGAGACTCCGTC 5976  
QY 770 TTA 772  
DB 5977 TCA 5979

RESULT 15  
US-09-362-230-33  
; Sequence 33, Application US/09362230  
; Patent No. 6352849  
; GENERAL INFORMATION:  
; APPLICANT: Tischfield, Jay A.  
; APPLICANT: Seilhamer, Jeffrey J.  
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide  
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences  
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide  
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &  
; ADDRESSEE: Russell PA  
; STREET: 200 East Broward Boulevard  
; CITY: Fort Lauderdale  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 33301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/362,230  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/888,497  
; FILING DATE:  
; APPLICATION NUMBER: US 08/097,354  
; FILING DATE: 26-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Manso, Peter J.  
; REGISTRATION NUMBER: 32,264

REFERENCE/DOCKET NUMBER: IN21044-5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 305-527-2498  
TELEFAX: 305-764-4996  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15328 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-362-230-33

Query Match 32.2%; Score 248.6; DB 4; Length 15328;  
Best Local Similarity 90.8%; Pred. No. 3.6e-60;  
Matches 275; Conservative 0; Mismatches 26; Indels 2; Gaps 1;  
QY 470 TAAAGATGTTGTAGAGCGCGCGGTGGCTCAGCCCTGTAAATCCAGCACTTTGGG 529  
DB 5679 TAAAGATGCTCTTGGCGCGCGGTGGCTCAGCTGTAAATCCAGCACTTTGGG 5738  
QY 530 AGGCGAGGCGTGGATCAGAGGTCAGGAGATCGAGACCATCTGGCTAACACGGTGA 589  
DB 5739 AGGCGAGGCGGCGGATCAGAGGTCAGGAGATCGAGACCATCTGGCTAACACGGTGA 5798  
QY 590 AACCCCGTCTCTACTTAAATAATCAAAAAAATTTAGCTGGGCGTGGTGGCGGCGCTG 649  
DB 5799 AACCCCGTCTCTACTTAAAT - ACATAAAAAATTTAGCGGCGTGGTGGCGGCGCTG 5856  
QY 650 TAGTCCAGCTATTCGGAGGCTAGGCGAGAGATGCGNTGAACTGGGAGGTGGAGCT 709  
DB 5857 TAGTCCAGCTACTCGGAGGCTAGGCGAGAGATGCGNTGAACTGGGAGGCGGAGCT 5916  
QY 710 TGCANTGAGCGAAGGTGCGGCCACTGCACTCCAGCTGGGCGACAGAGCGAGACTCCATC 769  
DB 5917 TGCAGTGAGCGGAGATTGGCCACTGCACTCCGCGCTGGGCCACAGAGCGAGACTCCGTC 5976  
QY 770 TTA 772  
DB 5977 TCA 5979

Search completed: May 6, 2004, 11:51:30  
Job time : 75.9822 secs





Query Match		99.7%; Score 770; DB 4; Length 772;
Best Local Similarity		100.0%; Pred. No. 9.9e-197;
Matches 772; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	AAAGGTTCTCGGCGGAGCGGCAACAACTAGAAACCGTGAGAACCGCTCCAGCAACCGCGA 60
DB	1	AAAGGTTCTCGGCGGAGCGGCAACAACTAGAAACCGTGAGAACCGCTCCAGCAACCGCGA 60
QY	61	CCACGAGCGTACCTCGGCGGAGCGGCAACAACTAGAAACCGCTCCAGCAACCGCGA 120
DB	61	CCACGAGCGTACCTCGGCGGAGCGGCAACAACTAGAAACCGCTCCAGCAACCGCGA 120
QY	121	AGCAGGGCTCCATGGCCCAAGCGTAGCGGAGCGGCTCCCGCGAGACCTCCCATCGACC 180
DB	121	AGCAGGGCTCCATGGCCCAAGCGTAGCGGAGCGGCTCCCGCGAGACCTCCCATCGACC 180
QY	181	CCAGGAGCCCTCTCTATGGGAGATGATCCGCTCGGACAGCAATGCCCATCGAGTGGT 240
DB	181	CCAGGAGCCCTCTCTATGGGAGATGATCCGCTCGGACAGCAATGCCCATCGAGTGGT 240
QY	241	TCCGCTTCTGCTGTGTGAGTCTCAACCAATAACCAAGCGCAAGTGTACTGTTCCAGAT 300
DB	241	TCCGCTTCTGCTGTGTGAGTCTCAACCAATAACCAAGCGCAAGTGTACTGTTCCAGAT 300
QY	301	GCCTGGGAAAGAACGATGGGCAAGCCCTTGAGAGTCCAGAAAAAAGGGCTTATA 360
DB	301	GCCTGGGAAAGAACGATGGGCAAGCCCTTGAGAGTCCAGAAAAAAGGGCTTATA 360
QY	361	ACAGGTAGTTTGGGACATGGTCTAATAGTGAGGAGAACAAATAGCCAGTGTGTGA 420
DB	361	ACAGGTAGTTTGGGACATGGTCTAATAGTGAGGAGAACAAATAGCCAGTGTGTGA 420
QY	421	TTACATTGCCCTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 480
DB	421	TTACATTGCCCTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 480
QY	481	CTTAGAGCGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB	481	CTTAGAGCGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY	541	GTCGGATCACGAGTTCAGGAGATCAGACCATCTGGGTAAACAGGTTGAAACCCCGCTC 600
DB	541	GTCGGATCACGAGTTCAGGAGATCAGACCATCTGGGTAAACAGGTTGAAACCCCGCTC 600
QY	601	TACTATAAATTCAAAAAATTTAGCTGGGCTGGTGGGCGGCGCTGAGTCCAGCT 660
DB	601	TACTATAAATTCAAAAAATTTAGCTGGGCTGGTGGGCGGCGCTGAGTCCAGCT 660
QY	661	ATTGGGAGCTGAGGAGGAGATGGTGAACCTGGGAGTGGAGCTTGCANTGAGCC 720
DB	661	ATTGGGAGCTGAGGAGGAGATGGTGAACCTGGGAGTGGAGCTTGCANTGAGCC 720
QY	721	AAGGTGCGGCCACTGCACTCCAGCTGGCGGACAGAGGAGACTCCATCTTA 772
DB	721	AAGGTGCGGCCACTGCACTCCAGCTGGCGGACAGAGGAGACTCCATCTTA 772

RESULT 2  
AAL37089  
ID AAL37089 standard; DNA; 8487 BP.  
XX  
AC  
XX  
DT  
DT 08-JAN-2002 (first entry)  
XX  
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3454.  
XX  
KW Cytostatic; immunosuppressive; nontropic; neuroprotective; antiviral;  
KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; antitumor;  
KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;  
KW cardiac; gene therapy; cancer; immune disorder; cardiovascular disorder;  
KW neurological disease; infection; human; secreted protein;

KW	musculoskeletal system; ds.
XX	
OS	Homo sapiens.
XX	
FN	WC200155367-Al.
XX	
PD	02-AUG-2001.
XX	
PF	17-JAN-2001; 2001WO-US001338.
XX	
PR	31-JAN-2000; 2000US-0179065P.
PR	04-FEB-2000; 2000US-0180628P.
PR	24-FEB-2000; 2000US-0184664P.
PR	02-MAR-2000; 2000US-0186350P.
PR	16-MAR-2000; 2000US-0189874P.
PR	17-MAR-2000; 2000US-0190076P.
PR	18-APR-2000; 2000US-0198123P.
PR	19-MAY-2000; 2000US-0205515P.
PR	07-JUN-2000; 2000US-0209467P.
PR	28-JUN-2000; 2000US-0214886P.
PR	30-JUN-2000; 2000US-0215135P.
PR	07-JUL-2000; 2000US-0216647P.
PR	07-JUL-2000; 2000US-0216880P.
PR	11-JUL-2000; 2000US-0217487P.
PR	11-JUL-2000; 2000US-0217496P.
PR	14-JUL-2000; 2000US-0218290P.
PR	26-JUL-2000; 2000US-0220363P.
PR	26-JUL-2000; 2000US-0220964P.
PR	14-AUG-2000; 2000US-0224518P.
PR	14-AUG-2000; 2000US-0224519P.
PR	14-AUG-2000; 2000US-0225213P.
PR	14-AUG-2000; 2000US-0225214P.
PR	14-AUG-2000; 2000US-0225266P.
PR	14-AUG-2000; 2000US-0225267P.
PR	14-AUG-2000; 2000US-0225268P.
PR	14-AUG-2000; 2000US-0225270P.
PR	14-AUG-2000; 2000US-0225477P.
PR	14-AUG-2000; 2000US-0225757P.
PR	14-AUG-2000; 2000US-0225758P.
PR	14-AUG-2000; 2000US-0225759P.
PR	18-AUG-2000; 2000US-0228279P.
PR	22-AUG-2000; 2000US-0228681P.
PR	22-AUG-2000; 2000US-0228686P.
PR	22-AUG-2000; 2000US-0227182P.
PR	23-AUG-2000; 2000US-0227009P.
PR	30-AUG-2000; 2000US-0228924P.
PR	01-SEP-2000; 2000US-0229287P.
PR	01-SEP-2000; 2000US-0229287P.
PR	01-SEP-2000; 2000US-0229344P.
PR	01-SEP-2000; 2000US-0229345P.
PR	05-SEP-2000; 2000US-0229509P.
PR	05-SEP-2000; 2000US-0229513P.
PR	06-SEP-2000; 2000US-0230437P.
PR	06-SEP-2000; 2000US-0230438P.
PR	08-SEP-2000; 2000US-0231242P.
PR	08-SEP-2000; 2000US-0231243P.
PR	08-SEP-2000; 2000US-0231244P.
PR	08-SEP-2000; 2000US-0231413P.
PR	08-SEP-2000; 2000US-0231414P.
PR	08-SEP-2000; 2000US-0232080P.
PR	08-SEP-2000; 2000US-0232081P.
PR	12-SEP-2000; 2000US-0231968P.
PR	14-SEP-2000; 2000US-0232397P.
PR	14-SEP-2000; 2000US-0232398P.
PR	14-SEP-2000; 2000US-0232399P.
PR	14-SEP-2000; 2000US-0232400P.
PR	14-SEP-2000; 2000US-0232401P.
PR	14-SEP-2000; 2000US-0233063P.
PR	14-SEP-2000; 2000US-0233064P.
PR	14-SEP-2000; 2000US-0233065P.
PR	21-SEP-2000; 2000US-0234223P.
PR	21-SEP-2000; 2000US-0234274P.
PR	25-SEP-2000; 2000US-0234997P.

PR	25-SEP-2000;	2000US-0234998P.	XX	(HUMA-) HUMAN GENOME SCI INC.
PR	26-SEP-2000;	2000US-0235484P.	XX	
PR	27-SEP-2000;	2000US-0235834P.	XX	Rosen CA, Barash SC, Ruben SM;
PR	29-SEP-2000;	2000US-0235836P.	XX	
PR	29-SEP-2000;	2000US-0236327P.	XX	WPI; 2001-451937/48.
PR	29-SEP-2000;	2000US-0236367P.	XX	
PR	29-SEP-2000;	2000US-0236368P.	XX	Isolated polypeptide for treating, preventing and/ or prognosing
PR	29-SEP-2000;	2000US-0236369P.	PT	disorders related to the musculoskeletal system including musculoskeletal
PR	29-SEP-2000;	2000US-0236370P.	PT	cancers and also for testing and detection e.g. diagnosis.
PR	02-OCT-2000;	2000US-0236802P.	XX	
PR	02-OCT-2000;	2000US-0237037P.	XX	Example 2; SEQ ID NO 3454; 781pp + Sequence Listing; English.
PR	02-OCT-2000;	2000US-0237038P.	XX	
PR	02-OCT-2000;	2000US-0237039P.	XX	
PR	13-OCT-2000;	2000US-0237040P.	XX	The invention relates to novel genes (AAU34669-AAU37666) and proteins
PR	13-OCT-2000;	2000US-0239933P.	CC	(ABB03087-ABB04109) associated with the musculoskeletal system useful for
PR	20-OCT-2000;	2000US-0239937P.	CC	preventing, treating or ameliorating medical conditions e.g. by protein
PR	20-OCT-2000;	2000US-0240960P.	CC	or gene therapy. The genes are isolated from a range of human tissues
PR	20-OCT-2000;	2000US-0240966P.	CC	disclosed in the specification. The nucleic acids, proteins, antibodies
PR	20-OCT-2000;	2000US-0242211P.	CC	and (ant)agonists are useful in the diagnosis, treatment and prevention
PR	20-OCT-2000;	2000US-0241785P.	CC	of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the
PR	20-OCT-2000;	2000US-0241786P.	CC	lung, or urogenital; (b) immune disorders e.g. Addison's disease,
PR	20-OCT-2000;	2000US-0241808P.	CC	adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,
PR	20-OCT-2000;	2000US-0241809P.	CC	allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
PR	20-OCT-2000;	2000US-0241826P.	CC	diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
PR	01-NOV-2000;	2000US-0244617P.	CC	arthritis and ulcerative colitis; (c) cardiovascular disorders such as
PR	08-NOV-2000;	2000US-0246474P.	CC	myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g.
PR	08-NOV-2000;	2000US-0246475P.	CC	cerebral anoxia and epilepsy; and (f) infectious diseases such as viral,
PR	08-NOV-2000;	2000US-0246476P.	CC	bacterial, fungal and parasitic infections. Note: the sequence data for
PR	08-NOV-2000;	2000US-0246477P.	CC	this patent did not form part of the printed specification, but was
PR	08-NOV-2000;	2000US-0246478P.	CC	obtained in electronic format directly from WIPO at
PR	08-NOV-2000;	2000US-0246523P.	CC	ftp.wipo.int/pub/published_pct_sequences
PR	08-NOV-2000;	2000US-0246524P.	XX	
PR	08-NOV-2000;	2000US-0246525P.	XX	Sequence 8487 BP; 1948 A; 1987 C; 2408 G; 2144 T; 0 U; 0 Other;
PR	08-NOV-2000;	2000US-0246526P.	XX	
PR	08-NOV-2000;	2000US-0246527P.	XX	
PR	08-NOV-2000;	2000US-0246528P.	XX	
PR	08-NOV-2000;	2000US-0246532P.	XX	
PR	08-NOV-2000;	2000US-0246609P.	XX	
PR	08-NOV-2000;	2000US-0246610P.	XX	
PR	08-NOV-2000;	2000US-0246611P.	XX	
PR	17-NOV-2000;	2000US-0249207P.	QY	2 AAGCGTTCTCGGCGGAGCGCAACACTAGAACCGGTGAGAACGGTCCAGCAACCGCGAC 61
PR	17-NOV-2000;	2000US-0249208P.	Db	5538 AAGCGTCTACGGCGGAGCGCAACACGAGAACCGGTGAGAACGGTCCAGCAACCGCA- 6596
PR	17-NOV-2000;	2000US-0249209P.	QY	62 CCACGACGAGCTCACCTCGGGCACGCCCAAGAGAGAAAGCCCGAGACCTCTAAGAGAA 121
PR	17-NOV-2000;	2000US-0249210P.	Db	6597 CCACGACGAGCGGCGCTCGGGCACACCCCAAGAGAGAAAGGCGCAAGACCTCCAAGAAGAA 6656
PR	17-NOV-2000;	2000US-0249211P.	QY	122 GCAGGGCTCCATGGCCCAAGCGGTAGCGGAGCGGTCCCGGAGAGCTCCCATCGACCC 181
PR	17-NOV-2000;	2000US-0249212P.	Db	6657 GAAGCGCTCCAGGCCAAGCGGAGCGGAGGCGTCCCTTGGGAGATGATGGGTGCGA 6716
PR	17-NOV-2000;	2000US-0249214P.	QY	182 CAGCGAGCC-----CTCTACTGGAGATGATCGGTGCGA 217
PR	17-NOV-2000;	2000US-0249218P.	Db	6717 CAACGAACCCACGCTACTGTCTGTGCAACACGAGTCTCTATGGGAGATGATGGGTGCGA 6776
PR	17-NOV-2000;	2000US-0249244P.	QY	218 CA---AGCAATGCCCATCGAGTGGTTCGGTCTCTGTGTGAGTCTCAACCAATAAAC 274
PR	17-NOV-2000;	2000US-0249245P.	Db	6777 CAACGACGAGTGGCCCATCGAGTGGTTCACACTTCTCGTGGGGCTCAATCATTAAC 6836
PR	17-NOV-2000;	2000US-0249297P.	QY	275 AAAGCGCAAGTGGTACTGTTTCCAGATGCGGGGGAAGAAAGACG-----ATGGGCAAGC 326
PR	17-NOV-2000;	2000US-0249300P.	Db	6837 CAAGGCAAGTGGTACTGTTCCCAAGTGGCGGGGAGAACGAGAGACCATGGACAAGC 6896
PR	01-DEC-2000;	2000US-0250160P.	QY	327 CTTGAGAGTCCAGAAAAAAGACGGCTTATAACAGTAGTTTGGGACATGGCTCTA 386
PR	05-DEC-2000;	2000US-0251030P.	Db	6897 CTTGGAGAAATCCA--AAAAAGAGAGGGGCTTACACAGTAGTTTGTGGAGGGCCCTG 6954
PR	06-DEC-2000;	2000US-0251479P.	QY	387 ATAGTGAGGAGAAACAAATAAGCCAGTGTGTGATTACATTGCCACTTGTGTAGGTGC 446
PR	08-DEC-2000;	2000US-0251868P.	Db	6955 GT-GTGGAGGAGCAAAATAAAC-GTGTATTATTATTACATTGCTGCTTTGTGAGGTGC 7012
PR	08-DEC-2000;	2000US-0251869P.	QY	447 AGGAAGTGTAATATATATTTTAAAGATGTGTAGAGG 488
PR	08-DEC-2000;	2000US-0251990P.	Db	7013 AAGGAGTGTAAATGTATATTTTAAAGATGTGTAGTAAAG 7054
PR	11-DEC-2000;	2000US-0254097P.		
PR	05-JAN-2001;	2001US-0259678P.		

## RESULT 3

ABX60077

ID ABX60077 standard; cDNA; 8487 BP.

XX AC ABX60077;

XX DT 26-FEB-2003 (first entry)

XX DE

XX cDNA encoding novel human musculoskeletal system antigen #2421.

Gene; ss; musculoskeletal system antigen; cancer; metastasis; re-vascularisation; thrombosis; arteriosclerosis; mineral content; cardiovascular condition; wound; injury; burn; angiogenesis; ulcer; post-operative tissue repair; limb regeneration; neuronal growth; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; AIDS-related complex; chondrocyte growth; bone regeneration; periodontal regeneration; tissue transport; bone graft; skin aging; keratinocyte growth; hair loss; melanocyte growth; cell proliferation; cell growth; organ transplant; cell differentiation; body height; weight; hair colour; eye colour; skin; percentage of adipose tissue; pigmentation; cosmetic surgery; metabolism; biorhythm; cardiac rhythm; depression; tendency for violence; pain; reproductive capability; hormone level; endocrine level; appetite; libido; memory; stress; storage capability; fat content; lipid content; protein content; carbohydrate content; vitamin content; cofactor content; nutritional component.

XX KW Homo sapiens.

XX OS

XX PN

XX PD

XX 10-OCT-2002.

XX 17-JAN-2001; 2001US-00764877.

XX 31-JAN-2000; 2000US-0179065P.

XX 04-FEB-2000; 2000US-0180628P.

XX 28-JUN-2000; 2000US-0214986P.

XX 07-JUL-2000; 2000US-0215647P.

XX 07-JUL-2000; 2000US-0216880P.

XX 11-JUL-2000; 2000US-0217487P.

XX 11-JUL-2000; 2000US-0217496P.

XX 14-JUL-2000; 2000US-0218290P.

XX 26-JUL-2000; 2000US-0220963P.

XX 14-AUG-2000; 2000US-0224518P.

XX 14-AUG-2000; 2000US-0224519P.

XX 14-AUG-2000; 2000US-0225268P.

XX 14-AUG-2000; 2000US-0225270P.

XX 14-AUG-2000; 2000US-0225447P.

XX 14-AUG-2000; 2000US-0225757P.

XX 22-AUG-2000; 2000US-0225758P.

XX 30-AUG-2000; 2000US-0228924P.

XX 01-SEP-2000; 2000US-0229287P.

XX 01-SEP-2000; 2000US-0229343P.

XX 01-SEP-2000; 2000US-0229344P.

XX 05-SEP-2000; 2000US-0229509P.

XX 08-SEP-2000; 2000US-0231133P.

XX 21-SEP-2000; 2000US-0234223P.

XX 23-SEP-2000; 2000US-0234977P.

XX 27-SEP-2000; 2000US-0235834P.

XX 29-SEP-2000; 2000US-0236327P.

XX 29-SEP-2000; 2000US-0236367P.

XX 29-SEP-2000; 2000US-0236368P.

XX 29-SEP-2000; 2000US-0236369P.

XX 29-SEP-2000; 2000US-0236370P.

PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
PR 02-OCT-2000; 2000US-0237040P.  
PR 13-OCT-2000; 2000US-0239935P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241805P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.

(ROSE/) ROSEN C A.

(RUBE/) RUBEN S M.

(BARA/) BARASH S C.

Rosen CA, Ruben SM, Barash SC;

WPI; 2003-128199/12.

XX Isolated nucleic acid molecules encoding musculoskeletal system  
PT associated polypeptides, useful for detecting disorders, e.g. cancer.

PS Disclosure; SEQ ID NO 3454; 321pp; English.

XX The invention describes an isolated nucleic acid molecule comprising a  
CC sequence encoding musculoskeletal system associated polypeptides useful  
CC for detecting disorders, e.g. cancer or cancer metastases, in animals or  
CC humans. The nucleic acid stimulates re-vascularisation of ischaemic  
CC tissues associated with conditions such as thrombosis, arteriosclerosis,  
CC and other cardiovascular conditions; treats wounds due to injuries,  
CC burns, post-operative tissue repair, and ulcers; stimulates angiogenesis  
CC and limb regeneration; stimulates neuronal growth; can treat and prevent  
CC neuronal damage occurring in certain disorders or neurodegenerative  
CC conditions, such as, Alzheimer's disease, Parkinson's disease, and AIDS-  
CC related complex; stimulates chondrocyte growth, thus they can be used to  
CC enhance bone and periodontal regeneration and aid in tissue transports or  
CC bone grafts; prevents skin aging due to sunburn by stimulating  
CC keratinocyte growth; prevents hair loss, since FGF family members  
CC activate hair-forming cells and promotes melanocyte growth; stimulates  
CC growth and differentiation of hematopoietic cells and bone marrow cells  
CC when used in combination with other cytokines; maintains organs before  
CC transplantation or for supporting cell culture of primary tissues;  
CC induces tissue of mesodermal origin to differentiate in early embryos;  
CC increases or decreases the differentiation or proliferation of embryonic  
CC stem cells, besides, haematopoietic lineage; modulates mammalian  
CC characteristics, such as, body height, weight, hair colour, eye colour,  
CC skin, percentage of adipose tissue, pigmentation, size, and shape (e.g.,  
CC cosmetic surgery); modulates mammalian metabolism; changes mammal's metal  
CC state or physical state by influencing biorhythms, cardiac rhythms,  
CC depression, tendency for violence, tolerance for pain, reproductive  
CC capabilities, hormonal or endocrine levels, appetite, libido, memory, or  
CC stress; increases or decreases storage capabilities, fat content, lipid,  
CC protein, carbohydrate, vitamins, minerals, cofactors or other nutritional  
CC components. This sequence encodes a novel human musculoskeletal system  
CC antigen. Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from the US patent office at  
CC ftp.segdata.uspto.gov/sequence.html?DocID=20020147140

SQ Sequence 8487 BP; 1948 A; 1987 C; 2408 G; 2144 T; 0 U; 0 Other;

## Query Match

36.0%; Score 277.6; DB 7; Length 8487;

Best Local Similarity 81.0%; Pred. No. 4e-64;

Matches 423; Conservative 0; Mismatches 59; Indels 40; Gaps 7;

OY 2 AAGCGTTCTCGGGGAGCGCAACAACTAGAACCGTGAGAACCGTCCAGCAACCGGAC 61  
|||||

Db 6538 AAGCGCTCAGCGGCGGAGCGCAACACAGAACCGTGAGAACCGTCCAGCAACCGA- 6596  
|||||





QY 62 CCACGACGACGTACCTCGGCGACGCCCAAGGAGAGAAAGCCAGACCTCTAAGAGAA 121  
DB 402 CCACGACGACGCGGCTCGGCGACACCCCAAGGAGAGAGGCGCAAGACCTTCAAGAGAA 461  
QY 122 CGAGGCTCCATGGCCAAAGGGGTACGCGCGAGCGCTCCCGCCAGACCTTCCCGCATCGACCC 181  
DB 462 GAAGCGCTCCAAAGGCCCAAGGGGAGCGAGGCGTCCCGACCTCCCGCATCGACCC 521  
QY 182 CAGCGAGCC-----CTCCTACTGGGAGATGATCCCTCGGA 217  
DB 522 CAACGAACCCACGTACTGTGTGTGCAACAGGTCTCTATGGGAGATGATCGGCTCGGA 581  
QY 218 CA---ACGAATGCCCATCGAGTGTCTCGCTTCTCGTGTGTGATCTTCAACCCATAAAC 274  
DB 582 CAACGACGAGTGCCCATCGAGTGTCTCACTTCTCGTGTGTGGGCTCAATATAAAC 641  
QY 275 AAAGCGCAAGTGTGTACTGTTCAGATGCGGGGGAAGAACG-----ATGGGCAAGC 326  
DB 642 CAAGGCGCAAGTGTGTACTGTCTCCAGTGTGGGGGGAAGAACGAGACCATGGGCAAGC 701  
QY 327 CTTGAGAGTCCAGAAAAAAGAGGCTTATAACAGTGTGTGTGGGAGATGCGTCTA 386  
DB 702 CTTGAGAGTCCAGAAAAAAGAGGCTTATAACAGTGTGTGTGGGAGATGCGTCTA 759  
QY 387 ATAGTGAGAGAACAAATAAGCCAGTGTGTGTGTATACATTCGCCACCTTGTGTAGGTGC 446  
DB 760 GT-GTGAGGAGGACAAATAAAC-GTGTATTATTATACATTCGCTTGTGTAGGTGC 817  
QY 447 AGGAGTGTAAATGTATATTTTAAAGATGTTGTAGAG 488  
DB 818 AAGGAGTGTAAATGTATATTTTAAAGATGTTGTAGAG 859

RESULT 7  
ID AAV62285  
XX AAV62285 standard; cDNA; 1902 BP.  
AC AAV62285;  
XX AAV62285;  
DT 18-JAN-1999 (first entry)  
XX Partial INGI partial cDNA sequence.  
DE INGI gene; p33ING1; human; apoptosis; cell death; breast cancer;  
KW brain tumour; gene therapy; tumour suppressor; ss.  
XX Homo sapiens.  
OS  
FH Key Location/Qualifiers  
FT CDS 109..741  
FT /\*tag= a  
XX  
FN WO9844102-A2.  
XX  
PD 08-OCT-1998.  
XX  
PF 26-MAR-1998; 98WO-CA000277.  
XX  
PR 27-MAR-1997; 97US-00828158.  
XX  
XX (UYTB-) UNIV TECHNOLOGIES INT INC.  
XX  
XX Helbing CC, Riabowol K, Johnston RN, Garkavtsev I;  
XX  
XX WPI; 1998-542700/46.  
XX P-PSDB; AAW79674.  
XX  
PT Modulating eukaryotic apoptosis by increasing p33ING1 activity - using  
PT p33ING1 derivatives, to induce apoptosis in cancer cells, and in the  
PT investigation of apoptotic pathways.  
XX  
XX Example 2; Fig 2; 66pp; English.  
PS

XX This is the nucleotide sequence of a human INGI (Inhibitor of Growth)  
CC partial cDNA clone that codes for a p33ING1 polypeptide (see AAW79674),  
CC a novel inhibitor of cell growth and a candidate tumour suppressor. INGI  
CC is a new gene that is expressed in normal mammary epithelial cells, but  
CC which is expressed only at lower levels in several cancerous mammary  
CC epithelial cell lines and is not expressed in many primary brain tumours.  
CC To isolate INGI, a subtractive hybridisation of breast cancer cell line  
CC cDNAs was performed with cDNA from normal mammary epithelial cells, and  
CC subtracted cDNAs were cloned into retrovirus vector pLNCX. Following  
CC passage through a packaging line, normal mouse mammary epithelial cells  
CC were infected, and infected cells were injected into nude mice. Putative  
CC transforming fragments from tumours were isolated by PCR (see AAV62290-  
CC 91) and subcloned into LNCX. An INGI fragment was obtained and used to  
CC screen normal human fibroblast and HeLa cell cDNA libraries. 2 Clones  
CC were sequenced to obtain the partial INGI sequence. The complete cDNA  
CC sequence (see AAV62292) was obtained by RACE. A claimed method to  
CC potentiate apoptosis in a eukaryotic cell involves administering an  
CC active p33ING1 peptide or an oligonucleotide encoding such as a peptide.  
CC A claimed method for inhibiting apoptosis in a eukaryotic cell involves  
CC administering an antisense oligonucleotide. Also claimed are a method for  
CC determining the apoptotic characteristics of a eukaryotic cell, an assay  
CC for determining the level of p33ING1 activity in a eukaryotic cell, and  
CC an isolated eukaryotic cell substantially free of p33ING1 biological  
CC activity. The invention discloses INGI derivatives or variants that may  
CC be used to induce apoptosis in eukaryotic cancer cells  
XX  
SQ Sequence 1902 BP; 574 A; 390 C; 462 G; 476 T; 0 U; 0 Other;  
Query Match 35.8%; Score 276; DB 2; Length 1902;  
Best Local Similarity 80.8%; Pred. No. 6.6e-64;  
Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;  
QY 2 AAGGTTCTCGGCGGAGCGCAACACTAGAACCTGTAGAACCGCTCCAGACCGCGAC 61  
DB 343 AAGCGCTCACGCGCGAGCGCAACACGAGAACCGTGAGAACGCGTCCAGACACCA- 401  
QY 62 CCACGACGACGTCACTCGGCGCACGCCCAAGAGAGAGAAAGCCAGACCTCTAAGAGAA 121  
DB 402 CCACGACGACGCGCGCTCGGCGCACCCCAAGAGAGAGAGGCGCAAGACCTCCAGAGAA 461  
QY 122 GCAGGGCTCATGGCCCAAGCGGTAGCGGAGAGGCTCCCGCGAGACCTCCCATCGACCC 181  
DB 462 GAAGCGCTCCAAAGGCCCAAGCGGAGGAGGCGTCCCGCGAGACCTCCCATCGACCC 521  
QY 182 CAGCGAGCC-----CTCCTACTGGGAGATGATCGCTGCGA 217  
DB 522 CAACGAACCCACGTACTGTCTGTGCAACAGGTCTCTATGGGAGATGATCGGCTGCGA 581  
QY 218 CA---ACGAATGCCCATCGAGTGTTCGCTTCTCGTGTGTGAGTCTCAACCATTAACC 274  
DB 582 CAACGACGAGTGTGCCCATCGAGTGTTCACACTTCTCGTGTGGGCTCAATATAAAC 641  
QY 275 AAAGCGCAAGTGTGTACTGTTCAGATGCGGGGAAAGAACG-----ATGGGCAAGC 326  
DB 642 CAAGGCAAGTGTGTACTGTCTCCAGTGTGGGGGAGAGACGAGAACCATGAGCAAGC 701  
QY 327 CTTGAGAGTCCAGAAAAAAGAGGCTTATAACAGGTTATTAACAGGTTGTGGGAGATGCGTCTA 386  
DB 702 CTTGAGAGTCCAGAAAAAAGAGGCTTATAACAGGTTATTAACAGGTTGTGGGAGATGCGTCTA 759  
QY 387 ATAGTGAGAGAACAAATAAGCCAGTGTGTGTGTATACATTCGCCACCTTGTGTAGGTGC 446  
DB 760 GT-GTGAGGAGGACAAATAAAC-GTGTATTATTATACATTCGCTTGTGTAGGTGC 817  
QY 447 AGGAGTGTAAATGTATATTTTAAAGATGTTGTAGAG 488  
DB 818 AAGGAGTGTAAATGTATATTTTAAAGATGTTGTAGAG 859  
RESULT 8  
AAD46126  
ID AAD46126 standard; cDNA; 1905 BP.

XX AAD46126;  
XX 27-DEC-2002 (first entry)  
XX Human tumour suppressor protein encoding cDNA.  
XX Human; tumour suppressor protein; cell proliferative disorder; vaccine;  
XX inflammation; brain cancer; adenocarcinoma; cervix cancer; bone cancer;  
XX apoptosis; leukaemia; lymphoma; melanoma; therapy; chromosome 13; gene;  
XX ss.  
XX Homo sapiens.  
XX Key  
XX 5'UTR  
XX Location/Qualifiers  
XX 1..160  
XX /\*tag= a  
XX 161..1036  
XX /\*tag= b  
XX /product= "Human tumour suppressor protein"  
XX 1037..1905  
XX /\*tag= c  
XX  
XX WO200268468-A2.  
XX  
XX 06-SEP-2002.  
XX  
XX 05-FEB-2002; 2002WO-US003235.  
XX  
XX 27-FEB-2001; 2001US-00793706.  
XX  
XX (PEKE ) PE CORP NY.  
XX  
XX Gong F, Yan C;  
XX  
XX MPI; 2002-698658/75.  
XX P-PSDB; AAE28633.  
XX  
XX New human tumor suppressor proteins, useful for developing human  
XX therapeutic agents, or preventing or treating inflammation, or disorders  
XX associated with cell proliferation, e.g. bone cancer, brain cancer,  
XX leukemia or lymphoma.  
XX  
XX Claim 4; Fig 1; 200pp; English.  
XX  
XX The invention relates to human tumour suppressor polypeptides and  
XX polynucleotides. Sequences of the invention are useful for diagnosing,  
XX preventing or treating inflammation, or disorders associated with cell  
XX proliferation and apoptosis e.g. bone cancer, brain cancer, cervix  
XX cancer, adenocarcinoma, leukaemia, lymphoma or melanoma. They are  
XX particularly useful as models for developing human therapeutic targets,  
XX identifying therapeutic proteins, or serving as targets for the  
XX development of human therapeutic agents that modulate tumour suppressor  
XX protein activity in cells and tissues that express the tumour suppressor  
XX protein. Polypeptides of the invention are used for identifying agents  
XX that modulate their activity. They are useful for raising antibodies or  
XX eliciting an immune response; as a reagent in assays designed to  
XX quantitatively determine levels of the protein (or its binding partner or  
XX ligand) in biological fluids; or as markers for tissues in which the  
XX corresponding protein is preferentially expressed. The invention is also  
XX used as vaccines. The present sequence is human tumour suppressor protein  
XX encoding cDNA. The tumour suppressor gene is located on chromosome 13  
XX  
XX Sequence 1905 BP; 532 A; 428 C; 528 G; 417 T; 0 U; 0 Other;  
XX  
XX Query Match 35.8%; Score 276; DB 6; Length 1905;  
XX Best Local Similarity 80.8%; Pred. No. 6 6e-64;  
XX Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;  
XX  
XX 2 AACGGTTCGGCGGAGGCGGCAAACTAGAACCGGTGAGACGGCTCAGGACCGGAC 61  
XX  
XX 638 AAGGGCTACGGCGGCGGAGGCGGCAAACTAGAACCGGTGAGACCGGTGAGACCGG 696

QY 62 CCACGACGAGCTCACCTCGGGCCACGCCAAGGAGAGAAAGCCACGACCTCTTAGAAGAA 121  
DB 697 CCACGACGACGGCGCTTCGGGCAACCCAAAGGAGAGAGAGCCCAAGACCTTCCAAAGAA 756  
QY 122 GCAGGGCTCCATGGCCAAAGCGGTAGCGGAGGAGGCTCCCGGAGAGCTCCCTCCCATCGACCC 181  
DB 757 GAACGGCTCCAAAGGCCAAGCGGAGGAGGCGTCCCTGCGGACCTCCCATCGACCC 816  
QY 182 CAGCGAGCC-----CTCCTACTGGGAGATGATCCGCTCGGA 217  
DB 817 CAACGAACCCACGCTACTGTCTGTGCAACCAAGGTCTCTATGGGAGATGATCGGCTCGGA 876  
QY 218 CA---ACGAATGCCCATCGAGTGGTTCGGTCTCGTGTGTGAGTCTCAACCATAAACC 274  
DB 877 CAACGACGAGTGGCCCATCGAGTGGTTCCTCTCTCTGCTGGGGGTCTCATATAAAC 936  
QY 275 AAAGCGCAAGTGGTACTGTTCCAGATCCCGGGGAAAGAACG-----ATGGGCAAGC 326  
DB 937 CAAGGGCAAGTGGTACTGTTCCAAAGTCCCGGGGAGAGACGAGAGACCATGGACAAAGC 996  
QY 327 CTTGAGAGTCCAGAAAACAGGGCTTAAACAGGTAGTTTGGGACATCGCTTA 386  
DB 997 CCTGGAGAAATCCA--AAAAAGAGAGGGCTTACCAACAGGTAGTTTGGACAGGCGCTG 1054  
QY 387 ATAGTGAGGAGAAACAAATAAGCCAGTGTGTGATTATTCATTCGCCACCTTTGCTGAGTGC 446  
DB 1055 GT-GTGGAGGAGCAAAATAAAC--GTGATTTATTATTCATTCGCTTGTGAGGTGC 1112  
QY 447 AGGAAGTGTAAATGATATATTTTAAAGAAATGTTGTTAGAGG 488  
DB 1113 AAGGAGTGTAAATGATATATTTTAAAGAAATGTTAGAAAGG 1154  
  
RESULT 9  
AAI69652  
ID AAT69652 standard; cDNA; 2061 BP.  
XX AC AAT69652;  
XX DT 27-AUG-1997 (first entry)  
XX DE Tumour suppressor gene INGI full-length cDNA.  
XX KW Tumour suppressor gene; INGI; p3ING1; breast cancer; brain cancer;  
XX diagnosis; gene therapy; ss.  
XX OS Homo sapiens.  
XX Key Location/Qualifiers  
XX CDS 16..900  
XX primer\_bind complement(474..494)  
XX /\*tag= a  
XX /\*tag= b  
XX /note= "direct primer 1"  
XX primer\_bind complement(763..782)  
XX /\*tag= c  
XX /note= "direct primer 2"  
XX primer\_bind 857..876  
XX /\*tag= d  
XX /note= "reverse primer 3"  
XX primer\_bind 890..900  
XX /\*tag= e  
XX /note= "reverse primer 4"  
XX  
XX WO9721809-A1.  
XX PD 19-JUN-1997.  
XX PF 06-DEC-1996; 96WO-CA000819.  
XX PR 08-DEC-1995; 95US-00569721.  
XX 15-NOV-1996; 96US-00751230.



PA	(UYTE-) UNIV TECHNOLOGIES INT INC.
XX	Garkavstev I, Riabowol K;
PI	WPI; 1997-332781/30.
DR	P-PSDB; AAW18119.
XX	Isolated tumour suppressor gene, INGI - useful to develop products for
PT	inhibiting or increasing cell proliferation, in particular for treatment
FT	of diagnosis of cancer.
XX	Claim 11; Fig 3; 63pp; English.
XX	A full-length cDNA clone (AAT69652), designated INGI, codes for a novel
CC	33 kDa tumour suppressor protein p33INGI (AAW19119), formerly p33IG1,
CC	that is a potent inhibitor of cell growth. A partial clone (AAT69651) was
CC	isolated by subtractive hybridisation between normal mammary and
CC	transformed epithelial cDNAs, isolation of an antisense INGI cDNA insert
CC	that caused increased cell proliferation, and use of the insert to screen
CC	normal human fibroblast and HeLa cDNA libraries. The complete INGI
CC	sequence was then obd. by 5'RACE. INGI is localised to the 13q33-34
CC	chromosome region, to which a number of human cancers have been mapped.
CC	INGI nucleic acids can be used in the diagnosis of breast cancer; a
CC	decreased level of INGI mRNA indicates cancerous cells. They can also be
CC	used in gene therapy methods to block the proliferation of cancer cells
XX	Sequence 2061 BP; 602 A; 439 C; 515 G; 505 T; 0 U; 0 Other;
SQ	Query Match 35.8%; Score 276; DB 2; Length 2061;
	Best Local Similarity 80.8%; Pred. No. 6.7e-64;
	Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;
QY	2 AAGCGTCTCGGCGCAGCGCAACACTAGAACCCTGTGAAGACCGCTCCAGCAACCGGCAC 61
Db	502 AAGCGTCTCACGGCGGCGAGCGCAACAACAGAGACCGGTGAGACGCCGTCCAGCACACCA- 560
QY	62 CCACGACGACGTCACCTCGGCGCAGCGCCCAAGGAGAGAACGCCACGACTCTTAAGAAGAA 121
Db	561 CCACGACGACGCGGCTCTCGGCGCAGCGCCCAAGGAGAGAACGCCACGACTCTTAAGAAGAA 620
QY	122 GCAGGGCTCATGCGCAAGCGTAGCGGAGGCGTCCCAGAGACCTCCCCATCGACCC 181
Db	621 GAAGCGCTCCAGGCCAGCGGAGCGAGAGGGTGCTCCCTCGGACCTCCCATGACCC 680
QY	182 CAGCGAGCC-----CTCCTACTGGGAGATGATCCGCTGCGA 217
Db	681 CAACGACCCACGCTACTGCTGTGCAACACGAGTCTCCTATGGGAGAGATGATCGGCTGGA 740
QY	218 CA---AGCATGCCCATCGAGTGGTTCGCTCTCTGCTGTGAGTCTCAACCATATAACC 274
Db	741 CAACGACGATGTCCTCCATCGAGTGGTTTCACTTCTGCTGCGGTGCTCATATAACC 800
QY	275 AAAGCGCAAGTGTGCTATTCTCCAGATGCCGGGAAAAGAACG-----ATGGGCAAGC 326
Db	801 CAAGGCGAAGTGTGCTATTCTCCAAAGTCCCGGGGAGAGACGAGACCATGGAACAAAGC 860
QY	327 CCTGTGAGAGTCCAGAAAAACAGGGCTTATAACAGTAGTTTGGGACATGCGTCTA 386
Db	861 CTGAGAAATCCA--AAAAAGAGAGGCTTACACAGTAGTTTGTGACAGGGGCGCTG 918
QY	387 ATAGTAGGAGAAACAAATAAGCCAGTGTCTTGAATTAATGTCATGTCACCTTTGTGAGGTGC 446
Db	919 GT-GTGAGGAGGACAAAATAAACCG-GTGTATTTATTACATTTGCTGCTTTGTTGAGGTGC 976
QY	447 AGGAAGTGTAAAGTATATTTTTAAAGATGTTGTTAGAGG 488
Db	977 AAGAGTGTAAAGTATATTTTTAAAGATGTTAGAAAGG 1018
RESULT 10	
AAV62292	
YY	AAV62292 standard; cDNA; 2061 BP.
YY	AC AAV62292;
DT	18-JAN-1999 (first entry)
DE	Human INGI full-length cDNA sequence.
KX	INGI gene; p33INGI; human; apoptosis; cell death; breast cancer;
KW	brain tumour; gene therapy; tumour suppressor; ss.
XX	Homo sapiens.
OS	Key Location/Qualifiers
PH	16..900
FT	/*tag= a
XX	WO9844102-A2.
PN	08-OCT-1998.
XX	26-MAR-1998; 98WO-CA000277.
PF	27-MAR-1997; 97US-00828158.
XX	(UYTE-) UNIV TECHNOLOGIES INT INC.
PA	Felbing CC, Riabowol K, Johnston RN, Garkavtsev I;
XX	WPI; 1998-542700/46.
XX	P-PSDB; AAW79675.
DR	Modulating eukaryotic apoptosis by increasing p33INGI activity - using
XX	p33INGI derivatives, to induce apoptosis in cancer cells, and in the
PT	investigation of apoptotic pathways.
FT	Claim 7; Fig 3; 66pp; English.
XX	This is the nucleotide sequence of a human INGI (Inhibitor of Growth)
CC	that codes for a p33INGI polypeptide (see AAW79675), a novel inhibitor
CC	of cell growth and a candidate tumour suppressor. INGI is a new gene that
CC	is expressed in normal mammary epithelial cells, but which is expressed
CC	only at lower levels in several cancerous mammary epithelial cell lines
CC	and is not expressed in many primary brain tumors. To isolate INGI, a
CC	subtractive hybridisation of breast cancer cell line cDNAs was performed
CC	with cDNA from normal mammary epithelial cells, and subtracted cDNAs were
CC	cloned into retrovirus vector pLNCX. Following passage through a
CC	packaging line, normal mouse mammary epithelial cells were infected, and
CC	infected cells were injected into nude mice. Putative transforming
CC	fragments from tumours were isolated by PCR (see AAV62290-91) and
CC	subcloned into LNCX. An INGI fragment was obtained and used to screen
CC	normal human fibroblast and HeLa cell cDNA libraries. 2 Clones were
CC	sequenced to obtain a partial INGI sequence (see AAV62285). The complete
CC	cDNA sequence was then obtained by RACE. A claimed method to potentiate
CC	apoptosis in a eukaryotic cell involves administering an active p33INGI
CC	peptide or an oligonucleotide encoding such as a peptide. A claimed
CC	method for inhibiting apoptosis in a eukaryotic cell involves
CC	determining the apoptotic characteristics of a eukaryotic cell, an assay
CC	for determining the level of p33INGI activity in a eukaryotic cell, and
CC	an isolated eukaryotic cell substantially free of p33INGI biological
CC	activity. The invention discloses INGI derivatives or variants that may
CC	be used to induce apoptosis in eukaryotic cancer cells
XX	Sequence 2061 BP; 602 A; 439 C; 515 G; 505 T; 0 U; 0 Other;
SQ	Query Match 35.8%; Score 276; DB 2; Length 2061;
	Best Local Similarity 80.8%; Pred. No. 6.7e-64;
	Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;
QY	2 AAGCGTCTCGGCGCAGCGCAACACTAGAACCCTGTGAAGACCGCTCCAGCAACCGGCAC 61
Db	502 AAGCGTCTCACGGCGGCGAGCGCAACAACAGAGACCGGTGAGACGCCGTCCAGCACACCA- 560
QY	62 CCACGACGACGTCACCTCGGCGCAGCGCCCAAGGAGAGAACGCCACGACTCTTAAGAAGAA 121
Db	561 CCACGACGACGCGGCTCTCGGCGCAGCGCCCAAGGAGAGAACGCCACGACTCTTAAGAAGAA 620
QY	122 GCAGGGCTCATGCGCAAGCGTAGCGGAGGCGTCCCAGAGACCTCCCCATCGACCC 181
Db	621 GAAGCGCTCCAGGCCAGCGGAGCGAGAGGGTGCTCCCTCGGACCTCCCATGACCC 680
QY	182 CAGCGAGCC-----CTCCTACTGGGAGATGATCCGCTGCGA 217
Db	681 CAACGACCCACGCTACTGCTGTGCAACACGAGTCTCCTATGGGAGAGATGATCGGCTGGA 740
QY	218 CA---AGCATGCCCATCGAGTGGTTCGCTCTCTGCTGTGAGTCTCAACCATATAACC 274
Db	741 CAACGACGATGTCCTCCATCGAGTGGTTTCACTTCTGCTGCGGTGCTCATATAACC 800
QY	275 AAAGCGCAAGTGTGCTATTCTCCAGATGCCGGGAAAAGAACG-----ATGGGCAAGC 326
Db	801 CAAGGCGAAGTGTGCTATTCTCCAAAGTCCCGGGGAGAGACGAGACCATGGAACAAAGC 860
QY	327 CCTGTGAGAGTCCAGAAAAACAGGGCTTATAACAGTAGTTTGGGACATGCGTCTA 386
Db	861 CTGAGAAATCCA--AAAAAGAGAGGCTTACACAGTAGTTTGTGAC











PR 08-NOV-2000; 2000US-0246525P.  
PR 08-NOV-2000; 2000US-0246526P.  
PR 08-NOV-2000; 2000US-0246527P.  
PR 08-NOV-2000; 2000US-0246528P.  
PR 08-NOV-2000; 2000US-0246532P.  
PR 08-NOV-2000; 2000US-0246609P.  
PR 08-NOV-2000; 2000US-0246610P.  
PR 08-NOV-2000; 2000US-0246611P.  
PR 08-NOV-2000; 2000US-0246613P.  
PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
PR 17-NOV-2000; 2000US-0249209P.  
PR 17-NOV-2000; 2000US-0249210P.  
PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
PR 17-NOV-2000; 2000US-0249213P.  
PR 17-NOV-2000; 2000US-0249214P.  
PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.  
PR 17-NOV-2000; 2000US-0249264P.  
PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249297P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 01-DEC-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250160P.  
PR 05-DEC-2000; 2000US-0250391P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
PR 06-DEC-2000; 2000US-0256719P.  
PR 06-DEC-2000; 2000US-0251479P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251989P.  
PR 11-DEC-2000; 2000US-0251990P.  
PR 05-JAN-2001; 2001US-0259678P.  
(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Disclosure; SEQ ID NO 39232; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAK62170 to AAK61921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patient's own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK67694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAK62169 CC represent sequences used in the exemplification of the present invention

Sequence 322 BP; 95 A; 84 C; 100 G; 43 T; 0 U; 0 Other;

Query Match 34.5%; Score 266.2; DB 4; Length 322;  
Best Local Similarity 94.8%; Pred. No. 1.6e-61;  
Matches 274; Conservative 0; Mismatches 15; Indels 0; Gaps 0;  
QY 484 AGAGCCGGGGCGGCTCAAGCCTGTATCCAGACATTTGGAGGCGGCGGTC 543  
DB 5 AAAGCCGGGGCGGCTCAAGCCTGTATCCAGACATTTGGAGGCGGCGGCGC 64  
QY 544 GGATCAGGAGTTCAGGAGATCGAGACCATCTGGCTAACCGGTGAACCCCGTCTTAC 603  
DB 65 GGATCAGGAGTTCAGGAGATCGAGACCATCTGGCTAACCGGTGAACCCCGTCTTAC 124  
QY 604 TAAAAATTCAAAAAAATAATTAGCTGGCGGTGGTGGCGGCGCCTGTAGTCCAGCTATT 663  
DB 125 TAAAAATACAAAAAATAATTAGCGGGCGTGGTGGCGGCGCCTGTAGTCCAGCTACT 184  
QY 664 CGGGAGGCTGAGGCGAGGAGATGCGTGAACCTGGGAGTGGAGCTTGCAATGAGCCAAG 723  
DB 185 CGGGAGGCTGAGGCGAGGAGATGCGGCTGAACCCGGAGGCGGAGCTTGCAATGAGCCAAG 244  
QY 724 GTGCGGCCACTGCACTCCAGGCTGGGCGACAGAGCGAGACTCCATCTTA 772  
DB 245 ATCGCACCACCTGCACTCCAGGCTGGGCGACAGAGCGAGACTCCGCTCA 293

Search completed: May 6, 2004, 08:19:39  
Job time : 385.55 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 6, 2004, 15:57:18 ; Search time 642 Seconds  
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Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2941586 seqs, 2264995651 residues

Total number of hits satisfying chosen parameters: 5883172

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPECL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=bloume2  
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Database : Published Applications NA:

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3:	/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq*
4:	/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq*
5:	/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq*
6:	/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq*
7:	/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq*
8:	/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq*
9:	/cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq*
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11:	/cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq*
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16:	/cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq*
17:	/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq*
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19:	/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
\$						

1	2589	99.6	4047	14	US-10-007-805-566	Sequence 566, App
2	2589	99.6	4047	15	US-10-076-622-566	Sequence 566, App
3	2589	99.6	4047	15	US-10-124-805-566	Sequence 566, App
4	2589	99.6	4458	13	US-10-058-270A-3	Sequence 3, Appli
5	2589	99.6	4458	14	US-10-007-805-564	Sequence 564, App
6	2589	99.6	4458	15	US-10-076-622-564	Sequence 564, App
7	2589	99.6	4458	15	US-10-177-293-333	Sequence 333, App
8	2589	99.6	4458	15	US-10-124-805-564	Sequence 564, App
9	2578	99.2	3288	14	US-10-007-805-490	Sequence 490, App
10	2578	99.2	3288	15	US-10-076-622-490	Sequence 490, App
11	2578	99.2	3288	15	US-10-124-805-490	Sequence 490, App
12	2578	99.2	3865	9	US-09-604-287A-474	Sequence 474, App
13	2578	99.2	3865	10	US-09-551-621-474	Sequence 474, App
14	2578	99.2	3865	14	US-10-007-805-474	Sequence 474, App
15	2578	99.2	3865	15	US-10-076-622-474	Sequence 474, App
16	2578	99.2	3865	15	US-10-124-805-474	Sequence 548, App
17	2576	99.1	3045	14	US-10-007-805-548	Sequence 548, App
18	2576	99.1	3045	15	US-10-076-622-548	Sequence 548, App
19	2576	99.1	3045	15	US-10-124-805-548	Sequence 548, App
20	2227.5	85.7	2307	9	US-09-825-301-24	Sequence 24, Appl
21	2227.5	85.7	2307	9	US-09-604-287A-468	Sequence 468, App
22	2227.5	85.7	2307	10	US-09-551-621-468	Sequence 468, App
23	2227.5	85.7	2307	14	US-10-007-805-468	Sequence 468, App
24	2227.5	85.7	2307	15	US-10-076-622-468	Sequence 468, App
25	2227.5	85.7	2307	15	US-10-124-805-468	Sequence 468, App
26	2227.5	85.7	2307	15	US-10-033-527-24	Sequence 24, Appl
27	2224.5	85.6	3681	9	US-09-825-301-19	Sequence 19, Appl
28	2224.5	85.6	3681	9	US-09-604-287A-463	Sequence 463, App
29	2224.5	85.6	3681	10	US-09-551-621-463	Sequence 463, App
30	2224.5	85.6	3681	14	US-10-007-805-463	Sequence 463, App
31	2224.5	85.6	3681	15	US-10-076-622-463	Sequence 463, App
32	2224.5	85.6	3681	15	US-10-124-805-463	Sequence 463, App
33	2224.5	85.6	3681	15	US-10-033-527-19	Sequence 19, Appl
34	2125	81.8	1337	9	US-09-825-301-23	Sequence 23, Appl
35	2125	81.8	1337	9	US-09-604-287A-467	Sequence 467, App
36	2125	81.8	1337	10	US-09-551-621-467	Sequence 467, App
37	2125	81.8	1337	14	US-10-007-805-467	Sequence 467, App
38	2125	81.8	1337	15	US-10-076-622-467	Sequence 467, App
39	2125	81.8	1337	15	US-10-124-805-467	Sequence 467, App
40	2125	81.8	1337	15	US-10-033-527-23	Sequence 23, Appl
41	2077.5	79.9	2043	15	US-10-133-757-3	Sequence 3, Appli
42	1781	68.5	3883	15	US-10-177-293-331	Sequence 331, App
43	1775	68.3	3720	14	US-10-007-805-576	Sequence 576, App
44	1775	68.3	3720	15	US-10-076-622-576	Sequence 576, App
45	1775	68.3	3720	15	US-10-124-805-576	Sequence 576, App

#### ALIGNMENTS

RESULT 1  
US-10-007-805-566  
; Sequence 566, Application US/10007805  
; Publication No. US20020150581A1  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Durham, Margarita  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER  
; FILE REFERENCE: 210121.470C10  
; CURRENT APPLICATION NUMBER: US/10/007,805  
; CURRENT FILING DATE: 2001-12-07  
; NUMBER OF SEQ ID NOS: 593  
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 566
; LENGTH: 4047
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-007-805-566

Alignment Scores:
  1.82e-225      Length: 4047
  Score: 2589.00  Matches: 510
  Percent Similarity: 100.00%  Conservative: 0
  Best Local Similarity: 100.00%  Mismatches: 0
  Query Match: 99.62%  Indels: 0
  DB: 14  Gaps: 0

US-09-451-739H-16 (1-512) x US-10-007-805-566 (1-4047)

QY 1 MetLysValSerIleProThrLysAlaLeuMetAspMetGlnThrPheLysAla 20
DB 2053 ATGAAGTTTCTATTCCAACTAAGCTTGAATGATGACATGCCAACTTCCAAAGCA 2112
QY 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
DB 2113 GAGCTCCCGAAGACCATCTGCCCTCGAGCTGCCATTGAAATGCCAAAGCTCTGTCCA 2172
QY 41 LenLysAlaLeuGluLysLeuLysAsnGlnThrLeuArgAlaAspGluLysLeuProSer 60
DB 2173 AATRAAGCTTGGAAATTGAGAAATGCAAACTTGAAGCAGATGATGATCTCCATCA 2232
QY 61 GluSerLysGlnLysAspTyrGluLysSerTrpAspSerGluSerLeuLysGluThr 80
DB 2233 GAATCCAAACAAAGGACTATGAAGAAAGTTCTGGGATTTCTGAGAGTCTCTGTGAGACT 2292
QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLysLysLysLys 100
DB 2293 GTTTCACAGAAGATGTGGTTTACCAGGCTACACATCAAAAGAAATAGATTAATA 2352
QY 101 AsnGlyLysLeuGluLysProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
DB 2353 AATGAAATATTAGAAGACTCTCTGATAATGATGCTTTCTGAAGCTCCCTCGAGATG 2412
QY 121 LysValSerIleProThrLysAlaLeuGluLysMetAspMetGlnThrPheLysAlaGlu 140
DB 2413 AAGATTTCTATTCCAACTTAAGCCCTTAGAATGATGAGCATGCAAACTTTCAAGCAGAG 2472
QY 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
DB 2473 CCTCCGAGAAGCCATCTGCCCTCGAGCTGCCATTGAAATGCCAAAGTCTGTTCCAAAT 2532
QY 161 LysAlaLeuGluLysLysGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
DB 2533 AAGACCTTGAATTGAAGAAATGAACAAACATTTGAGAGCAGATCAGATGTTCCCTTCAGAA 2592
QY 181 SerLysGlnLysLysValGluLysLysSerTrpAspSerGluSerLeuArgGluThrVal 200
DB 2593 TCAAAACAAAGAGTTGAAGAAATTTCTGGGATTTCTGAGACTCCGTGAGACTGTT 2652
QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluLysMetAspLysSer 220
DB 2653 TCACAGAAGGATGTGTGTATCCCAAGGCTACACATCAAAAGAAATGGATAAAATAGT 2712
QY 221 GlyLysLeuGluLysSerThrSerLysLysLysLeuAspThrValHisSerCysGlu 240
DB 2713 GGAATATTAGAGATTCACTAGCCTATCAAAATCTTGATACAGTTCACTTCTGTGA 2772
QY 241 ArgAlaArgGluLysGlnLysAspHisCysGluGlnArgThrGlyLysMetGluLysMet 260
DB 2773 AGAGCAAGGAACTTCAAAAGATCACTGTGAACACGCTACAGAGCAAAATGGCAAAATG 2832
QY 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluLysLysSerGln 280
DB 2833 AAAAAGAGTTTGTGTACTGAAACAACTGTGACAGCAAAAGAAATAAATACAG 2892
QY 281 LeuGluAsnGlnLysValLysTrpGluGlnLysLeuLysSerValArgLeuThrLeuAsn 300

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## RESULT 2

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US-10-076-622-566
; Sequence 566, Application US/10076622
; Publication No. US20030023036A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C11
; CURRENT APPLICATION NUMBER: US/10/076,622
; CURRENT FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 566
; LENGTH: 4047
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-076-622-566

```

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Alignment Scores:
Pred. No.: 1.82e-225      Length: 4047
Score: 2589.00  Matches: 510
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0

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Query Match: 99.62% Indels: 0
DB: 15 Gaps: 0
US-09-451-739H-16 (1-512) x US-10-076-622-566 (1-4047)

QY 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPhelYsAla 20
DB 2053 ATGAAGTTTCTATTCCAACTTAAGACCTTAGAATTGATGACATGCACAACTTTCAAAGCA 2112
QY 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
DB 2113 GAGCCTCCGAGAGCACTCTGCCCTTCGAGCTGCCATTGAAATGCAAAAGTCTGTTCGA 2172
QY 41 AsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 60
DB 2173 AATAAGCCTTGGAAATGAAGATGAACAAACATTGAGAGCAGATGAGATCTCCCATCA 2232
QY 61 GluSerLysGlnLysAspTyrGluLysSerTrpAspSerGluSerLeuCysGluThr 80
DB 2233 GAATCCCAACAAAGGACTATGAAGAAAGTTCTTGGGATCTCTGAGAGCTCTGTGAGACT 2292
QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100
DB 2293 GTTTCACAGAGGATGTGTGTTTACCCCAAGCTACACATCAAAAGAAATAGATAAATA 2352
QY 101 AsnGlyLysLeuGluLysProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
DB 2353 AATGAAATATAGAGAGCTCTCCGTGATAATGATGGTTTCTGAAGGCTCCCTCGAGATG 2412
QY 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPhelYsAlaGlu 140
DB 2413 AAAGTTTCTATTCCAACTTAAGCCTTAGAATTGATGACATGCACAACTTTCAAAGCAGAG 2472
QY 141 ProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
DB 2473 CCTCCGAGAGCCTCTGCCCTTCGAGCTGCCATTGAAATGCAAAAGTCTGTTCACAAAT 2532
QY 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
DB 2533 AAAGCCTTGGAAATGAAGATGAACAACTTAGAGAGCAGATCAGATGTTCCCTTCAGAA 2592
QY 181 SerLysGlnLysLysValGluLysSerTrpAspSerGluSerLeuArgGluThrVal 200
DB 2593 TCAAAACAAAGAGAGTTGAAGAAATTTCTTGGGATTTCTGAGAGTCTCCGTGAGACTGTT 2652
QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
DB 2653 TCACAGAGGATGTGTGTACCCAGGCTACACATCAAAAGAAATGGATAAATAGT 2712
QY 221 GlyLysLeuGluAspSerThrSerLysLysLeuAspThrValHisSerCysGlu 240
DB 2713 GGAAATTTAGAAGATTCAACTAGCCTATCAAAATCTTGGATACAGATTCATTTCTGTGAA 2772
QY 241 ArgAlaArgGluLeuGluLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
DB 2773 AGAGCAAGGAACTTCAAAAGATCCTGTGACCACTGACCACTAGCAAGAAATGGAAACAATG 2832
QY 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluIleLysSerGln 280
DB 2833 AAAAAGAGTTTGTGTACTGAAAGAAACTGTGAGAGCAAGAAAGAAATTAATCAAG 2892
QY 281 LeuGluAsnGlnLysValIleTrpGluGlnLysCysSerValArgLeuThrLeuAsn 300
DB 2893 TTAGAGAACCAAAAGTTAAATGGGAACAAGAGCTCTCGAGTGTGAGATTGACTTTAAAC 2952
QY 301 GlnGluGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320
DB 2953 CAAGAAGAGAGAGAGAGAAATCCCGATATATTAAATGAAATAATAGGAGAAATTA 3012
QY 321 GlyArgIleGluGlnHisArgGlyGlnLeuGluValLysGlnLeuGluGlnAla 340
DB 3013 CGAAGAAATCGAGAGCAGCATAGGAAGAGTTAGAAAGTGAACCAACTTGAACAGGCT 3072

QY 341 LeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis 360
DB 3073 CTCAGATACAAAGATATAGAATTGAGAGCTAGAAAAGTAAATTTGAAATCAGGTTTCTCAC 3132
QY 361 ThrHisGluAsnGluAsnTyrLeuHisGluAsnCysMetLeuLysLysGluIleAla 380
DB 3133 ACTCATGAATATGAATAATTAATCTTTACATGAAAATTCATGTTTGAAGAAAGAAATTCGC 3192
QY 381 MetLeuLysLeuGluIleAlaThrIleLysHisGlnTyrGlnGluLysGluAsnLysTyr 400
DB 3193 ATGCTAAACTGGAATAGCCACACTGAAACACCAATACCAAGGAAAAGGAAATAAATATAC 3252
QY 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
DB 3253 TTTGAGGACATTAAGATTTTAAAGAAAAGAAATGCTGAACTTCAGATGACCTTAAACTG 3312
QY 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle 440
DB 3313 AAAGAGGAATCATTAACATAAAGGCACTCTCAATATAGTGGCAGCTTAAAGTTCTGATA 3372
QY 441 AlaGluAsnThrMetLeuThrSerLysLysGlnLysGlnAspLysGluIleLeuGlu 460
DB 3373 GCTGAGACACAATGCTCCTTCTAAATTTGAAGGAAAACCAAGCAAAAGAAATCTAGAG 3432
QY 461 AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
DB 3433 GCAGAAATTAATCACACCATCTAGACTGGCTTCTGCTGTACAAAGACCATGATCAAAAT 3492
QY 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
DB 3493 GTGACATCAAGAAAAGTCAAGAACCTGCTTTCCACATTGCAGGAGATGCTTGTTCGAA 3552
QY 501 ArgLysMetAsnValAspValSerThr 510
DB 3553 AGAAAAATGAATGTTGATGTGAGTAGTAGG 3582

RESULT 3
US-10-124-805-566
; Sequence 566, Application US/10124805
; Publication No. US20030166022A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Sleath, Paul R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C12
; CURRENT APPLICATION NUMBER: US/10/124,805
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 566
; LENGTH: 4047
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-124-805-566

Alignment Scores: 1,82e-225 Length: 4047
Pred. No.: 2589.00 Matches: 510
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 99.62% Indels: 0
Query Match: 15 Gaps: 0
DB:

US-09-451-739H-16 (1-512) x US-10-124-805-566 (1-4047)

QY 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPhelYsAla 20
DB 2053 ATGAAGTTTCTATTCCAACTTAAGACCTTAGAATTGATGACATGCACAACTTTCAAAGCA 2112
QY 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
DB 2113 GAGCCTCCGAGAGCACTCTGCCCTTCGAGCTGCCATTGAAATGCAAAAGTCTGTTCGA 2172
QY 41 AsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 60
DB 2173 AATAAGCCTTGGAAATGAAGATGAACAAACATTGAGAGCAGATGAGATCTCCCATCA 2232
QY 61 GluSerLysGlnLysAspTyrGluLysSerTrpAspSerGluSerLeuCysGluThr 80
DB 2233 GAATCCCAACAAAGGACTATGAAGAAAGTTCTTGGGATCTCTGAGAGCTCTGTGAGACT 2292
QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100
DB 2293 GTTTCACAGAGGATGTGTGTTTACCCCAAGCTACACATCAAAAGAAATAGATAAATA 2352
QY 101 AsnGlyLysLeuGluLysProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
DB 2353 AATGAAATATAGAGAGCTCTCCGTGATAATGATGGTTTCTGAAGGCTCCCTCGAGATG 2412
QY 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPhelYsAlaGlu 140
DB 2413 AAAGTTTCTATTCCAACTTAAGCCTTAGAATTGATGACATGCACAACTTTCAAAGCAGAG 2472
QY 141 ProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
DB 2473 CCTCCGAGAGCCTCTGCCCTTCGAGCTGCCATTGAAATGCAAAAGTCTGTTCACAAAT 2532
QY 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
DB 2533 AAAGCCTTGGAAATGAAGATGAACAACTTAGAGAGCAGATCAGATGTTCCCTTCAGAA 2592
QY 181 SerLysGlnLysLysValGluLysSerTrpAspSerGluSerLeuArgGluThrVal 200
DB 2593 TCAAAACAAAGAGAGTTGAAGAAATTTCTTGGGATTTCTGAGAGTCTCCGTGAGACTGTT 2652
QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
DB 2653 TCACAGAGGATGTGTGTACCCAGGCTACACATCAAAAGAAATGGATAAATAGT 2712
QY 221 GlyLysLeuGluAspSerThrSerLysLysLeuAspThrValHisSerCysGlu 240
DB 2713 GGAAATTTAGAAGATTCAACTAGCCTATCAAAATCTTGGATACAGATTCATTTCTGTGAA 2772
QY 241 ArgAlaArgGluLeuGluLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
DB 2773 AGAGCAAGGAACTTCAAAAGATCCTGTGACCACTGACCACTAGCAAGAAATGGAAACAATG 2832
QY 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluIleLysSerGln 280
DB 2833 AAAAAGAGTTTGTGTACTGAAAGAAACTGTGAGAGCAAGAAAGAAATTAATCAAG 2892
QY 281 LeuGluAsnGlnLysValIleTrpGluGlnLysCysSerValArgLeuThrLeuAsn 300
DB 2893 TTAGAGAACCAAAAGTTAAATGGGAACAAGAGCTCTCGAGTGTGAGATTGACTTTAAAC 2952
QY 301 GlnGluGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320
DB 2953 CAAGAAGAGAGAGAGAGAAATCCCGATATATTAAATGAAATAATAGGAGAAATTA 3012
QY 321 GlyArgIleGluGlnHisArgGlyGlnLeuGluValLysGlnLeuGluGlnAla 340
DB 3013 CGAAGAAATCGAGAGCAGCATAGGAAGAGTTAGAAAGTGAACCAACTTGAACAGGCT 3072
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Db 2113 GAGCCTCCGAGAGCCATCTGCTCGAGCCTGCCATTCAAAATGCAAAAGTCTGTCCA 2172  
 Qy 41 AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluLeuLeuProSer 60  
 Db 2173 AATAAAGCCTTGGAAATGAAGAATGAACAACATTCAGAGCAGATGAGATCTCCCATCA 2232  
 Qy 61 GluSerLysGlnLysAspTyrGluGluSerSerTyrAspSerGluSerLysGluThr 80  
 Db 2233 GAATCCAAACAAGAGCTATGAAGAAGTCTTGGATTCAGAGAGTCTCTGTGAGAT 2292  
 Qy 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLeuLeuLysIle 100  
 Db 2293 GTTTCACAGAGGATGTGTGTTTACCACAGCTACACATCAAAAGAAATAGATAAATA 2352  
 Qy 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120  
 Db 2353 AATGGAAATAGAGAAGTCTCCCTGATAATGATGTTTCTGAAGGCTCCCTCCAGAAATG 2412  
 Qy 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140  
 Db 2413 AAGTTTCTATTCCAACTAAGCCTTAGAATTGATGACATGCAAACTTTCAAGCAGAG 2472  
 Qy 141 ProGlnLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160  
 Db 2473 CCTCCGAGAGCCATCTGCCTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTCAAAT 2532  
 Qy 161 LysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180  
 Db 2533 AAGCCTTGGAAATGAAGATGAACAACATTCAGAGCAGATGATTCCTCTCAGAA 2592  
 Qy 181 SerLysGlnLysLysValGluGluLysSerTrpAspSerGluSerLeuArgGluThrVal 200  
 Db 2593 TCAAAACAAAGAAGGTGGAAGAAATCTTGGATTCAGAGTCTCCGTGAGACTGTT 2652  
 Qy 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220  
 Db 2653 TCACAGAAGATGTGTGTACCCAGGCTACACATCAAAAGAAATGGATAAATAAGT 2712  
 Qy 221 GlyLysLeuGluAspSerThrSerLysSerLysIleLeuAspThrValHisSerCysGlu 240  
 Db 2713 GGAATAATTAGAAATTCAACTAGCTATCAAAATCTTGGATCAGTTCATCTTGTGAA 2772  
 Qy 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260  
 Db 2773 AGAGCAAGGAACTTCAAAAGATCACTGTGAACAGCTACAGCAAAATGGAACAATG 2832  
 Qy 261 LysLysLysPheCysValLeuLysLysLysSerGluAlaLysGluLeuLysSerGln 280  
 Db 2833 AAAAAGAAGTTTGTGTACTGAAAAGAACTGTCAAGCAAGCAAAAGAAATAAATCAAC 2892  
 Qy 281 LeuGluAsnGlnLysValLysTrpGluGlnLysCysSerValArgLeuThrLeuAsn 300  
 Db 2893 TTAGAGAACCAAAAGTTAAATGGGAACAGAGCTCTGCAGTGTGAGATTGACTTTAAAC 2952  
 Qy 301 GlnGluGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320  
 Db 2953 CAAGAAGAAGAGAGAGAAATGCCATATATTAATGAATAAATAGGGAAGAATTA 3012  
 Qy 321 GlyArgIleGluGluGlnHisArgLysGluValLysGlnLysGluGlnAla 340  
 Db 3013 GGAAGAATCGAAGACAGCATAGGAAGATTTAGAGTGAACAACAACACTTGAACAGCT 3072  
 Qy 341 LeuArgIleGlnAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360  
 Db 3073 CTCAGATACAGATATAGAATTGAAGAGTGTAGAAGTAATTTGAATCAGGTCTCTCAC 3132  
 Qy 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380  
 Db 3133 ACTCATGAATAAGAAATATCTCTTACATGAATAATGCATGTTGAAGAAGAAATTTGCC 3192  
 Qy 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400  
 Db 3193 ATGCTAAACTGGAAATACCCACACTGAACACCAATACCAGGAAAGAAAGAAATAAATAC 3252

Qy 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420  
 Db 3253 TTTGAGGACATTAGATTTTAAAGAAAGAAAGTCTGAACTTCAGATGACCTTAAAACTG 3312  
 Qy 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle 440  
 Db 3313 AAAGAGGAATCATTAACATAAAGGGCATCTCAATATAGTGGGAGCTTAAAGTTCTGATA 3372  
 Qy 441 AlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLysGluIleLeuGlu 460  
 Db 3373 GCTGAGAACACAACTCTCACTTCTTAATTCAGGAAACAAAGCAAAATATCTAGAG 3432  
 Qy 461 AlaGluIleGluSerHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480  
 Db 3433 GCAGAAATTAATCACACCATCTCTAGACTGGCTTCTGCTACAAAGACCATGATCAAT 3492  
 Qy 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500  
 Db 3493 GTGACATCAAGAAAGTCAAGAACCTGCTTTCACATTCAGGAGATGCTTGTTCGAA 3552  
 Qy 501 ArgLysMetAsnValAspValSerThr 510  
 Db 3553 AGAAAAATGAATGTGATGTGAGTAGTACG 3582

RESULT 4

US-10-058-270A-3  
 ; Sequence 3, Application US/10058270A  
 ; Publication No. US20040029114A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mack, David H.  
 ; APPLICANT: Gish, Kurt C.  
 ; APPLICANT: Afar, Daniel  
 ; APPLICANT: Eos Biotechnology, Inc.  
 ; TITLE OF INVENTION: Methods of Diagnosis of Breast Cancer, Compositions and  
 ; TITLE OF INVENTION: Methods of Screening for Modulators of Breast Cancer  
 ; FILE REFERENCE: 018501-005210US  
 ; CURRENT APPLICATION NUMBER: US/10/058,270A  
 ; CURRENT FILING DATE: 2002-01-24  
 ; PRIOR APPLICATION NUMBER: US 60/263,965  
 ; PRIOR FILING DATE: 2001-01-24  
 ; PRIOR APPLICATION NUMBER: US 60/265,928  
 ; PRIOR FILING DATE: 2001-02-02  
 ; PRIOR APPLICATION NUMBER: US 09/829,472  
 ; PRIOR FILING DATE: 2001-04-09  
 ; PRIOR APPLICATION NUMBER: US 60/282,698  
 ; PRIOR FILING DATE: 2001-04-09  
 ; PRIOR APPLICATION NUMBER: US 60/288,590  
 ; PRIOR FILING DATE: 2001-05-04  
 ; PRIOR APPLICATION NUMBER: US 60/294,443  
 ; PRIOR FILING DATE: 2001-05-29  
 ; NUMBER OF SEQ ID NOS: 141  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 3  
 ; LENGTH: 4458  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-058-270A-3

Alignment Scores:  
 Pred. No.: 2,06e-225 Length: 4458  
 Score: 2589.00 Matches: 510  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.62% Indels: 0  
 DB: 13 Gaps: 0

US-09-451-739H-16 (1-512) x US-10-058-270A-3 (1-4458)

Qy 1 MetLysValSerIleProThrLysAlaLeuLeuMetAspMetGlnThrPheLysAla 20  
 Db 2128 ATGAAAGTTTCTATTCTCAACTAAAGCCTTAGAATTGATGACATGCAAACTTTCAAGCA 2187

QY 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40  
Db 2188 GAGCTCCCGAGAGACCATCTGCCTTCGAGCCTGCCATTGAAATGCCAAAGATCTGTCCA 2247  
QY 41 AsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 60  
Db 2248 AATAAGGCTTGGAAATCGAAGATGAAACAACATTGAGAGCAGATGATGATCTCCCATCA 2307  
QY 61 GluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGluSerLeuLysGluThr 80  
Db 2308 GAATCCAAACAAAGGACTATGAGAAAGTCTCTGGGATTCGAGAGTCTCTGTGAGACT 2367  
QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100  
Db 2368 GTTTCACAGAGAGATGTGTGTTTACCAAGGCTACACATCAAAAGAAATAGATAAATA 2427  
QY 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120  
Db 2428 AATGGAAATATGAAAGAGTCTCTCATATGATGTTTCTGAAGGCTCCCTGCGAAGATG 2487  
QY 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140  
Db 2488 AAAGTTTCTATTCCAACTAAAGCCTTAGAATTTGATGGAATGCAACATTTTCAAGCGAG 2547  
QY 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160  
Db 2548 CTCCCGAGAGCCATCTGCCTTCGAGCCTGCCATTGAAATGCCAAAGTCTGTTCCTCAAT 2607  
QY 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180  
Db 2608 AAAGCCTTGGAAATGAAAGATGAACAACATTTGAGAGCAGATCAGATGTTCCCTTCAGAA 2667  
QY 181 SerLysGlnLysLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200  
Db 2668 TCARAACAAGAAGGTTGAAGAAATCTTCGGATTCGAGATCTCGTGAGACTGTT 2727  
QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220  
Db 2728 TCACAGAGAGATGTGTGTACCCAGGCTACACATCAAAAGAAATGCAATAAATAGT 2787  
QY 221 GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu 240  
Db 2788 GGAAATATGAGATTCACATAGCCTATCAAAATCTTGATACAGTTCATCTTGTGAA 2847  
QY 241 ArgAlaArgGluLysGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260  
Db 2848 AGAGCAAGGGAATCTCAAAAGATCACTGTGAACACGTACAGGAAATGCAACAAATG 2907  
QY 261 LysLysLysPheCysValLysLysLysLysLeuSerGluAlaLysGluIleLysSerGln 280  
Db 2908 AAAAAAGATTTTGTGTACTGAAAAAGAACTGTCAAGACCAAGAAATATAAATCACAG 2967  
QY 281 LeuGluAsnGlnLysValLysTrpGluGlnGluLeuLysCysSerValArgLeuThrLeuAsn 300  
Db 2968 TTAGAGAACCAAAAGTAAATGGGAACAAGAGCTCTGCAGTGTGAGATTCATTTAAAC 3027  
QY 301 GlnGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320  
Db 3028 CAAGAAGAAGAGAGAGAAATGCCGATATATTAAATGAAATAATAGGGAAGAATTA 3087  
QY 321 GlyArgIleGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGluGlnAla 340  
Db 3088 GGAAAGATCGAAGAGCAGCATAGAAAGAGTTAGAAAGTGAACAACAACATTCAGAGCT 3147  
QY 341 LeuArgIleGlnAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360  
Db 3148 CTCAGAATACAGATATAGAAATGAAAGGTGTAGAAAGTAATTTGAATCAGGTTCTCAC 3207  
QY 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380  
Db 3208 ACTCATGAATGAAATATATCTCTTACATGAATAATTCATGTTTGAAGAGGAATGCC 3267  
QY 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400

Db 3268 ATGCTAAAACCTGGAATAGCCACACTGAAACACCAATACCAGAAAAGAAATTAATAC 3327  
QY 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLysLysLeu 420  
Db 3328 TTTGAGGACATTAAGATTTTAAAGAAAAGAAATGCTGAATTCAGATGACCCCTAAAACCTG 3387  
QY 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLysLysValLeuIle 440  
Db 3388 AAAGAGGAATCATTAACATAAAGGGCATCTCAATATAGTGGCAGCTTAAAGTTCTGATA 3447  
QY 441 AlaGluAsnThrMetLeuThrSerLysLysLeuLysGluLysGlnAspLysGluIleLeuGlu 460  
Db 3448 GCTGAGACACCAATGCTCACTTCTAAATTTGAAGGAAAACCAAGACAAAGAAATACTAGAG 3507  
QY 461 AlaGluIleGluSerHisProArgLeuAlaSerAlaValGlnAspHisaspGlnIle 480  
Db 3508 GCAGAAATTTGAATCACACCATCTAGCTGGCTTCTGCTGTACAAAGACCATGATCAAT 3567  
QY 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500  
Db 3568 GTGACATCAAGAAAAGTCAAGAACCTGTTTCCACATTGCAGGAGATGCTTGTGTTGCAA 3627  
QY 501 ArgLysMetAsnValAspValSerSerThr 510  
Db 3628 AGAAAATGAATGTTGATGTGATGACG 3657

RESULT 5  
US-10-007-805-564  
; Sequence 564, Application US/10007805  
; Publication No. US20020150581A1  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yuqiu  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Farger, Gary R.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Durham, Margarita  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER  
; FILE REFERENCE: 210121.470C10  
; CURRENT APPLICATION NUMBER: US/10/007,805  
; CURRENT FILING DATE: 2001-12-07  
; NUMBER OF SEQ ID NOS: 593  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 564  
; LENGTH: 4458  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-10-007-805-564

Alignment Scores:  
Pred. No.: 2,06e-225 Length: 4458  
Score: 2589.00 Matches: 510  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.62% Indels: 0  
DB: 14 Gaps: 0

US-09-451-739H-16 (1-512) x US-10-007-805-564 (1-4458)

QY 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20  
Db 2128 ATGAAGATTTCTATTTCACCTTAAAGCCTTAGAATTTGATGACATGCAAACTTTCRAAGCA 2187  
QY 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40  
Db 2188 GAGCCTCCGAGAGACCATCTGCCTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTGTCCA 2247

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QY 41 AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluLeuProSer 60
Db 2248 AATAAGCCCTTGAAATGAGATGACAAACATTGAGAGCAGATGAGATCTCCCATCA 2307
QY 61 GluSerLysGlnLysAspTyrGluGluSerSerTyrAspSerGluSerLysGluThr 80
Db 2308 GAATCCAAACAAAGAGACTATGAGAAAGTCTCTGGGATCTCAGAGTCTCTGTGAGACT 2367
QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLeuAspLysIle 100
Db 2368 GTTTCACAGAGAGGATGTTGTTTACCCAGGCTACACATCAAAAGAAATAGATAAATA 2427
QY 101 AsnGlyLysLeuGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
Db 2428 AATGGAAAATAGAAAGAGTCTCTGATAATGATGGTCTTCTGAAGGCTCCCTCAGAATG 2487
QY 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140
Db 2488 AAGTTTCTATTCCAACTAAGCCCTTAGAATGATGACATGCAACTTTCAAAGCAGAG 2547
QY 141 ProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
Db 2548 CCTCCGAGAAAGCATCTGCCTTCAGCGCTGCCATTGAAATGCAAAAGTCTGTTCCAAAT 2607
QY 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
Db 2608 AAGCCTTGGAAATGGAAGATGAACAAACATTGAGAGCAGATCAGATGCCCTTCAGAA 2667
QY 181 SerLysGlnLysLysValGluGluAsnSerTyrAspSerGluSerLeuArgGluThrVal 200
Db 2668 TCAAAACAAAGAGGTTGAAGAAATCTCTGGGATCTCAGAGTCTCCGTGAGACTGTT 2727
QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
Db 2728 TCACAGAGAGGATGTGTGTACCCAGGCTACATCAAAAGAAATGGATAAATAGT 2787
QY 221 GlyLysLeuGluAspSerThrSerLysLysIleLeuAspThrValHisSerCysGlu 240
Db 2788 GGAAATATTAGAGATTCAACTAGCTATCAAAATCTTGATACAGTTCACTTCTGTGAA 2847
QY 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
Db 2848 AGAGCAAGGGAACTTCAAAAGATCACTGTGAACACGTACAGGAAATGGAAACAATG 2907
QY 261 LysLysLysPheCysValLeuLysLysLysLysLeuSerGluAlaLysGluLysSerGln 280
Db 2908 AAAAAGAGCTTTTGTGCTACTGAAAAGAACTGTCTAGAGCAAAAGAAATTAATTCACAG 2967
QY 281 LeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuThrLeuAsn 300
Db 2968 TTAGAGAACCAAAAGTTAAATGGGAACAGAGCTCTGCAGTGTGAGATTGACTTTAAAC 3027
QY 301 GlnGluGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320
Db 3028 CAAGAAGAAGAGAGAGAAATGCCGATATATTAAATGAAAAAATTAGGAGAAATTA 3087
QY 321 GlyArgIleGluGlnGlnHisArgLysGluLeuGluValLysGlnGlnLeuGluGlnAla 340
Db 3088 GGAAGAATCGAAGCAGCAGCATAGGAAGAGTTAGAAGTGAACCAACAACACTTGAACAGGCT 3147
QY 341 LeuArgIleGluAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis 360
Db 3148 CTCAGAAATCAAGATATAGATTGAAGATGTAGAAAGTAATTTGAATCAGGTTTCTCAC 3207
QY 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380
Db 3208 ACTCATGAAATGAAATATCTCTTACATGAAATTCATGTAATTCGAAAAAGGAAATGCG 3267
QY 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400
Db 3268 ATGCTAAACTGGAATAGCCACTGAAACCAATACCAGAAAGGAAATTAATATAC 3327
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QY 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
Db 3328 TTTGAGACATTTAAGATTTTAAAGAAAGAAATGCTGAATCTCAGATGACCTTAAACCTG 3387
QY 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle 440
Db 3388 AAAGAGGAATCATTAACATAAAGGCGCATCTCAATATAGTGGCAGCTTAAAGTCTTGATA 3447
QY 441 AlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLysGluIleLeuGlu 460
Db 3448 GCTGAGAACCAATGCTCACTTCTAAATTTGAAGAAACAAACAGCAAGAAATCTAGAG 3507
QY 461 AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
Db 3508 GCAGAAATGATCACACCATCTCTAGACTGGCTTCTGCTGTACAGACCATGATCAAT 3567
QY 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
Db 3568 GTGACATCAAGAAAGATCAAGAACCTGCTTCCACATTCAGGAGATGCTTGTTCGAA 3627
QY 501 ArgLysMetAsnValAspValSerSerThr 510
Db 3628 AGAAATAATGAATGTTGATGTAGTAGTAG 3657

RESULT 6
US-10-076-622-564
; Sequence 564, Application US/1007622
; Publication No. US20030023036A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C11
; CURRENT APPLICATION NUMBER: US/10/076, 622
; CURRENT FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 564
; LENGTH: 4458
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-076-622-564

Alignment Scores:
Pred. No.: 2,06e-225 Length: 4458
Score: 2589.00 Matches: 510
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.62% Indels: 0
DB: 15 Gaps: 0

US-09-451-739H-16 (1-512) x US-10-076-622-564 (1-4458)
QY 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20
Db 2128 ATGAAGATTTCTATTCCAACTAAAGCCTTAGAATTCAGATGCAATCTTCAAGCA 2187
QY 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
Db 2188 GAGCCTCCGAGAGCGCATCTGCTCTCGAGCGCTGCAATTCGAAATGCAAAAGTCTGTCCA 2247
QY 41 AsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 60
Db 2248 AATAAGCCCTTGGAAATGAGATGAAACAAACATTGAGAGCAGATGAGATCTCCCATCA 2307
QY 61 GluSerLysGlnLysAspTyrGluGluSerSerTyrAspSerGluSerLysGluThr 80
Db 2308 GAATCCAAACAAAGAGACTATGAGAAAGTCTCTGGGATCTCAGAGTCTCTGTGAGACT 2367
QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100
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Db 2128 ATGAAAGTTTCTATTCCAACTAAAGCCTTAGAATTGATGGACATGCCAAACTTTCAAGCA 2187  
Qy 21 GluProGluLysProSerAlaPheGluProAlaileGluMetGlnLysSerValPro 40  
Db 2188 GAGCCTCCGAGAGCCATCTGCCTTCGAGCCTGCCATTCAAATGCAAAAGTCTGTTC 2247  
Qy 41 AsnLysAlaLeuGluLysAsnGluThrLeuArgAlaAspGluLeuLeuProSer 60  
Db 2248 AATAAAGCCTTGGAAATGGAAGATGAACAACATTGAGACGACATGATACCTCCATCA 2307  
Qy 61 GluSerLysGlnLysAspGluSerGluSerSerTrpAspSerGluSerLysGluThr 80  
Db 2308 GAATCCAAACAAAGGACTATGAAGAAAGTTCTTGGGATTCTGAGAGCTCTGTGAGACT 2367  
Qy 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLeuAspLysLe 100  
Db 2368 GTTTCACAGAAGGATGTGTGTTTACCAGGCTACATCAAAAGAAATGATTAATA 2427  
Qy 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120  
Db 2428 AATGGAAATATGAAGAGTCTCTGATTAATGATGTTTCTGAAGGCTCTGTCGAGATG 2487  
Qy 121 LysValSerLeuProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140  
Db 2488 AAAGTTTCTATTCCAACTAAAGCCTTAGAATTGATGGACATGCCAACTTTCAAGCAGAG 2547  
Qy 141 ProProGluLysProSerAlaPheGluProAlaileGluMetGlnLysSerValProAsn 160  
Db 2548 CTCTCCGAGAGCCATCTGCCTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAAT 2607  
Qy 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180  
Db 2608 AAAGCCTTGGAAATGAAGAAATGAACAAACATTGAGACGATGATGTTCCCTTCAGAA 2667  
Qy 181 SerLysGlnLysLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200  
Db 2668 TCAAACCAAGAAGGTTGAAGAAATCTTGGGATCTTGAGAGTCTCCGTGAGAGCTTT 2727  
Qy 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysLeSer 220  
Db 2728 TCACAGAAGGATGTGTGTGATCCCAAGGCTACACATCAAAAGAAATGGATAAATAAGT 2787  
Qy 221 GlyLysLeuGluAspSerThrSerLysLysLysLeuAspThrValHisSerCysGlu 240  
Db 2788 GGAAATATGAAAGATTCAACTAGCTATCAAAATCTTGGATACAGTTCTATCTTGTGAA 2847  
Qy 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260  
Db 2848 AGAGCAAGGCAACTTCAAAAGATCACTGTGAACCAACCTACAGGCAAAATGGAAACAATG 2907  
Qy 261 LysLysLysPheCysValLysLysLysLysLysLysLysLysLysLysLysLysLys 280  
Db 2908 AAAAAGAGTTTGTGTCTGTAAGAAAGAACTGTGAGAGCGCAAGAAATTAATCAAG 2967  
Qy 281 LeuGluAsnGlnLysValLysTrpGluGlnLysCysSerValArgLeuThrLeuAsn 300  
Db 2968 TTAGAGAACCAAAAGTTAAATGGGAAACAAAGAGCTCTGAGTGTGAGATTGACTTTAAAC 3027  
Qy 301 GlnGluGluLysArgArgAlaAspLeuLeuAsnGluLysLeuArgGluGluLeu 320  
Db 3028 CAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3087  
Qy 321 GlyArgileGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGluGlnAla 340  
Db 3088 GGAAGAAATCGAAGAGCAGCATAGGAAGAGTTAGAGTGAAGTGAACAAACAACCTTCAACAGGCT 3147  
Qy 341 LeuArgileGlnAspLysGlnLysSerValGluSerAsnLeuAsnGlnValSerHis 360  
Db 3148 CTGAGAAATCAAGATATAGAAATGGAAGGTGAGAAAGTAATTTGAATCAGGTTTCTCAC 3207  
Qy 361 ThrHisGluAsnGluAsnTrpLeuLeuHisGluAsnCysMetLysLysGluLeuAla 380  
Db 3208 ACTCATGAAATCAAAATATCTCTTACATGAAATTCATGTAATTCGATGTAAGAAAGAAATGCC 3267

Qy 381 MetLeuLysLeuGluLeuAlaThrLeuLysHisGlnTrpGlnGluLysGluAsnLysTr 400  
Db 3268 ATGCTAAACCTGGAAATATAGCCACTGAAACCACTATCCAGGAAAGGAAATAAATAC 3327  
Qy 401 PheGluAspLysLysLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420  
Db 3328 TTTGAGGACATTAAGATTTTAAAGAGAAAGAAATGCTGAATTCAGATGACCCCTAAACCTG 3387  
Qy 421 LysGluGluSerLeuThrLysArgAlaSerGlnTrpSerGlyGlnLeuLysValLeuLe 440  
Db 3388 AAAGAGGAATCATTAACCTAAAGGCGCATCTCAATATAGTGGCAGCTTAAAGTTCTGATA 3447  
Qy 441 AlaGluAsnThrMetLeuThrSerLysLysLysGlnLysGlnAspLysGluLeuGlu 460  
Db 3448 GCTGAGAACACAACTGCTCACTTCTAAATTTGAAGGAAAAACAAGCAAGAAATACTAGAG 3507  
Qy 461 AlaGluLeuGluSerHisProArgLeuAlaSerAlaValGlnAspHisAspGlnLe 480  
Db 3508 GCAGAAATGGAATCACCATCTAGACTTGGCTTCTGCTGTACAGACCATGATCAAT 3567  
Qy 481 ValThrSerArgLysSerGlnGluProAlaPheHisLeuAlaGlyAspAlaCysLeuGln 500  
Db 3568 GTGACATCAAGAAAAAGTCAAGAACCTGCTTTCCACATTCGAGGAGATGCTTGTTCGAA 3627  
Qy 501 ArgLysMetAsnValAspValSerSerThr 510  
Db 3628 AGAAAAATGAATGATGTGATGTGAGTAGTAGC 3657

## RESULT 8

US-10-124-805-564  
; Sequence 564, Application US/10124805  
; Publication No. US20030166022A1  
; GENERAL INFORMATION:  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Sleath, Paul R.  
; APPLICANT: Persing, David H.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.470C12  
; CURRENT APPLICATION NUMBER: US/10/124,805  
; CURRENT FILING DATE: 2002-04-15  
; NUMBER OF SEQ ID NOS: 627  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 564  
; LENGTH: 4458  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-124-805-564

Alignment Scores:  
Pred. No.: 2,06e-225 Length: 4458  
Score: 2589.00 Matches: 510  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.62% Indels: 0  
DB: 15 Gaps: 0

US-09-451-739H-16 (1-512) x US-10-124-805-564 (1-4458)

Qy 1 MetLysValSerLeuProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20  
Db 2128 ATGAAAGTTTCTATTCCAACTAAAGCCTTAGAATTGATGGACATGCCAAACTTTCAAGCA 2187  
Qy 21 GluProGluLysProSerAlaPheGluProAlaileGluMetGlnLysSerValPro 40  
Db 2188 GAGCCTCCGAGAGCCATCTGCCTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTC 2247  
Qy 41 AsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluLeuLeuProSer 60  
Db 2248 AATAAAGCCTTGGAAATGGAAGATGAACAACATTGAGACGACATGATACCTCCATCA 2307  
Qy 61 GluSerLysGlnLysAspTrpGluGluSerSerTrpAspSerGluSerLysGluThr 80

Db 2308 GAATCCAAACAAAGGACATATGAAGAAAGTTCTGGGATTCAGAGATCTCTGTGAGACT 2367  
QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLeuAspLysLeu 100  
Db 2368 GTTTCACAGAAGGATGTGTGTTATCCCAAGGCTACACATCAAAAAGAAATAGATAAATA 2427  
QY 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120  
Db 2428 AATGGAAATATAGAAGAGTCTCTGATATATGATGTTTTCTGAAGGCTCCCTGCAGAAATG 2487  
QY 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140  
Db 2488 AAGATTTCTATTCCAACTAAAGCCCTTAGAATTGATGGACATGCCAACTTTTCAAAAGCAGAG 2547  
QY 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160  
Db 2548 CCTCCCGAGAGCCATCTGCCTTCAGGCTGCCATTGAATGCAAAAGTCTGTTCCAAAT 2607  
QY 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180  
Db 2608 AAGAGCTTTGGAAATGAAGAAATGAACAAACATTTGAGAGCAGATCGATGTTCCCTTCAGAA 2667  
QY 181 SerLysGlnLysLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200  
Db 2668 TCAAAACAAAGAAGGTTGAAGAAATTTCTTGGGATTCAGAGCTCCCGTGAGACTGTT 2727  
QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysLeuSer 220  
Db 2728 TCACAGAAGGATGTGTGTATCCCAAGGCTACACATCAAAAGAAATGATTAATAATAGT 2787  
QY 221 GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu 240  
Db 2788 GGAATAATTAGAGATTCACTAGCTATCAAAATCTTGGATACAGTTCACTCTGTGAA 2847  
QY 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260  
Db 2848 AGAGCAAGGAACTTCAAAAGATCACTGTGAACACGTACAGGAAAAAATGGAACAATG 2907  
QY 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluLeuLysSerGln 280  
Db 2908 AAAAAGAAGTTTTGTGTACTGAAAAGAAACTGTGAGAACCAAGAAATTAATCAAG 2967  
QY 281 LeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuThrLeuAsn 300  
Db 2968 TTAGAGAACCAAAAGTTAAATGGGAAACAAGGCTCTGCAGTGTGAGATTGACTTTAAAC 3027  
QY 301 GlnGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluLeu 320  
Db 3028 CAAGAAGAGAGAGAGAGAAATCCGATATATTAAATGAAAAAATTAGGGAAGAATTA 3087  
QY 321 GlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGluGlnAla 340  
Db 3088 GGAAGAATCGAAGAGCAGCATAGGAAGAGTTAGAAGTGAACACAACTTGAACAGGCT 3147  
QY 341 LeuArgIleGluAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360  
Db 3148 CTCAGAATAACAAGATATAGAAATGAGAGTGTAGAAAGTAATTTGAATCAGGTTTCTCAC 3207  
QY 361 ThrHisGluAsnGluAsnTrpLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380  
Db 3208 ACTCATGAATGAAATATCTCTACATGAATTTGATGTTGAAAAGAAATTTGCC 3267  
QY 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTrpGlnGluLysGluAsnLysTrp 400  
Db 3268 ATGCTAAAACCTGGAATAGCCACACTGAAACCAATACCAAGAAAGAAATTAATATAC 3327  
QY 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420  
Db 3328 TTTGAGGACATTAAGATTTTAAAGAAAGAAATGCTGAACCTTCAGATGACCCCTAAATCTG 3387  
QY 421 LysGluGluSerLeuThrLysArgAlaSerGlnTrpSerGlyGlnLeuLysValLeuIle 440

Db 3388 AAAGAGGAATCAATTAACTAAAGGCGCATCTCAATATAGTGGCAGCTTAAAGTTCTGATA 3447  
QY 441 AlaGluAsnThrMetLeuThrSerLysLeuLysGlnAspLysGlnLeuLeuGlu 460  
Db 3448 GCTGAGACACAAATGCTCCTTCTTAATTTGAAGGAAAAACAGACAAAGAAATCTAGAG 3507  
QY 461 AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480  
Db 3508 GCAGAAATTTGAATCACACCATCTAGATGGCTTCTGTCTGACAAAGACCATGATCAAT 3567  
QY 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500  
Db 3568 GTGACATCAAGAAAGATCARGAACCTGTTTCCACATTCGAGGAGATGCTTGTGTTGCAA 3627  
QY 501 ArgLysMetAsnValAspValSerSerThr 510  
Db 3628 AGAAAAATGAATGTTGATGTGAGTAGTAG 3657

## RESULT 9

US-10-007-805-490  
; Sequence 490, Application US/10007805  
; Publication No. US20020150581A1  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Dillion, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Durham, Margarita  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.470C10  
; CURRENT APPLICATION NUMBER: US/10/007,805  
; CURRENT FILING DATE: 2001-12-07  
; NUMBER OF SEQ ID NOS: 593  
; SOFTWARE: FastSeq for Windows Version 4.0.  
; SEQ ID NO 490  
; LENGTH: 3288  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-007-805-490

Alignment Scores:  
Pred. No.: 1.4e-224 Length: 3288  
Score: 2578.00 Matches: 506  
Percent Similarity: 99.61% Conservative: 2  
Best Local Similarity: 99.61% Mismatches: 0  
Query Match: 99.19% Indels: 0  
DB: Gaps: 0

US-09-451-739H-16 (1-512) x US-10-007-805-490 (1-3288)

QY 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspValGlnThrPheLysAla 20  
Db 1291 ATGAAAGCTTTCTATTCCAACTAAAGGCTTAGAATTGATGACATGCAAACTTTCAAAGCA 1350  
QY 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40  
Db 1351 GAGCTCCCGAAGCAATCTGCTTCGAGCGCTGCCATTGAAATGCAAAAGTCTGTCCA 1410  
QY 41 AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluLeuProSer 60  
Db 1411 AATAAGCTTTGGAATTTGAAGAATGAACAACATTGAGAGCAGATGAGATCTCCCATCA 1470  
QY 61 GluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGluSerLeuCysGluThr 80  
Db 1471 GAATCCAAACAAAGGACTATGAGAAAGTCTTGTGGATCTCTGTGAGACT 1530

QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLeuLeuLeuLeuLys 100  
Db 1531 GTTTCAGAGAGATGTTGTTTACCAAGGCTRCRCATCAAAAAGAAATAGATAAATA 1590  
QY 101 AsnGlyLysLeuGluGlnSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120  
Db 1591 AATGGAAATTTAGAGAGCTCTCGTATATGATGATGTTTCTGAAGGCTCCCTGCGAATG 1650  
QY 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140  
Db 1651 AAAGTTTCTATTCCAACTAAAGCCTTTAGAAATTCATGATGCATGCACAACTTTCAAAGCAGAG 1710  
QY 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetClnLysSerValProAsn 160  
Db 1711 CCTCCCGAGAGAGCATCTGCTTCAGAGCTGCGCAATGAAATGCAAAAGTCTGTTCCAAAT 1770  
QY 161 LysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180  
Db 1771 AAAGCCTTGGAAATGAAGATGAACAAACATTCAGAGAGCATCAGATGTTCCCTTCAGAA 1830  
QY 181 SerLysGlnLysLysValGluGlnLysAsnSerTrpAspSerGluSerLeuArgGlnThrVal 200  
Db 1831 TCAAAAACAAAGAAAGTTGAAGAAATTTCTGGATTCGAGAGTCTCCGTGAGACTGTT 1890  
QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220  
Db 1891 TCACAGAGAGTGTGTGTACCCAGGCTACACATCAAAAGAAATGATGATAAATAAGT 1950  
QY 221 GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu 240  
Db 1951 GGAATAATTAGAGATTCACATAGCCATCAAAAATCTTGATACAGTTCATTTCTGTGA 2010  
QY 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260  
Db 2011 AGACCAAGGNACTTCAAAAGATCACTGTGAACACGTACAGCAAAATGGAACAAATG 2070  
QY 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluLysLeuLysGluLysSerGln 280  
Db 2071 AAAAAGAAGTTTCTGTACTGAAAAGAACTGTGCAAGCAAAAGAAATAAATAACACAG 2130  
QY 281 LeuGluAsnGlnLysValLysTrpGluGlnLeuCysSerValArgLeuThrLeuAsn 300  
Db 2131 TTAGAGAACCAAAAGTTAAATGGAAACAGAGCTCTGCAAGTGTGAGATTGACTTTAATC 2190  
QY 301 GlnGluGluLysArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320  
Db 2191 CAAGAGAGAGAGAGAGAGAGATCCGATATTAATGAAATAATAGGGAAGATTA 2250  
QY 321 GlyArgIleGluGlnGlnHisArgLysGluLeuValLysGlnGlnLeuGluGlnAla 340  
Db 2251 GGAAGATCGAAGAGCAGCATAGGAAGAGTTAGAGTGAACAACTTGACAGGCT 2310  
QY 341 LeuArgIleGlnAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360  
Db 2311 CTCAGATACAGATATAGAAATTCAGAGTGTAGAAAGTAAATTTGAATCAGGTTCTCAC 2370  
QY 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380  
Db 2371 ACTCATGAAATGAAATAATTTCTTACATGAAATTTGATGTTGAAAGGAAATTCGC 2430  
QY 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400  
Db 2431 ATGCTAAACTGGAAATAGCCACACTGAAACACCAATACAGGAAAGAAATAAATAAC 2490  
QY 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420  
Db 2491 TTTGAGGACATTAAGATTTTAAAGAAAGAAATGCTGAACCTTCAGATGACCCATAAACTG 2550  
QY 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle 440  
Db 2551 AAAGAGGATCATTAACCTAAAGGGCATCTCAATATAGTGGCAGCTTAAAGTTCTGATA 2610  
QY 441 AlaGluAsnThrMetLeuThrSerLysLysLeuLysGlnAspLysGluIleLeuGlu 460

Db 2611 GCTGAGAACCAATGCTCACTTCTAAATTTAGAGAAAAACAGACAAAGAAATACAGAG 2670  
QY 461 AlaGluIleGluSerHisProArgLeuAlaSerAlaValGlnAspHisGlnIle 480  
Db 2671 CGAAATTTGAATCACACCATCTAGACTGGCTTCGCTGTACAGACCATGATCAAT 2730  
QY 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGluAspAlaCysLeuGln 500  
Db 2731 GTGACATCAAGAAAAAGTCAAGAACTGCTTTCCATTCGAGAGATGCTGTGTTGCA 2790  
QY 501 ArgLysMetAsnValAspValSerSerThr 510  
Db 2791 AGAAAAATGAATGTTGATGTAGTAGTACG 2820  
RESULT 10  
US-10-076-622-490  
; Sequence 490, Application US/10076622  
; Publication No. US20030023036A1  
; GENERAL INFORMATION:  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Sleath, Paul R.  
; APPLICANT: Peising, David H.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER  
; FILE REFERENCE: 210121.470C11  
; CURRENT APPLICATION NUMBER: US/10/076.622  
; CURRENT FILING DATE: 2002-02-13  
; NUMBER OF SEQ ID NOS: 627  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 490  
; LENGTH: 3288  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-076-622-490  
Alignment Scores:  
Pred. No.: 1,48-224 Length: 3288  
Score: 2578.00 Matches: 508  
Percent Similarity: 99.61% Conservative: 0  
Best Local Similarity: 99.61% Mismatches: 2  
Query Match: 99.19% Indels: 0  
DB: 15 Gaps: 0  
US-09-451-739H-16 (1-512) x US-10-076-622-490 (1-3288)  
QY 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20  
Db 1291 ATGAAAGTTTCTATTCCAACTAAAGCCTTAGAATTTGATGGACATGCAAACTTTCAAAGCA 1350  
QY 21 GluProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40  
Db 1351 GAGCCTCCGAGAGAGCCATCTGCCCTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCTCA 1410  
QY 41 AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 60  
Db 1411 AATAAAGCCTTGGAAATTTGAAGATGAACAAACATTTAGAGCAGATGAGATCTCCCATCA 1470  
QY 61 GluSerLysGlnLysAspTyrClnLysSerTrpAspSerGluSerLeuCysGluThr 80  
Db 1471 GAATCAACAAAGAGACTATGAGAAAGTCTTCGGATTCGAGAGTCTCTGTGAGACT 1530  
QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100  
Db 1531 GTTTCAGAGAGATGTTGTTTACCAAGGCTRCRCATCAAAAGAAATAAATAAATA 1590  
QY 101 AsnGlyLysLeuGluGlnSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120  
Db 1591 AATGGAAATTTAGAGAGTCTCCCTGATATGATGTTTCTGAAGGCTCCCTGCGAATG 1650  
QY 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140  
Db 1651 AAAGTTTCTATTCCAACTAAAGCCTTAGAATTTAGAGATGAGACATGCAAACTTTCAAAGCAGAG 1710



QY 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160  
DB 1711 CCTCCGAGAGCCATCTGCTTGGAGCTGCCATTGAAATGCAAAAGTCTGTTCCTCAAT 1770  
QY 161 LysAlaLeuGluLysLeuLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180  
DB 1771 AAAGCCTTGGAAATGAAGAATGACACACATTTGAGAGCAGATCAGATCTTCCCTTCAGAA 1830  
QY 181 SerLysGlnLysLysValGluLysValGluLysSerTrpAspSerGluSerLeuArgGluThrVal 200  
DB 1831 TCACAAACAAAGAGAGTTGAGAAATTTCTTGGAGTCTCGAGTCTCCGTCGACATGTT 1890  
QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220  
DB 1891 TCACAGAGGATGTGTGTACCCAGGCTACACATCAAAAGAAGTGAATAAATAGT 1950  
QY 221 GlyLysLeuGluAspSerThrSerLeuSerLysLysLeuAspThrValHisSerCysGlu 240  
DB 1951 GGAAATTTAGAGATTCAACTAGCTATCAAAAATCTTGGATACAGTTTCATTTGTGAA 2010  
QY 241 ArgAlaArgGluLysGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260  
DB 2011 ACAGCAAGGAACTTCAAAAGATCCTGTGACACGCTACAGAAATGCAACAATG 2070  
QY 261 LysLysLysPheCysValLeuLysLysLysLysLeuSerGluAlaLysGluLysSerGln 280  
DB 2071 AAAAAGAGTCTTGTGTACTGAAAAAGAACTGTGAGAGCAAAAGAAATTAATTCACAG 2130  
QY 281 LeuGluAsnGlnLysValLysTrpGluGlnGluLysCysSerValArgLeuThrLeuAsn 300  
DB 2131 TTAGAGAACCAAAAGTTAAATGGGACAAAGAGCTCTCGAGTGTGAGATTGACTTTAAAC 2190  
QY 301 GlnGluGluGluLysArgArgAsnAlaAspLeuAsnGluLysIleArgGluGluLeu 320  
DB 2191 CAAGAAGAAGAGAGAGAAATCCCGATATATTAAATGAAAAATTAGGAGAAATTA 2250  
QY 321 GlyArgIleGluGluGlnHisArgLysGluLysValLysGlnLysGlnGluAla 340  
DB 2251 GGAAGAAATCGAAGAGCAGATAGGAAGAGTTAGAAAGTGAACACAACTTGAACAGCT 2310  
QY 341 LeuArgIleGlnAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360  
DB 2311 CTCAGATACAGATATAGATTGAAGAGTGTAGAAAGTAAATTTGAATCAGGTTCTCAC 2370  
QY 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluLysAla 380  
DB 2371 ACTCATGAAATGAAATTTATCTTACATGAAATTCATGTGTAAGAAAGAAATTTGCC 2430  
QY 381 MetLeuLysLeuGluLysAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400  
DB 2431 ATGCTAAACTGGAATAGCCACACTGAACACCATACAGGAAAGAAATTAATATAC 2490  
QY 401 PheGluAspIleLysLysLysLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420  
DB 2491 TTTGAGGACATTAAGATTTTAAAGAAAGAAATGCTGAATTCAGATGACCTTAAACTG 2550  
QY 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyLysValLeuLysValLeu 440  
DB 2551 AAAGAGGAATCATTAACATAAAGGGCACTCATATAGTGGCAGCTTAAAGTTCTGATA 2610  
QY 441 AlaGluAsnThrMetLeuThrSerLysLysLysGluLysGlnAspLysGluLysLeuGlu 460  
DB 2611 GCTGAGAACACAAATGCTCACTTAAATTTGAAGGAAAAACAGACAAAGAAATATACAG 2670  
QY 461 AlaGluLysSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480  
DB 2671 GCAGAAATTTGAATCACACCATCTAGCTGGTCTCTGTGTACAAAGACCATGATCAAAAT 2730  
QY 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500  
DB 2731 GTGACATCAAGAAAAAGTCAAGAACTGCTTTCCACATTCAGGAGATGCTGTGTTGCAA 2790

QY 501 ArgLysMetAsnValAspValSerSerThr 510  
DB 2791 AGAAAAATGAATGTTGATGTGAGTAGTAGC 2820

## RESULT 11

US-10-124-805-490  
; Sequence 490, Application US/10124805  
; Publication No. US20030166022A1  
; GENERAL INFORMATION:  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Sleath, Paul R.  
; APPLICANT: Slesing, David H.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.470C12  
; CURRENT APPLICATION NUMBER: US/10/124,805  
; CURRENT FILING DATE: 2002-04-15  
; NUMBER OF SEQ ID NOS: 627  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 490  
; LENGTH: 3288  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-124-805-490

Alignment Scores: 1.4e-224 Length: 3288  
Pred. No.: 2578.00 Matches: 508  
Score: 2578.00  
Percent Similarity: 99.61% Conservative: 0  
Best Local Similarity: 99.61% Mismatches: 2  
Query Match: 99.19% Indels: 0  
DB: 15 Gaps: 0

US-09-451-739H-16 (1-512) x US-10-124-805-490 (1-3288)

QY 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20  
DB 1291 ATGAAAGTTTCTATTCCAACTAAAGCCTTAGAATTTGATGGACATGCAAACTTCAAGCA 1350  
QY 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40  
DB 1351 GAGCCTCCCGAGAGCCATCTGCTTCGAGCTGCCATTTGAAATGAAAGTCTGTTC 1410  
QY 41 AsnLysAlaLeuLysLysAsnGluGlnThrLeuArgAlaAspGluLysLeuProSer 60  
DB 1411 AATAAGCCTTCGAATTTGAAGATGAACAAACATTTGAGAGCAGATGAGATCTCCATCA 1470  
QY 61 GluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGluSerLeuCysGluThr 80  
DB 1471 GAATCCAAACAAAGAGACTATGAAGAAAGTCTTGGGATTTCTGAGAGTCTCTGAGAGCT 1530  
QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLysLysIle 100  
DB 1531 GTTTCAGAGAGATGTGTGTTTACCAGGCTTCRCATCAAAAGAAATAGATAAATA 1590  
QY 101 AsnGlyLysLeuGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120  
DB 1591 AATGGAATTTAGAGAGCTCTCCTGATAATGATGGTTTCTGAGGCTCCCTCGCAAGT 1650  
QY 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140  
DB 1651 AAAGTTTCTATTCCAACTAAAGCCTTAGAATTTGATGGACATGCAAACTTCAAGCAGAG 1710  
QY 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160  
DB 1711 CCTCCGAGAGCACTCTGCTTCGAGCCTGCCATTTGAAATGCAAAAGTCTGTTCCTCAAT 1770  
QY 161 LysAlaLeuLysLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180  
DB 1771 AAAGCCTTGAATTTGAAGAAATGAACAAACATTTGAGAGCAGATCAGATGTTCCCTTCAGAA 1830  
QY 181 SerLysGlnLysLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200



Db 1831 TCAAAACAAAAGASGTTGAAGAAAATCTTGGGATCTCGAGAGTCTCCGTGAGACTGTT 1890  
Qy SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220  
Db 1891 TCACAGAGGATGTGTGTACCAAGCTACACATCAAAAGAAATGGATAAAATAGT 1950  
Qy GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu 240  
Db 1951 GGAATAATTAGAAAGATTCACTAGGCTATCAAAAATCTTGATACAGTTCACTTTGGAA 2010  
Qy 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260  
Db 2011 AGAGCAAGGGAACCTCAAAAAGATCACTGTGAACAACGTACAGGAAAAATGGAACAAATG 2070  
Qy 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluLysSerGln 280  
Db 2071 AAAAAGAAGTTTGTGTACTGAAAAGAAATCTGTCAGAACCAAGAAATAAAATCACAG 2130  
Qy 281 LeuGluAsnGlnLysValLysValLysGlnGlnLeuLysCysSerValArgLeuThrLeuAsn 300  
Db 2131 TTAGAGAACCAAAAAGTTAAATGGGAACAAGAGCTCTGCAGTGTGAGATTGACTTTAAAC 2190  
Qy 301 GlnGluGluGluLysArgArgAsnAlaAspIleLeuAsnGlnLysIleArgGluGluLeu 320  
Db 2191 CAAGAGAGAGAGAGAGAGAAATGCCGATATATTAATGAAAATAATAGGGAAGATTA 2250  
Qy 321 GlyArgIleGluGluGlnHisArgLysGluLeuValLysGlnGlnLeuGluGlnAla 340  
Db 2251 GGAAGATCGAAGAGCAGCATAGAAAGATTAGAACTGAAACAACTTTGACAGGCT 2310  
Qy 341 LeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis 360  
Db 2311 CTCAGATACAGATATAGAAATGAGAGATGAGAAAGTAATTTGAATCAGGTTCTCTAC 2370  
Qy 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380  
Db 2371 ACTCATGAAATGAAATTAATCTTATCATGAAATTCGATGTTGAAAAGGAAATGTC 2430  
Qy 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400  
Db 2431 ATGCTAAACTGGAATAGCCACACTGAAACCAATACCAGGAAAAGGAAAATAAATAC 2490  
Qy 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420  
Db 2491 TTTGAGGACATTAGATTTTAAAGAAAGAAATGCTGAACTTCAGATGACCTTAAACTG 2550  
Qy 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle 440  
Db 2551 AAAGAGGAATCATTAACATAAAGGCACTCTCAATATAGTGGGAGCTTAAAGTTCTGATA 2610  
Qy 441 AlaGluAsnThrMetLeuThrSerLysLysGlnLysGlnAspLysGluIleLeuGlu 460  
Db 2611 GCTGAGAACACAATGCTCCTCCTTCTAAATTTGAAGGAAAACAAAGACAAAGAAATCTAGAG 2670  
Qy 461 AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480  
Db 2671 GCAGAAATTTGAATCACACCATCTAGAGCTGCTCTCTGTGTACAGACCATGATCAAT 2730  
Qy 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500  
Db 2731 GTGACATCAAGAAAAGTCAAGAACCTGCTTTCACATTCGAGAGATGCTTGTGTTGCAA 2790  
Qy 501 ArgLysMetAsnValAspValSerSerThr 510  
Db 2791 AGAAAATGAATGTTGATGTGAGTAGTACG 2820

## RESULT 12

US-09-604-287A-474  
; Sequence 474, Application US/09604287A  
; Patent No. US20020064872A1  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yuqiu  
; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Hepler, William T.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE OF INVENTION: DIAGNOSIS OF BREAST CANCER  
; FILE REFERENCE: 210121.470C7  
; CURRENT APPLICATION NUMBER: US/09/604,287A  
; SOFTWARE: FastSeq for Windows Version 3.0  
; NUMBER OF SEQ ID NOS: 489  
; CURRENT FILING DATE: 2000-06-22  
; SEQ ID NO 474  
; LENGTH: 3865  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (2448)...(2631)  
; OTHER INFORMATION: 184 bp insert of B726P splice form  
US-09-604-287A-474

Alignment Scores:  
Pred. No.: 1,728-224 Length: 3865  
Score: 2578.00 Matches: 508  
Percent Similarity: 99.61% Conservative: 2  
Best Local Similarity: 99.61% Mismatches: 2  
Query Match: 99.19% Indels: 0  
DB: 9 Gaps: 0

US-09-451-739H-16 (1-512) x US-09-604-287A-474 (1-3865)

Qy 1 MetLysValSerIleProThrLysAlaLeuGluMetAspMetGlnThrPheLysAla 20  
Db 1563 ATGAAAGTTTCTATTCCAACTAAAGCCCTTAGAATGTGACATGCAAACTTTCAAAGCA 1622  
Qy 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40  
Db 1623 GAGCTCTCCGAGAGCCATCTGCCTTCGAGCTGCCATTGAAATGCAAAAGTCTGTTCCA 1682  
Qy 41 AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 60  
Db 1683 AATAAAGCCTTGGAAATGAAGATGACAAACATTTGAGAGCAGATGAGACTCCCATCA 1742  
Qy 61 GluSerLysGlnLysAspTyrGluLysSerSerTrpAspSerGluSerLeuCysGluThr 80  
Db 1743 GAATCCAAACAAAGAGACTATGAAGAAATTTCTGGGATTTCTGAGAGTCTCTGTGAGACT 1802  
Qy 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100  
Db 1803 GTTTCACAGAGAGTGTGTGTTTACCCCAAGGCTRCRCATCAAAAAGAAATAGATAAAATA 1862  
Qy 101 AsnGlyLysLeuGluLysProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120  
Db 1863 AATGAAAATTAGAAGAGTCTCCTGATATGATGTTTCTGAAAGGCTCCCTGCAGAAATG 1922  
Qy 121 LysValSerIleProThrLysAlaLeuGluMetAspMetGlnThrPheLysAlaGlu 140  
Db 1923 AAAGTTTCTATTCCAACTAAAGCCTTAGAATGTGAGACTGCAAACTTTCAAAGCAGAG 1982  
Qy 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160  
Db 1983 CCTCCGAGAGAGCCATCTGCCTTCGAGGCTGCCATTTGAAATGCAAAAGTCTGTGTTCCAAAT 2042  
Qy 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180  
Db 2043 AAAGCCTTGGAAATGAAGATGAACAAACATTTGAGAGCAGATCAGATGTTCCCTTCAGAA 2102  
Qy 181 SerLysGlnLysLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200  
Db 2103 TCAAAACAAAAGASGTTGAAGAAAATCTTGGGATTTCTGAGAGTCTCCGAGACTGTT 2162  
Qy 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220

Db 2163 TCACAGAGGATGTGTGTCCCAAGGCTACACATCAAAAGAAATGATAAATAAGT 2222  
Qy GlyLysLeuGluAspSerThrSerLeuSerLysLysLeuAspThrValHisSerCysGlu 240  
Db 2223 GGAAAAATTAGAGATTCACATAGCTATCAAAAATCTTGGATACAGTTTCATCTGTGAA 2282  
Qy 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260  
Db 2283 AGAGCAAGGGAACCTTCAAAAGATCCTGTGACACACCTGACAGAAAAATGGAACAATG 2342  
Qy LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluLysSerGln 280  
Db 2343 AAAAACAAGTTTGTGTACTGAAAGAAATCTGTGAGAGCAAGAAAGAAATTAATCAAG 2402  
Qy 281 LeuGluAsnGlnLysValLysTrpGluGlnGluLeuLysCysSerValArgLeuThrLeuAsn 300  
Db 2403 TTAGAGAACCAAAAGATTAAATGGGCAACAGAGCTCTGCAGTGTGAGATTGACTTTAAAC 2462  
Qy GlnGluGluGluLysArgArgAsnAlaAspLeuLeuAsnGluLysLysLeuGluGluLeu 320  
Db 2463 CAAGAAGAGAGAGAGAGAAATCCGATATATTTAAATGAAATAATTAGGGAAGAAATTA 2522  
Qy 321 GlyArgGluGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGluAla 340  
Db 2523 GGAAGATCGAGAGACAGCATAGGAAGATTAGAGTGAACACACAACTTGAACAGCT 2582  
Qy 341 LeuArgGlnAspLeuLysSerValGluSerAsnLeuAsnGlnValSerHis 360  
Db 2583 CTCAGATACAGATATAGATTGAAGAGTGTAGAAAGTAAATTTGAATCAGGTTTCTCAC 2642  
Qy 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluLeuAla 380  
Db 2643 ACTCATGAAATGAAATATCTTACATGAAATTTGCATGTTGAAAGAGAAATTTGCC 2702  
Qy 381 MetLeuLysLeuGluLeuAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400  
Db 2703 ATGTAAAACTGGAAATAGCCACACTGAAACACCAATACCAGAAAGAAAGAAATAATAC 2762  
Qy 401 PheGluAspLysLysLysLysLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420  
Db 2763 TTGTAGGACATTAGATTTTAAAGAAAGAAATGCTGAACCTTCAGATCACCTTAAACCTG 2822  
Qy 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuLeu 440  
Db 2823 AAAGAGGATCATTAACTAAGAGGCACTCTCAATATAGTGGCAGCTTAAGTCTGATA 2882  
Qy 441 AlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLysGluLeuLeuGlu 460  
Db 2883 GCTGAGAACACATGCTCACTTCTTAATTTGAAGGAAACCAAGACAAAGAAATACATAGAG 2942  
Qy 461 AlaGluLeuGluSerHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480  
Db 2943 GCAGAAATTTGAATCACACCATCTAGACTGGCTTCTGTGTACAGACCATGATCAATTT 3002  
Qy 481 ValThrSerArgLysSerGlnGluProAlaPheHisLysLeuAlaGlyAspAlaCysLeuGln 500  
Db 3003 GTGACATCAAGAAAAAGTCAAGAACCTGCTTTCCCACTTGCAGGAGATGCTTTGTTGAA 3062  
Qy 501 ArgLysMetAsnValAspValSerSerThr 510  
Db 3063 AGAAAAATGAATGTTGATGTGAGTAGTACG 3092

## RESULT 13

US-09-551-621-474  
; Sequence 474, Application US/09551621  
; Publication No. US20030104366A1  
; GENERAL INFORMATION:  
; APPLICANT: Yuqi, Jiang  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND

; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE  
; FILE REFERENCE: 210121.470C5  
; CURRENT APPLICATION NUMBER: US/09/551,621  
; CURRENT FILING DATE: 2000-04-17  
; NUMBER OF SEQ ID NOS: 479  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 474  
; LENGTH: 3865  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (2448)...(2631)  
; OTHER INFORMATION: 184 bp insert of B726P splice form  
; US-09-551-621-474  
Alignment Scores:  
Pred. No.: 1,72e-224 Length: 3865  
Score: 2578.00 Matches: 508  
Percent Similarity: 99.61% Conservative: 0  
Best Local Similarity: 99.61% Mismatches: 2  
Query Match: 99.19% Indels: 0  
DB: 10 Gaps: 0  
US-09-451-739H-16 (1-512) x US-09-551-621-474 (1-3865)

Qy 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20  
Db 1563 ATGAAAGTTTCTATTCCAACTAAGCCTTAGAATTTGATGACATGCAAACTTTCAAAGCA 1622  
Qy 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40  
Db 1623 GAGCTTCCCGAGAGGCATCTGCTTCGAGCTGCCATTGAATGCAAAAGTCTGTTCCTCA 1682  
Qy 41 AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluLeuLeuProSer 60  
Db 1683 AATAAAGCCTTGGAAATTGAAGAATGAACAACATTCAGAGCAGATGAGATCTCCCATCA 1742  
Qy 61 GluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGluSerLeuCysGluThr 80  
Db 1743 GAATCCAAACAAGAGCACTATGAGAAAGTCTTGGGANTCTCGAGTCTCTGTGAGACT 1802  
Qy 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLeuAspLysIle 100  
Db 1803 GTTTCACAGAGGATGTGTGTTTACCAAGGCTTCRCATCAAAAGAAATAGATAAAATA 1862  
Qy 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120  
Db 1863 AATGGAAAAATAGAGAGTCTCTGATAATGATGGTTTTCTGAAGGCTCCCTGCAGAAATG 1922  
Qy 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140  
Db 1923 AAAGTTTCTATTCCAACTAAGCCTTAGAATTCAGATGACATGCAAACTTTCAAAGCAGAG 1982  
Qy 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160  
Db 1983 CTTCCCGAGAGGCATCTGCTTCGAGCTGCGCAATGAAATGAAAGTCTGTGTCCAAAT 2042  
Qy 161 LysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180  
Db 2043 AAAGCCTTGAATTTGAAGATGAACAACATTCAGAGCAGATCAGATGTTCCCTTCAGAA 2102  
Qy 181 SerLysGlnLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200  
Db 2103 TCAAAACAAAAGAAAGTTGAAGAAAAATCTTGGGATTTCTGAGAGTCTCCGTGAGACTGT 2162  
Qy 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220  
Db 2163 TCACAGAGGATGTGTGTGTACCAAGGCTTACATCAAAAGAAATGATTAATAGT 2222  
Qy 221 GlyLysLeuGluAspSerThrSerLeuSerLysLysLeuAspThrValHisSerCysGlu 240  
Db 2223 GGAAAAATTAGAGATTCAACTAGCTATCAAAATCTTGATACAGTTCATTCTTGTGAA 2282

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Qy 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
Db 2283 AGAGCAAGGGAACTTCAAAAGATCACTGTGAACAACGTACAGAAAATGGAAACAATG 2342
Qy 261 LysLysLysPheCysValLeuLysLysLysSerGluAlaLysGluLysSerGln 280
Db 2343 AAAAGAAGTTTGTGTACTGAAAAAGAACTGTCAAGACAAAGAAATAAATCACAG 2402
Qy 281 LeuGluGlnLysValLysThrGluGlnLeuGlnCysSerValArgLeuThrLeuAsn 300
Db 2403 TTAGAGAACCAAAAGTTAAATGGGAACAAGAGCTCTGCAGTGTGAGATTGACCTTAAAC 2462
Qy 301 GlnGluGluGluLysArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320
Db 2463 CAGAGAGAGAGAGAGAGAGAAATGCCGATATTAATGAATAATAGGAGAAATTA 2522
Qy 321 GlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGluGlnAla 340
Db 2523 GGAAGAATCGAAGAGCAGCATAGGAAGAGTAGAAGTGAACCAACCACTTGAAACGGCT 2582
Qy 341 LeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis 360
Db 2583 CTCAGATACAGATATAGAAATGAGAGGTGAGAAAGTAAATTTGAATCAGGTTCTCAC 2642
Qy 361 ThrHisGluAsnGluAsnThrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380
Db 2643 ACTCATGAAATGAAATATATCTCTTACATGAAATTCGATGTTGAAAAAGGAAATGTC 2702
Qy 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnThrGlnGluLysGluAsnLysTyr 400
Db 2703 ATGCTAAACCTGGAATAGCCACACTGAAACCAACATACCAGGAAGAAAGAAATAATAC 2762
Qy 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
Db 2763 TTGGAGACATTAAGATTTTAAAGAAAGAAATGCTGAACCTTCAGATGACCTAAAACTG 2822
Qy 421 LysGluGluSerLeuThrLysArgAlaSerGlnThrSerGlyGlnLeuLysValLeuIle 440
Db 2823 AAAGAGGAATCAATTAACATAAGGGCATCTCAATATAGTGGCAGCTTAAAGTTCTGATA 2882
Qy 441 AlaGluAsnThrMetLeuThrSerLysLysLysGluLysGlnAspLysGluIleLeuGlu 460
Db 2883 GCTGAGACACAACTCTCACCTTCTAAATTTGAAGGAAACCAAGCAAGAAATACTAGAG 2942
Qy 461 AlaGluIleGluSerHisArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
Db 2943 GCAGAAATGAAATCAACCATCTAGACTGGCTTCTGCTGTACAGACCATGATCAAT 3002
Qy 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
Db 3003 GTGACATCAAGAAAGTCAGAACTGCTTCCACATTCGAGGAGATGCTTGTGTCNA 3062
Qy 501 ArgLysMetAsnValAspValSerSerThr 510
Db 3063 AGAAAAATGAATGTTGATGTGAGTAGTAGC 3092
RESULT 14
US-10-007-805-474
; Sequence 474, Application US/10007805
; Publication No. US20020150581A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Durham, Margarita
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; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.470C10
; CURRENT APPLICATION NUMBER: US/10/007.805
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 593
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 474
; LENGTH: 3865
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-007-805-474
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Alignment Scores:
Pred. No.: 1,72e-224 Length: 3865
Score: 2578.00 Matches: 508
Percent Similarity: 99.61% Conservative: 0
Best Local Similarity: 99.61% Mismatches: 2
Query Match: 99.19% Indels: 0
DB: 14 Gaps: 0
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US-09-451-739H-16 (1-512) x US-10-007-805-474 (1-3865)

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Qy 1 MetLysValSerIleProThrLysAlaLeuGluMetAspMetGlnThrPheLysAla 20
Db 1563 ATGAAGTTTCTATTCCAACTTAAGCCTTAGAATTGATGGACATGCAAACTTTCARAGCA 1622
Qy 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
Db 1623 GAGCCTCCGAGAGACCATCTGCCCTTCGAGCTGCCATTGAATGCAAAAGCTGTCTCCA 1682
Qy 41 AsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 60
Db 1683 AATAAGCCTTGGAAATGAAGAAATGAACAACATTTGAGAGCAGATGAGATCTCCATCA 1742
Qy 61 GluSerLysGlnLysAspTyrGluGluSerTyrTrpAspSerGluSerLeuCysGluThr 80
Db 1743 GAATCCAAACAAAGAGACTATGAAGAAGTTCTTGGATTCTGAGAGTCTCTGTGAGACT 1802
Qy 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100
Db 1803 GTTTCACAGAGAGATGTGTGTTTACCCAGGCTRCATCAAAAGAAATAGATAAATA 1862
Qy 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
Db 1863 AATGGAAATTTAGAGAGTCTCTCTGATATGATGTTTCTGAAGGCTCCCTGCAGAAATG 1922
Qy 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140
Db 1923 AAAGTTTCTATTCCAACTTAAAGCCTTAGAATTTGATGGACATGCAAACTTTCAGAGCAG 1982
Qy 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
Db 1983 CTCCCGAGAGGCATCTGCCCTTCGAGCTGCCATTGAAATGCAAAAGTCTGTCCCAAT 2042
Qy 161 LysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluMetPheProSerGlu 180
Db 2043 AAAGCCTTGGAAATGAAGAATGAACAACATTTGAGAGCAGATCAGATGTTCCTTCAGAA 2102
Qy 181 SerLysGlnLysLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200
Db 2103 TCAAAACAAAGAGAGTTGAAGAAATTTCTGGATTCTGAGAGTCTCCGTGAGACTGT 2162
Qy 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
Db 2163 TCACAGAGAGATGTGTGTGTACCAAGGCTACACATCAAAAGAAATGATGATAATAAGT 2222
Qy 221 GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu 240
Db 2223 GGAATAATTAAGATTAACACTAGCCTATCAAAATCTTGGATACAGTTCATCTCTGTGAA 2282
Qy 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
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Db 2283 AGACGAAGGGAACCTTCAAAAGATCACTGTGAACAACGTACAGGAAAAATGGAAACAATG 2342  
Qy 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluLysSerGln 280  
Db 2343 AAAAAGAAGTTTCTGTACTGAAAGAAAGAACTGTGACAGCAAGAAAGAAATATAATCACAG 2402  
Qy 281 LeuGluAsnGlnLysValLysTrpGluGlnGluLysSerValArgLeuThrLeuAsn 300  
Db 2403 TTAGAGAACCAAAAGTTAAATGGAGCAAGAGCTCTGCAGTGTGAGATTGACTTTAAAC 2462  
Qy 301 GlnGluGluGluLysArgAsnAlaAspLysLeuAsnGluLysLysLeuArgGluLeu 320  
Db 2463 CAAGAAGAAGAGAGAGAGAAATGCCGATATATTAATGAAAAATATAGGGAAGAAATTA 2522  
Qy 321 GlyArgLysGluGlnGlnHisArgLysGluLysGluLysGlnGlnLeuGluGlnAla 340  
Db 2523 GGAAGAATCGAAGACAGCAGCATAGAAAGAGTTGAAGTGAACCAACACATGTGAACAGCT 2582  
Qy 341 LeuArgLysGlnAspLysLysGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360  
Db 2593 CTCAGATACAGATATAGATTGAAGAGTGTAGAAAGTAAATTTGAATCAGGTTTCTCAC 2642  
Qy 361 ThrHisGluAsnGluAsnTyLeuLeuHisGluLysCysMetLeuLysLysGluLysAla 380  
Db 2643 ACTCATGAAATGAAATATATCTCTTACATGAAATTTGCATGTTGAAAAAGGAAATTGCC 2702  
Qy 381 MetLeuLysLeuGluLysLeuLysHisGlnTyLeuGlnGluLysGluAsnLysTy 400  
Db 2703 ATGCTTAAATCTGGAATATAGCACTGAAACCAACATACAGGAAAGGAAATATAATAC 2762  
Qy 401 PheGluAspLysLysLysLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420  
Db 2763 TTTGAGGACATTAAGATTTTAAAGAAAGAAATGCTGAACCTTCAGATGACCTTAAACTG 2822  
Qy 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyLeuGlnGluLysValLeuLeu 440  
Db 2823 AAAGAGGAATCATTAACATAAAGGCATCTCAATATAGTGGCAGCTTAAAGTTCTGATA 2882  
Qy 441 AlaGluAsnThrMetLeuThrSerLysLysLysGluLysGlnAspLysGluLysLeu 460  
Db 2883 GCTGAGACACAATGCTCCTCAATTAATGAAGGAAACCAAGCAAAAGAAATACTAGAG 2942  
Qy 461 AlaGluLysGluSerHisProArgLeuAlaSerAlaValGlnAspHisAspGlnLe 480  
Db 2943 CGAGAAATGAATCACCATCTAGACTGGCTTCTGCTGACAGACCATGATCAATTT 3002  
Qy 481 ValThrSerArgLysSerGlnGluProAlaPheHisLysLysAlaGlyAspAlaCysLeuGln 500  
Db 3003 GTGACATCAAGAAAAAGTCAAGAACCTGCTTCCACATTCGAGGAGATGCTTTGTTGCA 3062  
Qy 501 ArgLysMetAsnValAspValSerThr 510  
Db 3063 AGAAAAATGAATGTTGATGTGAGTAGTAGC 3092

## RESULT 15

US-10-076-622-474  
; Sequence 474, Application US/10076622  
; Publication No. US20030023036A1  
; GENERAL INFORMATION:  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Sleath, Paul R.  
; APPLICANT: Persing, David H.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER  
; FILE REFERENCE: 210121.470C11  
; CURRENT APPLICATION NUMBER: US/10/076,622  
; CURRENT FILING DATE: 2002-02-13  
; NUMBER OF SEQ ID NOS: 627  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 474  
; LENGTH: 3865  
; TYPE: DNA  
; ORGANISM: Homo sapiens

## US-10-076-622-474

Alignment Scores:  
Pred. No.: 1,72e-224 Length: 3865  
Score: 2578.00 Matches: 508  
Percent Similarity: 99.61% Conservative: 0  
Best Local Similarity: 99.61% Mismatches: 2  
Query Match: 99.19% Indels: 0  
DB: 15 Gaps: 0

## US-09-451-739H-16 (1-512) x US-10-076-622-474 (1-3865)

Qy 1 MetLysValSerLysIleProThrLysAlaLeuMetAspMetGlnThrPheLysAla 20  
Db 1563 ATGAAAGTTTCTATTCCAACTAAGCCCTTAGAATGTATGGACATGCAAACTTCAAAGCA 1622  
Qy 21 GluProGluLysProSerAlaPheGluProAlaLysGluMetGlnLysSerValPro 40  
Db 1623 GAGCCTCCGGAAGAACCATCTGCCTTCGAGCCTGCCATTTGAATGCAAAAGTCTGTTCCA 1682  
Qy 41 AsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluLysLeuProSer 60  
Db 1683 AATAAAGCCTTGGAATTTGAAGATGAACAACATTTGAGACGATGAGATATCCCATCA 1742  
Qy 61 GluSerLysGlnLysAspTyLeuGluSerSerTrpAspSerGluSerLeuCysGluThr 80  
Db 1743 GAATCCAAACAAAAGGACTATGAGAAAGTTCTTGGGATTTCTGAGAGTCTCTGTGAGACT 1802  
Qy 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLysLysIle 100  
Db 1803 GTTTCACAGAGATGTGTGTTTACCAAGGCTCCCATCAAAAGAAATAGATAAATA 1862  
Qy 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120  
Db 1863 AATGGAATATTAGAAGAGTCTCTGATATGATGTTTCTGAGGCTCCCTGCAAGATG 1922  
Qy 121 LysValSerLysProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140  
Db 1923 AAAGTTTCTATTCCAACTAAGCCCTTAGAATTTGATGACATGCAAACTTCAAAGCAG 1982  
Qy 141 ProProGluLysProSerAlaPheGluProAlaLysGluMetGlnLysSerValProSer 160  
Db 1983 CCTCCGGAAGAACCATCTGCCTTCGAGCCTGCCATTTGAATGCAAAAGTCTGTTCCAAT 2042  
Qy 161 LysAlaLeuGluLysLysAsnGluGlnThrLeuArgAlaAspGluMetPheProSerGlu 180  
Db 2043 AAAGCCTTGGAATTTGAAGATGAACAACATTTGAGAGCGATCAGATGTTCCCTTCAGAA 2102  
Qy 181 SerLysGlnLysLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200  
Db 2103 TCAAAACAAAAGAAAGCTTGAAGAAATTTCTGGGATTTCTGAGAGTCTCCGTGAGACTGT 2162  
Qy 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220  
Db 2163 TCACGAAGGATGTGTGTATCCCAAGGCTACATCAATCAAAAGAAATGATATAAATAGT 2222  
Qy 221 GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu 240  
Db 2223 GGAATATTAGAGATTTCAACTAGCCTATCAAAATCTTGGATACAGTTTCATCTTTGTGAA 2282  
Qy 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGlnMet 260  
Db 2283 AGAGCAAGGGAACCTCAAAAGATCACTGTGAACACGTCACAGGAAAAATGAAACAAATG 2342  
Qy 261 LysLysLysPheCysValLeuLysLysLysLysLeuSerGluAlaLysGluLysSerGln 280  
Db 2343 AAAAAGAAGTTTGTGTACTGAAAAAGAAACTGTGAGAGCAAAAGAAATATAATCACAG 2402  
Qy 281 LeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuThrLeuAsn 300  
Db 2403 TTAGAGAACCAAAAGTTAAATGGGAACAAGAGCTCTGCAGTGTGAGATTGACTTTAAAC 2462  
Qy 301 GlnGluGluLysArgAsnAlaAspLysLeuAsnGluLysLysIleArgGluLeu 320

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Db      2463  CAAGAAGAGAGAGAGAGAAATGCCGATATATTAATGAAAAAATTAGGGAAGAAATTA 2522
Qy      321  GlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGluGlnAla 340
Db      2523  GGAAGAATCGAAGAGCAGCATAGGAAAGAGTTAGAGTGAACAACAACCTTGAACAGGCT 2582
Qy      341  LeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis 360
Db      2583  CTCAGAATACAGAATATAGAAATTTAGAGAGTGTAGAAAGTAAATTTGAATCAGGTTTCTCAC 2642
Qy      361  ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380
Db      2643  ACTCATGAAATGAAATTTATCTCTTACATGAAATTTGCATGTTGAAAAAGGAAATTGCC 2702
Qy      381  MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGlnLysGluAsnLysTyr 400
Db      2703  ATGCTAAACCTGGAATAGCCACACTGAAACACCAATACCAGGAAAGGAAATAAATAC 2762
Qy      401  PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
Db      2763  TTTGAGGACATTAAAGATTTTAAAGAAAGAAAGAAATGCTGAACCTTCAGATGACCTAAACTG 2822
Qy      421  LysGlnGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle 440
Db      2823  AAGAGGAATCATTAACCTAAAGGGGCATCTCAATATAGTGGGAGCTTAAAGTTCTGATA 2882
Qy      441  AlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLysGluIleLeuGlu 460
Db      2883  GCTGGAACACACATGCTCCTCTTAATTTGAAGGAAACAAAGACAAAGAAATACTAGAG 2942
Qy      461  AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
Db      2943  GCAGAAATTGAATCACACCATCTAGACTGGCTTCTGCTGTACAAGACCATGATCAAATT 3002
Qy      481  ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
Db      3003  GTGACATCAAGAAAAAGTCAGAAACCTGCTTTCACATTTGCAGGAGATGCTTCTTGCAA 3062
Qy      501  ArgLysMetAsnValAspValSerSerThr 510
Db      3063  AGAAAAATGAATGTTGATGTGAGTAGTACG 3092

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Search completed: May 6, 2004, 18:38:46  
 Job time : 681 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 6, 2004, 13:51:33 ; Search time 110 Seconds  
(without alignments)

2583.044 Million cell updates/sec

Title: US-09-451-739H-16

Perfect score: 2599

Sequence: 1 MKVSIPTKALELMDMQTFKA.....IAGDACLQRXNVDSSTDI 512

Scoring table:

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgm2\_1/USPRO.spool/US09451739/runat 05052004 101645 18712/app query.fasta\_1.711  
-DB=Issued\_Patents\_NA -QWMT-rascap -SUFFIX=rni -MINMATCH=0.1 -LOOFCU=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=BL0SUM62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09451739 @CGN 1 1 56 @runat 05052004 101645 18712 -NCPU=6 -ICPU=3  
-NO.MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:  
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2: /cgm2\_6/ptodata/2/ina/5B.COMB.seq:  
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5: /cgm2\_6/ptodata/2/ina/PTCUS.COMB.seq:  
6: /cgm2\_6/ptodata/2/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2578	99.2	3288	4	US-09-620-405B-490 Sequence 490, App
2	2578	99.2	3288	4	US-09-834-759-490 Sequence 490, App
3	2578	99.2	3865	4	US-09-620-405B-474 Sequence 474, App
4	2578	99.2	3865	4	US-09-604-287A-474 Sequence 474, App
5	2578	99.2	3865	4	US-09-834-759-474 Sequence 474, App
6	2227.5	85.7	2307	4	US-09-620-405B-468 Sequence 468, App
7	2227.5	85.7	2307	4	US-09-433-826B-468 Sequence 468, App
8	2227.5	85.7	2307	4	US-09-604-287A-468 Sequence 468, App
9	2227.5	85.7	2307	4	US-09-834-759-468 Sequence 468, App
10	2224.5	85.6	3681	4	US-09-620-405B-463 Sequence 463, App
11	2224.5	85.6	3681	4	US-09-433-826B-463 Sequence 463, App
12	2224.5	85.6	3681	4	US-09-604-287A-463 Sequence 463, App

13	2224.5	85.6	3681	4	US-09-834-759-463 Sequence 463, App
14	2125	81.8	1337	4	US-09-620-405B-467 Sequence 467, App
15	2125	81.8	1337	4	US-09-433-826B-467 Sequence 467, App
16	2125	81.8	1337	4	US-09-604-287A-467 Sequence 467, App
17	2125	81.8	1337	4	US-09-834-759-467 Sequence 467, App
18	1556.5	59.9	2232	4	US-09-620-405B-491 Sequence 491, App
19	1556.5	59.9	2232	4	US-09-834-759-491 Sequence 491, App
20	1532.5	59.0	1665	4	US-09-389-681-178 Sequence 178, App
21	1532.5	59.0	1665	4	US-09-620-405B-178 Sequence 178, App
22	1532.5	59.0	1665	4	US-09-339-338-178 Sequence 178, App
23	1532.5	59.0	1665	4	US-09-433-826B-178 Sequence 178, App
24	1532.5	59.0	1665	4	US-09-604-287A-178 Sequence 178, App
25	1532.5	59.0	1665	4	US-09-285-480-178 Sequence 178, App
26	1532.5	59.0	1665	4	US-09-834-759-178 Sequence 178, App
27	1384	53.3	1681	4	US-09-389-681-180 Sequence 180, App
28	1384	53.3	1681	4	US-09-620-405B-180 Sequence 180, App
29	1384	53.3	1681	4	US-09-339-338-180 Sequence 180, App
30	1384	53.3	1681	4	US-09-433-826B-180 Sequence 180, App
31	1384	53.3	1681	4	US-09-604-287A-180 Sequence 180, App
32	1384	53.3	1681	4	US-09-285-480-180 Sequence 180, App
33	1384	53.3	1681	4	US-09-834-759-180 Sequence 180, App
34	1032	39.7	1729	4	US-09-620-405B-466 Sequence 466, App
35	1032	39.7	1729	4	US-09-433-826B-466 Sequence 466, App
36	1032	39.7	1729	4	US-09-604-287A-466 Sequence 466, App
37	1032	39.7	1729	4	US-09-834-759-466 Sequence 466, App
38	889.5	34.2	1206	4	US-09-389-681-175 Sequence 175, App
39	889.5	34.2	1206	4	US-09-620-405B-175 Sequence 175, App
40	889.5	34.2	1206	4	US-09-339-338-175 Sequence 175, App
41	889.5	34.2	1206	4	US-09-433-826B-175 Sequence 175, App
42	889.5	34.2	1206	4	US-09-604-287A-175 Sequence 175, App
43	889.5	34.2	1206	4	US-09-285-480-175 Sequence 175, App
44	889.5	34.2	1206	4	US-09-834-759-175 Sequence 175, App
45	780.5	30.0	1233	4	US-09-620-405B-492 Sequence 492, App

#### ALIGNMENTS

#### RESULT 1

US-09-620-405B-490  
; Sequence 490, Application US/09620405B  
; Patent No. 6528054  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yuguu  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Repler, William T.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER  
; FILE REFERENCE: 21021.470C8  
; CURRENT APPLICATION NUMBER: US/09/620,405B  
; CURRENT FILING DATE: 2000-07-20  
; NUMBER OF SEQ ID NOS: 495  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 490  
; LENGTH: 3288  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-620-405B-490

Alignment Scores:  
Pred. No.: 2,23e-270 Length: 3288  
Score: 2578.00 Matches: 508  
Percent Similarity: 99.61% Conservative: 0  
Best Local Similarity: 99.61% Mismatches: 2  
Query Match: 99.19% Indels: 0  
DB: 4 Gaps: 0

US-09-451-739H-16 (1-512) x US-09-620-405B-490 (1-3288)

Oy 1 MetLysValSerIleProThrIysAlaLeuMetAspMetGlnThrPhelysAla 20

Db 1291 ATGAAAGTTCTTATTCCTCAACTAAAGCCTTAGAATGTAGTGGACATGCACAACTTTCAGAGCA 1350  
 Qy 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetClnLysSerValPro 40  
 Db 1351 GAGCCTCCCGAGAGGCACTCTGCTTCGAGCCTGCCATTGAAATGCAAAAGTCTCTTCCA 1410  
 Qy 41 AsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluLysLeuProSer 60  
 Db 1411 AATAAAGCCTTGAAATTGAAGATGAACAAACATTGAGAGCAGATGAGATATCCCATCA 1470  
 Qy 61 GluSerLysGlnLysAspTyrGluGluSerSerTyrAspSerGluSerLeuCysGluThr 80  
 Db 1471 GATCCAAACAAAGGACATGATGAAGAAAGTCTCTGGGATTCTGAGAGTCTCTGTGAGACT 1530  
 Qy 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLysLeuLysIle 100  
 Db 1531 GTTTCACAGAGATGTGTGTTTACCAGGCTTCFCATCAAAAGAAATAGATAAATA 1590  
 Qy 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120  
 Db 1591 AATGGAATAATAGAGAGTCTCTGATATGATGTTTCTGAGGCTCCCTGCAGATG 1650  
 Qy 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140  
 Db 1651 AAAGTTTCTATTCCAACTAAAGCCTTAGAATTGATGACATGCACAACTTTCAGAGCAG 1710  
 Qy 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160  
 Db 1711 CCTCCCGAGAGCCTCTGCTTCGAGCTGCCATTGAATGCAGAACTGTGTCCAAAT 1770  
 Qy 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180  
 Db 1771 AAAGCCTTGGAAATGAAGAATGAACAAACATTGAGAGCAGATGATGTTCCCTTCAGAA 1830  
 Qy 181 SerLysGlnLysValGluGluAsnSerTyrAspSerGluSerLeuArgGluThrVal 200  
 Db 1831 TCAAAACAAAGAGAGTTGAGAAATCTCTGGATTCTGAGAGTCTCCGTGAGAGTGT 1890  
 Qy 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220  
 Db 1891 TCAGAGAGGATGTGTGTGTACCCAGGCTACATCAAAAGAAATGGATAAATGAAT 1950  
 Qy 221 GlyLysLeuGluAspSerThrSerLysSerLysIleLeuAspThrValHisSerCysGlu 240  
 Db 1951 GGAAATTTGAAGATTCACTAGCTATCAAAATCTGGATACAGTTCATCTTGTGAA 2010  
 Qy 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260  
 Db 2011 AGAGCAAGGAACTTCAAAAGATCACTGTGAACAACGTACAGGAAATGGACAAATG 2070  
 Qy 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluLysSerGln 280  
 Db 2071 AAAAAGAGTTTGTGTACTGAAAGAACTGTGAGAGCAAAAGAAATGAATATCAG 2130  
 Qy 281 LeuGluAsnGlnLysValLysTyrPgluGlnLysCysSerValArgLeuThrLeuAsn 300  
 Db 2131 TTAGAGACCAAAAGTTAAATGGAAACAGAGCTCTGAGTGTGAGATTGACTTTAAAC 2190  
 Qy 301 GlnGluGluGluLysArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320  
 Db 2191 CAAGAGAGAGAGAGAGAAATCCCATATATTAATGAAATTAATTTAGGAGAGATTA 2250  
 Qy 321 GlyArgIleGluGluGlnHisArgLysGluLeuValLysGlnGlnLeuGluAla 340  
 Db 2251 GGAAGATCGAAGAGCAGCATAGGAAGAGTTAGAGTGAACAACTTGAACAGGCT 2310  
 Qy 341 LeuArgIleGlnAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360  
 Db 2311 CTCAGAAATCAAGATATGAATGAGAGTGTAGAAAGTAAATTTGAATCAGTTTCTCAC 2370  
 Qy 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380  
 Db 2371 ACTCATGAATGAAATTAATCTTACATGAATTTGCATGTTTGAAGAGAAATTCGCC 2430

Qy 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400  
 Db 2431 ATGCTAAACTGGAATATGCCACACTGAAACCACTATCCAGGAAAGGAAATTAATAC 2490  
 Qy 401 PheGluAspIleLysLeuLysGluLysAsnAlaGluLysGlnMetThrLeuLysLeu 420  
 Db 2491 TTTGAGGACATTAAAGATTTTAAAGAAAGATGCTGAACTTCAGATGACCCCTAAACCTG 2550  
 Qy 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLysValLeuIle 440  
 Db 2551 AAGAGGAATCATTAATAAAGGCTCTCATATATAGTGGCAGCTTAAAGTTCTTGATA 2610  
 Qy 441 AlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLysGluIleLeuGlu 460  
 Db 2611 GCTGAGAAACAATGCTCACTTCTTAATTTGAAGGAAACCAAGACAAAGAAATCTAGAG 2670  
 Qy 461 AlaGluIleGluSerHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480  
 Db 2671 GCAGAAATTAATCAACCATCTCTAGCTGGCTTCTGCTACAGACCATGATCAAT 2730  
 Qy 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500  
 Db 2731 GTGACATCAAGAAAGTCAAGAACCTGCTTCCACATTCAGGAGATGCTTGTTCGAA 2790  
 Qy 501 ArgLysMetAsnValAspValSerThr 510  
 Db 2791 AGAAATGAATGTTGATGTTGAGTAGTAGC 2820

RESULT 2  
 US-09-834-759-490  
 ; Sequence 490, Application US/09834759  
 ; Patent No. 6680197  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jiang, Yugu  
 ; APPLICANT: Dillon, David C.  
 ; APPLICANT: Mitcham, Jennifer L.  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Harlocker, Susan L.  
 ; APPLICANT: Hepler, William T.  
 ; APPLICANT: Henderson, Robert A.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 ; FILE REFERENCE: 210121.470C9  
 ; CURRENT APPLICATION NUMBER: US/09/834.759  
 ; CURRENT FILING DATE: 2001-04-13  
 ; NUMBER OF SEQ ID NOS: 547  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 490  
 ; LENGTH: 3288  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-834-759-490

Alignment Scores:  
 Pred. No.: 2,238-270 Length: 3288  
 Score: 2578.00 Matches: 508  
 Percent Similarity: 99.61% Conservatives: 0  
 Best Local Similarity: 99.61% Mismatches: 2  
 Query Match: 99.19% Indels: 0  
 DB: 4 Gaps: 0

US-09-451-739H-16 (1-512) x US-09-834-759-490 (1-3288)

Qy 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20  
 Db 1291 ATGAAAGTTTCTTATTCCTCAACTAAAGCCTTAGAATGTAGTGGACATGCACAACTTTCAGAGCA 1350  
 Qy 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetClnLysSerValPro 40  
 Db 1351 GAGCCTCCCGAGAGGCACTCTGCTTCGAGCCTGCCATTGAAATGCAAAAGTCTCTTCCA 1410  
 Qy 41 AsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluLysLeuProSer 60  
 Db 1411 AATAAAGCCTTGAAATTGAAGATGAACAAACATTGAGAGCAGATGAGATATCCCATCA 1470  
 Qy 61 GluSerLysGlnLysAspTyrGluGluSerSerTyrAspSerGluSerLeuCysGluThr 80  
 Db 1471 GATCCAAACAAAGGACATGATGAAGAAAGTCTCTGGGATTCTGAGAGTCTCTGTGAGACT 1530  
 Qy 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLysLeuLysIle 100  
 Db 1531 GTTTCACAGAGATGTGTGTTTACCAGGCTTCFCATCAAAAGAAATAGATAAATA 1590  
 Qy 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120  
 Db 1591 AATGGAATAATAGAGAGTCTCTGATATGATGTTTCTGAGGCTCCCTGCAGATG 1650  
 Qy 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140  
 Db 1651 AAAGTTTCTATTCCAACTAAAGCCTTAGAATTGATGACATGCACAACTTTCAGAGCAG 1710  
 Qy 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160  
 Db 1711 CCTCCCGAGAGCCTCTGCTTCGAGCTGCCATTGAATGCAGAACTGTGTCCAAAT 1770  
 Qy 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180  
 Db 1771 AAAGCCTTGGAAATGAAGAATGAACAAACATTGAGAGCAGATGATGTTCCCTTCAGAA 1830  
 Qy 181 SerLysGlnLysValGluGluAsnSerTyrAspSerGluSerLeuArgGluThrVal 200  
 Db 1831 TCAAAACAAAGAGAGTTGAGAAATCTCTGGATTCTGAGAGTCTCCGTGAGAGTGT 1890  
 Qy 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220  
 Db 1891 TCAGAGAGGATGTGTGTGTACCCAGGCTACATCAAAAGAAATGGATAAATGAAT 1950  
 Qy 221 GlyLysLeuGluAspSerThrSerLysSerLysIleLeuAspThrValHisSerCysGlu 240  
 Db 1951 GGAAATTTGAAGATTCACTAGCTATCAAAATCTGGATACAGTTCATCTTGTGAA 2010  
 Qy 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260  
 Db 2011 AGAGCAAGGAACTTCAAAAGATCACTGTGAACAACGTACAGGAAATGGACAAATG 2070  
 Qy 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluLysSerGln 280  
 Db 2071 AAAAAGAGTTTGTGTACTGAAAGAACTGTGAGAGCAAAAGAAATGAATATCAG 2130  
 Qy 281 LeuGluAsnGlnLysValLysTyrPgluGlnLysCysSerValArgLeuThrLeuAsn 300  
 Db 2131 TTAGAGACCAAAAGTTAAATGGAAACAGAGCTCTGAGTGTGAGATTGACTTTAAAC 2190  
 Qy 301 GlnGluGluGluLysArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320  
 Db 2191 CAAGAGAGAGAGAGAGAAATCCCATATATTAATGAAATTAATTTAGGAGAGATTA 2250  
 Qy 321 GlyArgIleGluGluGlnHisArgLysGluLeuValLysGlnGlnLeuGluAla 340  
 Db 2251 GGAAGATCGAAGAGCAGCATAGGAAGAGTTAGAGTGAACAACTTGAACAGGCT 2310  
 Qy 341 LeuArgIleGlnAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360  
 Db 2311 CTCAGAAATCAAGATATGAATGAGAGTGTAGAAAGTAAATTTGAATCAGTTTCTCAC 2370  
 Qy 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380  
 Db 2371 ACTCATGAATGAAATTAATCTTACATGAATTTGCATGTTTGAAGAGAAATTCGCC 2430



Db 1411 AATAAGCCTTGGATTTGAAGATGAACAAACATTGAGACGATGAGATCTCCCATCA 1470  
 Qy 61 GluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGluSerLeuCysGluThr 80  
 Db 1471 GAATCCCAACAAAGGACATATGAAGAAAGTCTCTGGAGATCTCTGAGACT 1530  
 Qy 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLysLeuAspLysLe 100  
 Db 1531 GTTTCACAGAGGATGTGTGTTTACCCAGGCTRCATCAAAAAGAAATAGATATAATA 1590  
 Qy 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120  
 Db 1591 AATCGAAATATGAGAGGATCTCTGATATGATGTTTCTGGAAGGCTCCCTGAGAAATG 1650  
 Qy 121 LysValSerIleProThrLysAlaLeuGluMetAspMetGlnThrPheLysAlaGlu 140  
 Db 1651 AAGATTTCTATTCMACTTAAGCCTTAGAATTGATGACATGCAAACTTTCAAGCAGAG 1710  
 Qy 141 ProProGluLysProSerAlaPheGluProLalleGluMetGlnLysSerValProAsn 160  
 Db 1711 CCTCCGAGAGGACCATCTGCCTTCGAGCCTGCATTTGAAATGCAAAAAGTCTGTTCCAAAT 1770  
 Qy 161 LysAlaLeuGluLysLeuLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180  
 Db 1771 AAGCCTTGGATTTGAAGATGAACAAACATTGAGAGCATCAGATGTTCCCTTCAGAA 1830  
 Qy 181 SerLysGlnLysValGluGluLysSerTrpAspSerGluSerLeuArgGluThrVal 200  
 Db 1831 TCAAAACAAAGAAAGGTTGAAGAAATCTTGGGATCTGAGAGTCTCCGTGAGACTGTT 1890  
 Qy 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspValLeuSer 220  
 Db 1891 TCACAGAGGATGTGTGTATCCCAAGGCTACACATCAAAAAGAAATGATTAATTAAGT 1950  
 Qy 221 GlyLysLeuGluAspSerThrSerLysSerLysIleLeuAspThrValHisSerCysGlu 240  
 Db 1951 GGAAATATAGAGATCAACTAGCTATCAAAAATCTTGGATACAGTTCATCTTGTGAA 2010  
 Qy 241 ArgAlaArgGluGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260  
 Db 2011 AGAGCAAGGGAACTTCAAAAGATCACTGTGTGAACCAAGTACAGGAAATGGAACAAATG 2070  
 Qy 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluLysSerGln 280  
 Db 2071 AAAAAGATTTGTGTACTGAAAGAAAGAACTGTGAGAGCAAAAGAAATTAATCAAG 2130  
 Qy 281 LeuGluAsnGlnLysValLysTrpGluGlnGluLeuLysSerValArgLeuThrLeuAsn 300  
 Db 2131 TTAGAACCAAAAAGTAAATGGGAACCAAGAGCTCTGCAGTGTGAGATTTGACTTTAAAC 2190  
 Qy 301 GlnGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320  
 Db 2191 CAGAAGAGAGAGAGAGAGAAATGCCGATATATTAAATGAAGAAATTAGGGAAGATTA 2250  
 Qy 321 GlyArgIleGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGluGlnAla 340  
 Db 2251 GGAAGAATCGAGAGCAGCATAGAAAGAGTTAGAAAGTGAACCAACAACTTGAACAGGCT 2310  
 Qy 341 LeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis 360  
 Db 2311 CTGAGAAATCAAGATATAGATTTGAAGATGTAGAAAGTAAATTTGAATCAGTTTCTAC 2370  
 Qy 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluLeuAla 380  
 Db 2371 ACTCATGAAATGAAATATCTCTTACATGAAATTTGCATTTGAAAAAGGAAATTCGC 2430  
 Qy 381 MetLeuLysLeuGluLeuAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400  
 Db 2431 ATGCTAAATCTGGAATAGCCACCTGAAACCAATATACAGGAAAGGAAATTAATATAC 2490  
 Qy 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420

RESULT 3

US-09-620-405B-474  
 : Sequence 474, Application US/09620405B  
 : Patent No. 6528054  
 : GENERAL INFORMATION:  
 : APPLICANT: Jiang, Yuguo  
 : APPLICANT: Dillon, Davin C.  
 : APPLICANT: Mitcham, Jennifer L.  
 : APPLICANT: Xu, Jiangchun  
 : APPLICANT: Harlocker, Susan L.  
 : APPLICANT: Hepler, William T.  
 : TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 : TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER  
 : FILE REFERENCES: 210121.470C6  
 : CURRENT APPLICATION NUMBER: US/09/620,405B  
 : CURRENT FILING DATE: 2000-07-20  
 : NUMBER OF SEQ ID NOS: 495  
 : SOFTWARE: FastSeq for Windows Version 3.0  
 : SEQ ID NO 474  
 : LENGTH: 3865  
 : TYPE: DNA  
 : ORGANISM: Homo sapien  
 : FEATURE:  
 : NAME/KEY: misc\_feature  
 : LOCATION: (2448)...(2631)  
 : OTHER INFORMATION: 184 bp insert of B726P splice form  
 US-09-620-405B-474

Alignment Scores:  
 Pred. No.: 2,86e-270 Length: 3865  
 Score: 2578.00 Matches: 508  
 Percent Similarity: 99.61% Conservative: 0  
 Best Local Similarity: 99.61% Mismatches: 2  
 Query Match: 99.19% Indels: 0  
 DB: 4 Gaps: 0  
 US-09-451-739H-16 (1-512) x US-09-620-405B-474 (1-3865)

Qy 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20  
 Db 1563 ATGAAAGTTTCTATTCTCAACTTAAGCTTAGAATTGATGACATGCAAACTTTCAAAGCA 1622  
 Qy 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40  
 Db 1623 GAGCTCCGAGAGAGCCATCTGCCTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCTCA 1682  
 Qy 41 AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluLysLeuProSer 60  
 Db 1693 AATAAAGCCTTGGATTTGAAGATGAACAAACATTGAGAGCAGATGAGATCTCCCATCA 1742  
 Qy 61 GluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGluSerLeuCysGluThr 80



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Db 1743 GAATCCAAACAAAGGACTATGAGAAAGTTCTTGGGATTTGAGAGTCTCTGTGAGACT 1802
Qy 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLeuAspLysLeu 100
Db 1803 GTTTCACAGAGGATGTGTGTTTACCAAGGCTRCRCATCAAAAAGAAATAGATAAATA 1862
Qy 101 AsnGlyLysLeuGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
Db 1863 AATGGAAAATAGAGAGTCTCTGATAATGATGGTTTCTGAAGGCTCCCTGCAAGATG 1922
Qy 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140
Db 1923 AAGTTTCTATTCCAACTAAGGCTTAGAATTCGACATGCACAACTTTCAAAGCAGAG 1982
Qy 141 ProProGlnLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
Db 1983 CCTCCCGAGAGGACCTCGCTTTCGAGCTGCCATTGAAATGCAAAAGTCTGTTCAAAT 2042
Qy 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
Db 2043 AAGCCCTTGGANTTGAAGANTGACAAACATCTGAGAGCATCAGATGTTCCCTTCAGAA 2102
Qy 181 SerLysGlnLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200
Db 2103 TCAAAAACAAAAGASGTTGAAGAAATTTCTTGGATTCTGAGAGTCTCCGTGAGACTGT 2162
Qy 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
Db 2163 TCACAGAGAGTGTGTGTACCAAGGCTCACATCAAAAAGAAATGATGATAAATAGT 2222
Qy 221 GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu 240
Db 2223 GGAATAATTAGAGATTCAACTAGCTATCAAAAATCTTGGATACAGTTCATTCTTGTGAA 2282
Qy 241 ArgAlaArgGluLeuGlnLysAsnHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
Db 2283 AGACCAAGGGAACTTCAAAAAGATCTCTGACCACTGACCACTACAGGAAAATGGACAAATG 2342
Qy 261 LysLysLysPheCysValLeuLysLysLysSerGluAlaLysGluLysSerGln 280
Db 2343 AAAAAGAGTTTCTGTACTGAAAGAAATCTGTCAGAACCAAAAGAAATATAAATCACAG 2402
Qy 281 LeuGluAsnGlnLysValLysTrpGluGlnLeuCysSerValArgLeuThrLeuAsn 300
Db 2403 TTAGAGAACCAAAAGTTTAATGGACCAAGAGCTCTGAGTGTGAGATTGACTTTAAAC 2462
Qy 301 GlnGluGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320
Db 2463 CAAGAAGAGAGAGAGAGAGAAATGCCATATATTAATGAAAAAATTAGGAGAAATTA 2522
Qy 321 GlyArgIleGluGluGlnHisArgLysGluLeuValLysGlnGlnLeuGluGlnAla 340
Db 2523 GGAAGAATCGAAGAGCAGCATAGGAAGAGTTAGAGTGAACCAACACTTTGAACAGGCT 2582
Qy 341 LeuArgIleGlnAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360
Db 2583 CTCAGATACAGATATAGATTGAAGAGTGTAGAAAGTATATTTGAATCAGTTCTTCAC 2642
Qy 361 ThrHisGluAsnGluAsnTyrlleuLeuHisGluAsnCysMetLeuLysLysGluLysAla 380
Db 2643 ACTCATGAAATGAAATATATCTCTTATGAAATTCATGAAATTCATGTTGAAAGAAATGGCC 2702
Qy 381 MetLeuLysLeuGluLysAlaThrLeuLysHisGlnTyrlleuGlnLysGluAsnLysTy 400
Db 2703 ATGCTTAAATGGAATAGCCACACTGAAACCAATACCAAGGAAAGAAATATAATATC 2762
Qy 401 PheGluAspIleLysIleLeuLysGlnLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
Db 2763 TTTGAGGACATTAAGATTTTAAAGAAAGAAATGCTGAACCTTCAGATACCCCTAAAATG 2822
Qy 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrlleuGlnLysValLeuLysValLeu 440
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Db 2823 AAAGAGGAATCATTAATAAGGGCATCTCAATATAGTGGCAGCTTAAAGTTCTGATA 2882
Qy 441 AlaGluAsnThrVetLeuThrSerLysLeuLysGluLysGlnAspLysGluLysLeuGlu 460
Db 2883 GCTGAGAACCAATGCTCACTTCTTAATTCAGAGGAAAAACACAGACAAAGAAATACAGAG 2942
Qy 461 AlaGluLysGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
Db 2943 GCAGAAATTCGAATCACACCATCTAGACTGGCTTCTGCTGTACACAGACCATGATCAAAAT 3002
Qy 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
Db 3003 GTGCATCAAGAAAAAGTCAAGAACCTGCTTTCCATTCGAGGAGATGCTTCTTTGCAA 3062
Qy 501 ArgLysMetAsnValAspValSerSerThr 510
Db 3063 AGAAAATGAATGTTGATGTAGTAGTACG 3092

RESULT 4
US-09-604-287A-474
; Sequence 474, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604, 287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 474
; LENGTH: 3865
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2448)...(2631)
; OTHER INFORMATION: 184 bp insert of B726P splice form
US-09-604-287A-474

Alignment Scores:
Pred. No.: 2,866-270 Length: 3865
Score: 2578.00 Matches: 508
Percent Similarity: 99.61% Conservatives: 0
Best Local Similarity: 99.61% Mismatches: 2
Query Match: 99.13% Indels: 0
DB: 4 Gaps: 0

US-09-451-739H-16 (1-512) X US-09-604-287A-474 (1-3865)
Qy 1 MetLysValSerIleProThrLysAlaLeuGlnLeuMetAspMetGlnThrPheLysAla 20
Db 1563 ATGAAAGTTTCTTATTCCAACTTAAAGCCTTAGAATTTGATGGACATGCAAACTTTCAAAGCA 1622
Qy 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
Db 1623 GAGCTTCCGAGAGCCATCTGCTTCGAGCTGCCATTGAAATGCAAAAGTCTGTTCCA 1682
Qy 41 AsnLysAlaLeuGluLysAsnGluGlnThrLeuAlaAspGluLysLeuProSer 60
Db 1683 AATAAGCCCTTGAATTTGAAGAAATGAACAAACATTCAGAGACGATGAGATATCCCATCA 1742
Qy 61 GluSerLysGlnLysAspTyrlleuGluSerSerTrpAspSerGluSerLeuCysGluThr 80
Db 1743 GAATCCAAACAAAGAGACTATGAGAAAGTCTTGGGATTTGAGAGTCTCTGTGAGACT 1802
Qy 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLysLeuLysIle 100
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Db 1803 GTTTCAGAGGATGTGTGTTCACCAAGGCTRCRCATCAAAAAGAAATAGATAATA 1862  
Qy 101 AsnGlyLysLeuGluGluSerProAspAsnArgGlyPheLeuLysAlaProCysArgMet 120  
Db 1863 AATGGAATAATTAGAGAGTCTCTGATATATGATGGTGTCTGAAGGCTCCCTGCAGAAATG 1922  
Qy 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetClnPheLysAlaGlu 140  
Db 1923 AAAGTTCTTCAATCCAACTAAAGGCTTAGAAATGATGACATGCAAACTTTCAAGCAGAG 1982  
Qy 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160  
Db 1983 CCTCCGAGAGCCATCTGCTTCGAGCTGCCATTGAAATGCAAAAGTCTGTTCCAAT 2042  
Qy 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspClnMetPheProSerGlu 180  
Db 2043 AAAGCCTTGGAAATGAGAAATGACAAACATTCAGAGCAGATCAGATGTCCCTTCAGAA 2102  
Qy 181 SerLysGlnLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200  
Db 2103 TCAAAACAAAGAAAGTGTGAGAAATCTTGGATTCAGAGTCTCCGTGAGACTGT 2162  
Qy 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220  
Db 2163 TCAGAGAGATGTGTGTACCAAGCTACATCAAAAGAAATGGATAAAATAGT 2222  
Qy 221 GlnLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu 240  
Db 2223 GGAATATTAGAGATTCACTAGCTATCAAAATCTTGATACAGTTCATTTCTGTGA 2282  
Qy 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260  
Db 2283 AGAGCAAGGAACTTCAAAAGATCACTGTGAACACGCTACAGGAAATGGAAACAAATG 2342  
Qy 261 LysLysLysPheCysValLeuLysLysLeuSerGluAlaLysGluLysSerGln 280  
Db 2343 AAAAGAGATTTTGTGTACTGAAAGAAATGCGCATATATAATGAAATAATAGGAAGAAITA 2402  
Qy 281 LeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuThrLeuAsn 300  
Db 2403 TTAGAGAACCAAAAGTTAAATGGAAACAGAGCTCTGCAGTGTGAGATTGACTTTAAAC 2462  
Qy 301 GlnGluGluLysArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320  
Db 2463 CAAGAAGAGAGAGAGAGAAATGCGCATATATAATGAAATAATAGGAAGAAITA 2522  
Qy 321 GlyArgIleGluGluGlnHisArgLysGluLeuValLysGlnGlnLeuGluGlnAla 340  
Db 2523 GGAAGATCGAAGAGCAGCATAGGAAGAGTTAGAGTGAACAAACAACTTGAACAGGCT 2582  
Qy 341 LeuArgIleGlnAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360  
Db 2583 CTCAGATACAGATATAGAAATGGAAGAGTGAAGAGTAAATTTGAATCAGGTTCTCAC 2642  
Qy 361 ThrHisGluAsnGluAsnTrpLeuHisGluAsnCysMetLeuLysLysGluIleAla 380  
Db 2643 ACTCATGAAATGAAATTTCTTCTTACATGAAATTTGCAATTTGAAAGAAATTTGCC 2702  
Qy 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTrpGlnGluLysGluAsnLysTrp 400  
Db 2703 ATGCTAAACCTGGAATAGCCACACTGAAACACCACTACCAAGAAAGAAATAAATAC 2762  
Qy 401 PheGluAspIleLysLysLysLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420  
Db 2763 TTTGAGGACATTAAGATTTTAAAGAAAGAAATGCTGAACTTCAGATGACCTTAACACTG 2822  
Qy 421 LysGluGluSerLeuThrLysArgAlaSerGlnTrpSerGlyGlnLeuLysValLeu 440  
Db 2823 AAAGAGGAATCAATTAACATAAGGCACTCAATATAGTGGGCACTTAAAGTTCTGTATA 2882  
Qy 441 AlaGluAsnThrMetLeuThrSerLysLysGluLysGlnAspLysGluLysLeuGlu 460

Db 2883 GCTGAGAACCAATGCTCTCACTTCTAAATTGAGGAAAAAACAAGCAAAATACTAGAG 2942  
Qy 461 AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGluIle 480  
Db 2943 GCAGAAATTAATCACCACTCTAGACTGGCTTCTGCTGTACAGACCAATGATCAAT 3002  
Qy 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500  
Db 3003 GTGACATCAAGAAAAAGTCAAGAACCTGCTTCCACATTCAGAGATGCTTGTGTGCAA 3062  
Qy 501 ArgLysMetAsnValAspValSerSerThr 510  
Db 3063 AGAAAAATGAATGTGTGATGTAGTAGTACG 3092  
RESULT 5  
US-09-834-759-474  
; Sequence 474, Application US/09834759  
; Patent No. 6860197  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Dillon, David C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Henderson, Robert A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.470C9  
; CURRENT APPLICATION NUMBER: US/09/834,759  
; CURRENT FILING DATE: 2001-04-13  
; NUMBER OF SEQ ID NOS: 547  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 474  
; LENGTH: 3865  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (2448)...(2631)  
; OTHER INFORMATION: 184 bp insert of B726p splice form  
US-09-834-759-474  
Alignment Scores:  
Pred. No.: 2,866-270 Length: 3865  
Score: 2578.00 Matches: 508  
Percent Similarity: 99.61% Conservative: 0  
Best Local Similarity: 99.61% Mismatches: 2  
Query Match: 99.19% Indels: 0  
DB: 4 Gaps: 0  
US-09-451-739H-16 (1-512) x US-09-834-759-474 (1-3865)  
Qy 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20  
Db 1563 ATGAAAGTTCTTATTCACAACTAAAGCCTTAGAATTTAGTGAGCATGCAAACTTTCAAGCA 1622  
Qy 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40  
Db 1623 GAGCCTCCCGAGAGCCATCTGCTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTGCA 1682  
Qy 41 AsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 60  
Db 1683 AATAAAGCCTTGAATTTGAAGAAATGAACAAACATTCAGAGCAGATGAGATCTCCATCA 1742  
Qy 61 GluSerLysGluLysAspTrpGluSerSerTrpAspSerGluSerLeuCysGluThr 80  
Db 1743 GAATCCCAACAAAGAGCTATGAGAAAGTCTTGGATTTCTGAGAGTCTCTGTGAGACT 1802  
Qy 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLysLeuLys 100  
Db 1803 GTTTCAGAGAGATGTGTGTTTTACCAAGGCTRCRCATCAAAAGAAATAGATAATA 1862

QY 101 AsnGlyLysLeuGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120  
Db 1863 AATGGAAATTTAGAGAGCTCTCTGATATATGTTTCTGAAGGCTCCCTGCAGAATG 1922  
QY 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140  
Db 1923 AAGTTTCTATTCCAACTAAGCTTTAGAAATTTGATGGACATCAAACTTTCAAGCAGAG 1982  
QY 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160  
Db 1983 CTTCCCGAGAGAGCCATCTGCTTCGAGCTGCCATTGAAATGCAAAAGTCTCTTCCAAAT 2042  
QY 161 LysAlaLeuGluLysAsnGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180  
Db 2043 AAAGCCTTGGAAATGGAAGATGAACAAACATTTAGAGCAGATCAGATGTCCTTCAGAA 2102  
QY 181 SerLysGlnLysLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200  
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QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220  
Db 2163 TCACAGAGGATGTGTGTACCAAGGCTACATCAAAAGAAATGATGATAAATAAGT 2222  
QY 221 GlyLysLeuGluAspSerThrSerLysLysIleLeuAspThrValHisSerCysGlu 240  
Db 2223 GGAATAATTAGAGATTCACATGACCTATCAAAAATCTTGATACAGTTCATTCTTGAA 2282  
QY 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260  
Db 2283 AGAGCAAGGAAGTTCAAAAGATCACTGTGAACAGTACAGGAAAAATGGAAACAAATG 2342  
QY 261 LysLysLysPheCysValLeuLysLysLysLysLeuSerGluAlaLysGluLysLysSerGln 280  
Db 2343 AAAAGAAGTTTGTGTACTGAAAGAGAAACTGTGAGAACCAAGAAATATAATCACAG 2402  
QY 281 LeuGluAsnGlnLysValLysTrpGluGlnGluLysCysSerValArgLeuThrLeuAsn 300  
Db 2403 TTAGAGAACCAAAAGTTAAATGGGAACAAGAGCTCTGCAGTGTGAGATGACTTTAAAC 2462  
QY 301 GlnGluGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320  
Db 2463 CAAGAGAGAGAGAGAGAGAAATGCCGATATATTAATGAAGAAATAGCGAGAAATTA 2522  
QY 321 GlyArgIleGluGluGlnHisArgLysGluLeuValLysGlnLysGlnLysGlnAla 340  
Db 2523 CGAAGAAATCGAAGAGCAGCATAGAAAGAGTTAGAGTGAACAAACAACTTGAACAGGCT 2582  
QY 341 LeuArgIleGlnAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360  
Db 2583 CTCAGAAATACAGATATAGAAATTTGAAGAGTGAAGATTAATTTGAATCAGGTTCTCAC 2642  
QY 361 ThrHisGluAsnGluAsnTrpLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380  
Db 2643 ACTCATGAAATGAAATATATCTTCAATGAAATTTGCATGTTGAAAGAAAGAAATGACC 2702  
QY 381 MetLeuLysLeuGluIleAlaThrLysHisGlnTrpGlnGluLysGluAsnLysTrp 400  
Db 2703 ATGCTAAACATGGAATAGCCACACTGAACACCAATACACAGGAAAGAAATTAATATAC 2762  
QY 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420  
Db 2763 TTTGAGGACATTAGATTTTAAAGAAAGAAATGCTGAACCTCAGATGACCCATAAACTG 2822  
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Db 2823 AAAGAGGAATCATTAACATAAGGCGCATCTCAATATAGTGGCAGCTTAAAGTTCTGATA 2882  
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Db 2883 GCTGAGAACACAACTGCTCATTCTTAATTTGAAGGAAAGAAACAAAGACAAAGAAATCTAGAG 2942  
QY 461 AlaGluIleGluSerHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480

Db 2943 GCAGAAATTTGAATCAACCATCTCTAGACTGGCTTCTGCTGTACAAGACCATCAAAATT 3002  
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Db 3003 GTGACATCAAGAAAAAGTCAAGAACCTGCTTTCCACATTCAGAGGAGATCTGTTTTCGAA 3062  
QY 501 ArgLysMetAsnValAspValSerSerThr 510  
Db 3063 AGAAAAATGAATGTTGATGTAGTAGTAG 3092  
RESULT 6  
US-09-620-405B-468  
; Sequence 468, Application US/09620405B  
; Patent No. 5528054  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yudi  
; APPLICANT: Dillon, Devin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Hepler, William T.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER  
; FILE REFERENCE: 210121.470C8  
; CURRENT APPLICATION NUMBER: US/09/620,405B  
; CURRENT FILING DATE: 2000-07-20  
; NUMBER OF SEQ ID NOS: 495  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 468  
; LENGTH: 2307  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-620-405B-468  
Alignment Scores:  
Pred. No.: 1,81e-232 Length: 2307  
Score: 2227.50 Matches: 446  
Percent Similarity: 87.65% Conservative: 1  
Best Local Similarity: 87.45% Mismatches: 2  
Query Match: 85.71% Indels: 62  
DB: Gaps: 1  
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QY 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20  
Db 206 ATGAAAGTTTCTATTCCAACTTAAAGCCTTAGAATTTGATGGACATGCAAACTTTCAAAGCA 265  
QY 21 GluProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40  
Db 266 GAGCCTCCGAGAGAGCCATCTGCTTCGAGCTGCCATTGAAATGCAAAAGTCTGTTCCTCA 325  
QY 41 AsnLysAlaLeuGluLysAsnGlnThrLeuArgAlaAspGluIleLeuProSer 60  
Db 326 AATRAAGCCTTGGAAATGGAAGATGAACAAACATTTAGAGCAGATGAGATCTCCATCA 385  
QY 61 GluSerLysGlnLysAspTrpGluSerSerTrpAspSerGluSerLeuCysGluThr 80  
Db 386 GAATCCAAACAAAGAGACTATGAAGAAAGTTCTTGGGATTTCTGAGAGTCTCTGTGAGACT 445  
QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100  
Db 446 GTTTCACAGAGAGATGTGTGTTTACCCAGGCTCACATCAAAAGAAATAGATAAATA 505  
QY 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120  
Db 506 AATGGAATAATTAGAGAGTCTCTGATATATGATGTTTCTGAAGTCTCCCTGCAGAATG 565  
QY 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140  
Db 566 AAAAGTTTCTATTCCAACTAAGCCTTAGAATTTGATGGACATGCAAACTTTCAAAGCAGAG 625

141 ProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160  
Db CCTCCGAGAGCCATCTGCTTCAGCCGCAATGAAATGCAAAAGTCTGTCCAAAT 695  
161 LysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180  
Db AAACCCCTTGAATTTGAAGATGAACAAACATTTAGAGCAGATGATGCTCCCTCAGAA 745  
181 SerLysGlnLysLysValGluGluAsnSerTrpAspSerGluSerLysArgGluThrVal 200  
Db TCAAAACAAAGAACGTTGAAGAAATTTCTTGGATTTCTGAGAGTCTCCGTGAGACTGTT 805  
201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220  
Db TCACAGAGGATGTTGTGTGTACCCAGCTACACATCAAAAGAAATGGAATAAATAGT 865  
221 GlyLysLeuGluAspSerThrSerLysSerLysIleLeuAspThrValHisSerCysGlu 240  
Db GGAATAATTAGAAGATTTCAACTAGCTATCAAAATCTTGGATACAGTTCAATCTTGTGAA 925  
241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260  
Db AGACCAAGGAACTTCAAAAGATCACGTGTGAACACGTACAGGAAATGGAACAAATG 985  
261 LysLysLysPheCysValLeuLysLysLysSerGluAlaLysGluLysSerGln 280  
Db AAAAAGAAAGTTTGTGTACTGAAAGAAACTGTGAGAGCAAAAGAAATAAAATCACAG 1045  
281 LeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuThrLeuAsn 300  
Db TTAGAGAACCAAAAGTTAAATGGACACAGCTCTGCACTGTGAGTT----- 1095  
301 GlnGluGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320  
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321 GlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGluAla 340  
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341 LeuArgIleGlnAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360  
Db -----TCTCAC 1101  
361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluLysAla 380  
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381 MetLeuLysLeuGluLysAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400  
Db ATGCTAAACCTGAAATAGCCACACTGAAACACCAATACCAGGAAAGGAAATATAATAC 1221  
401 PheGluAspIleLysIleLeuLysGlnLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420  
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421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle 440  
Db AAAGAGGAATCATTAACATAAGGCACTCATATAGTGGCAGCTTAAAGTTCTGATA 1341  
441 AlaGluAsnThrMetLeuThrSerLysLysGluLysGlnAspLysGluLysLeuGlu 460  
Db GTTGAGAACACAAATGCTCATTTCTTAATTTGAAGGAAACACAGACAAAGAAATACATAG 1401  
461 AlaGluLysSerHisGlnProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480  
Db GAGAAATTTCAATCACCATCTGTAGCTGGCTTTCTGCTGTACAGACATGATCAATATT 1461  
481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaLysAlaCysLeuGln 500  
Db GTGACATCAAGAAAGTCAAGAACTGCTTTCCACATTCAGAGGAGATGCTTGTGTGCAA 1521  
501 ArgLysMetAsnValAspValSerSerThr 510

1522 AGAAATGAATGTTGATGTGAGTAGTACG 1551  
RESULT 7  
US-09-433-826B-468  
; Sequence 468, Application US/09433826B  
; Patent No. 6579973  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yuqi  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND  
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE  
; FILE REFERENCE: 210121.470C4  
; CURRENT APPLICATION NUMBER: US/09/433,826B  
; CURRENT FILING DATE: 1999-11-03  
; NUMBER OF SEQ ID NOS: 474  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 468  
; LENGTH: 2307  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-433-826B-468  
Alignment Scores:  
Pred. No.: 1,818-232 Length: 2307  
Score: 2227.50 Matches: 446  
Percent Similarity: 87.65% Conservative: 1  
Best Local Similarity: 87.45% Mismatches: 2  
Query Match: 85.71% Indels: 62  
Gaps: 4  
US-09-451-739H-16 (1-512) x US-09-433-826B-468 (1-2307)  
QY 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20  
Db 206 ATGAAAGTTTCTTATCCCACTAAAGCTTAGAATGTAGGACATGCAAACTTTCAAAGCA 265  
QY 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40  
Db 266 GAGCCTCCGAGAGCCATCTGCTTCGAGCTGCAATGAAATGCAAAAGTCTGTTCGA 325  
QY 41 AsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluLysLeuProSer 60  
Db 326 ATAAAGCCCTTGGATTTGAAGATGACAAACATTTAGAGCAGATGAGATCTCCATCA 385  
QY 61 GluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGluSerLysCysGluThr 80  
Db 386 GAATCAAAACAAAGGACTATGAAGAAAGTTCTTGGATTTCTGAGAGTCTCTGTGAGACT 445  
QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLysLysIle 100  
Db 446 GTTTCACAGAGGATGTTGTTTACCAAGGCTACACATCAAAAGAAATAGATAATA 505  
QY 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120  
Db 506 AATGGAATAATTAGAGAGTCTCTGATAATGATGTTTCTGAGTCTCCCTGCGAAGT 565  
QY 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140  
Db 566 AAGTTTCTTATTCACAACTAAGCCTTAGATTTGATGAGCATGCAAACTTTCAAAGCAG 625  
QY 141 ProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160  
Db 626 CTTCCCGAGAGGCACTCTGCTTCGAGCTGCAATGAAATGCAAAAGTCTGTTCCTCAAT 685  
QY 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180  
Db 686 AAGCCTTGAATTTGAAGATGAACAAACATTTAGAGCAGATGAGATGTTTCCCTTCAGAA 745  
QY 181 SerLysGlnLysValGluGluAsnSerTrpAspSerGluSerLysArgGluThrVal 200

```
Db 746 TCAAAACAAAGAACGTTGAAGAAATTTCTGGATCTCAGAGTCTCCGTGAGACTGTT 805
Qy 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
Db 806 TCACAGAGGATGTGTGTACCCAGGCTACACATCAAAAGAAATGGATATAAATAGT 865
Qy 221 GlyLysLeuGluAspSerThrSerLysLysIleLeuAspThrValHisSerCysGlu 240
Db 866 GGAATAATTAGAAATCAACTAGCTTCAAAATCTTGATACAGTTCATCTCTGTGA 925
Qy 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
Db 926 AGACGAAGGAACTTCAAAAGATCACTGTGAACAGCTACAGAAATGGAAACAAATG 985
Qy 261 LysLysLysPheCysValLeuLysLysLeuSerGluAlaLysGluIleLysSerGln 280
Db 986 AAAAAGAGTTTGTGTACTGAAAAGAACTGTGAGAGCAAGAAAGAAATAAATCACAG 1045
Qy 281 LeuGluAsnGlnLysValLysTrpGluGlnLeuCysSerValArgLeuThrLeuAsn 300
Db 1046 TTAGAGAACCAAAAGTTAAATGGGAACAGAGCTCTGCAGTGTGAGGTT----- 1095
Qy 301 GlnGluGluGluLysArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320
Db 1095 ----- 1095
Qy 321 GlyArgIleGluGluGlnHisArgLysGluLeuValLysGlnGlnLeuGluGlnAla 340
Db 1095 ----- 1095
Qy 341 LeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis 360
Db 1096 -----TCTCAC 1101
Qy 361 ThrHisGluAsnGluAsnTyrIleLeuHisGluAsnCysMetLeuLysLysGluIleAla 380
Db 1102 ACTCATGAAATGAAATATATCTTTACATGAAATTTGCATGTTGAAAGAAATGCTCC 1161
Qy 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400
Db 1162 ATGCTAAAACTGGAATAGCCACTGAAACACCAATACAGGAAGAAAGAAATAAATAC 1221
Qy 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
Db 1222 TTTGAGGACATTAGATTTAAAGAAAGAAATGCTGAACCTTCAGATGACCTTAAACTG 1281
Qy 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle 440
Db 1282 AARGAGGAATCAATTAACATAAAGGCACTCTCAATATAGTGGCAGCTTAAAGTTCTGATA 1341
Qy 441 AlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLysGluIleLeuGlu 460
Db 1342 GCTGAGAACACAATGCTCACTTCTAAATTAAGGAAACAAAGCAAAAGAAATACTAGAG 1401
Qy 461 AlaGluIleGluSerHisHisProArgIleAlaSerAlaValGlnAspHisAspGlnIle 480
Db 1402 GCAGAAATGAATCAACCATCTAGACGCGTCTGCTGTACAGACCATGATCAATTT 1461
Qy 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
Db 1462 GTGACATCAAGAAAGTCAAGAACTGCTTTCCACATTCGAGGAGATGCTTGTGTGCAA 1521
Qy 501 ArgLysMetAsnValAspValSerSerThr 510
Db 1522 AGAAAAATGAATGTTGATGTAGTAGTAGC 1551
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## RESULT 8

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US-09-604-287A-468
; Sequence 468, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
```

```
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
```

```
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
```

```
; NUMBER OF SEQ ID NOS: 489
```

```
; SOFTWARE: FastSeq for Windows Version 3.0
```

```
; SEQ ID NO 468
```

```
; LENGTH: 2307
```

```
; TYPE: DNA
```

```
; ORGANISM: Homo sapiens
```

```
US-09-604-287A-468
```

## Alignment Scores:

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Pred. No.: 1,81e-232 Length: 2307
Score: 2227.50 Matches: 446
Percent Similarity: 87.65% Conservative: 1
Best Local Similarity: 87.45% Mismatches: 2
Query Match: 85.71% Indels: 62
DB: 4 Gaps: 1
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US-09-451-739H-16 (1-512) x US-09-604-287A-468 (1-2307)
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Qy 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20
Db 206 ATGAAAGTTTCTATTCCAACTAAAGCCTTAGAATTGATGGACATGCAAACTTTCAAGCA 265
Qy 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
Db 266 GAGCCTCCGAGAGCCATCTGCTTCGAGCGCTGCAATGAAATGCAAAAGTCTGTCTCCA 325
Qy 41 AsnLysAlaLeuGluLeuLysAsnGlnThrLeuArgAlaAspGluIleuProSer 60
Db 326 AATAAAGCCTTCGAAATGAAGAAATGAACAAACATTGAGAGCAGATGAGATATCCCATCA 385
Qy 61 GluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGluSerLeuCysGluThr 80
Db 386 GAATCCAAACAAAGGACTATGAGAAAGTTCTTGGATTCTGAGAGTCTCTGTGAGACT 445
Qy 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLysLeuAspLysIle 100
Db 446 GTTTCACAGAGGATGTGTGTTTACCCAGGCTCACATCAAAAGAAATAGATAAATA 505
Qy 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
Db 506 AATGGAAATTTAGAGAGTCTCTGTATATGATGTTTCTGAACTCTCCCTGCAGAAATG 565
Qy 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140
Db 566 AAAGTTTCTATTCCAACTAAAGCCTTAGAATTGATGGACATGCAAACTTTCAAGACAGAG 625
Qy 141 ProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
Db 626 CTTCCGAGAGCCATCTGCTTCGAGCTGCAATGAAATGCAAAAGTCTTCTTCCAAAT 685
Qy 161 LysAlaLeuGluLeuLysAsnGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
Db 686 AAAGCCTTGAATTTAAGAAATGAACAAACATTGAGAGCAGATCAGATGTTCCCTTCAGAA 745
Qy 181 SerLysGlnLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200
Db 746 TCAAAACAAAGAACTTGAAGAAATTTCTTGGATTCTGAGAGTCTCGTGAGACTGTT 805
Qy 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
Db 806 TCACAGAGGATGTGTGTGTACCCAGGCTACACATCAAAAGAAATGATAAATAAATAGT 865
Qy 221 GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu 240
```

Db	866	GGAAAAATTAGAAAGATTCAACTAGCCCTATCAAAAATCTTTGGATACAGTTTCATTCTTTGTGAA	925
Qy	241	ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet	260
Db	926	AGAGCAAGGGAACCTTCAAAAAGATCACTGTGTGAACAACGTACAGAGAAAAATGGAAACAAATG	985
Qy	261	LysIlyLysPheCysValLeuLysLysLysLeuSerGlnAlaLysGluIleLysSerGln	280
Db	986	AAAAAGAAAGTTTGTGTACTGAAAAAGAAACTGTCAAGCAAAAGAAATAAAATCACAG	1045
Qy	281	LeuGluAsnGlnLysValLysTTPGluGlnGluLeuCysSerValArgLeuThrLeuAsn	300
Db	1046	TTAGAGAACCAAAAAAGTTAAATGGAAACAAGAGCTCTGCAGTGTGAGGTT	1095
Qy	301	GlnGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu	320
Db	1095	-----	1095
Qy	321	GlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGluGlnAla	340
Db	1095	-----	1095
Qy	341	LeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis	360
Db	1096	-----	1101
Qy	361	ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla	380
Db	1102	ACTCATGAAATGAAATTAATTCCTTACATGAAATTTGCATGTTTGAAGAAAGGAATTTGCC	1161
Qy	381	MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGlnLysGluAsnLysTyr	400
Db	1162	ATGCTAAACCTGGAAATAGCCACACTGAAACCCAAATACACAGGAAAGGAAATAAATAC	1221
Qy	401	PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu	420
Db	1222	TTTGAGGCATTAGATTTTAAAGAAAAAGAAATGCTGAACCTCAGATGACCTTAAACACTG	1281
Qy	421	LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle	440
Db	1282	AAAGAGGAATCATTTAACTTAAAGGGCATCTCAATATATGTGGCAGCTTAAAGTTCTGATA	1341
Qy	441	AlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLysGluIleLeuGlu	460
Db	1342	GCTGAGAACAACAATGCTCATTCTTAATTGAAGGAAAAACAAGACAAGAAATACTAGAG	1401
Qy	461	AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle	480
Db	1402	GCAGAAATTTGAATCACACCATCTAGACTGGCGTTCTGCTGTACAGACCATGATCAATT	1461
Qy	481	ValThrSerArgLysSerGlnLysProAlaPheHisIleAlaGlyAspAlaCysLeuGln	500
Db	1462	GTGACATCAAGAAAAAGTCAAGACCTGCTTCCCATTTGCAGGAGATGCTTTGTTGCCAA	1521
Qy	501	ArgLysMetAsnValAspValSerSerThr	510
Db	1522	AGAAAAATCAATGTTGATGTCAGTAGTACG	1551

## RESULT 9

US-09-834-759-468  
; Sequence 468, Application US/09834759  
; Patent No. 6680197  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Hazlocker, Susan L.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Henderson, Robert A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER

```

QY 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluLeuLysSerGln 280
DB 986 AAAAAAGAGTTTGTGTACTGAAAGAAAGAACTGTGAGAGCAAAAGAAATAAAATCACAG 1045
QY 281 LeuGluAsnGlnLysValLysTrpGluGlnGluLeuLysSerValArgLeuThrLeuAsn 300
DB 1046 TTAGAGAACCAAAAGTTAAATGGGAACAGAGCTCTGAGGTGAGGTT----- 1095
QY 301 GlnGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320
DB 1095 ----- 1095
QY 321 GlyArgIleGluGlnHisArgLysGluLeuValLysGlnGlnLeuGlnAla 340
DB 1095 ----- 1095
QY 341 LeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis 360
DB 1096 -----TCTCAC 1101
QY 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380
DB 1102 ACTCATGAAATGAAATTAATCTCTTACATGAAATTCATGTTGAAAGGAAATTCGC 1161
QY 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400
DB 1162 ATGCTAAACTGGAATAGCCACACTGAACACCATACAGGAAGGAATTAATATAC 1221
QY 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuMetThrLeuLysLeu 420
DB 1222 TTTGAGGACATTAAGATTTTAAAGAGAAAGAAATGCTGAATTCAGATGACCTTAAACTG 1281
QY 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlnGlnLeuLysValLeuIle 440
DB 1282 AAGAGGAATCATTAATAAAGGCACTCAATATAGTGGCAGCTTAAGTTCTGATA 1341
QY 441 AlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLysGluIleLeuGlu 460
DB 1342 GCTGAGACACAATGCTCACTTCTTAAATTAAGGAAAGAAAGAAAGAAATTAATAGAG 1401
QY 461 AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
DB 1402 CGAGAAATTAATCACACCATCTAGACTGCTTCTGCTGTACAGACCATGATCAAT 1461
QY 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
DB 1462 GTGACATCAAGAAAGTCAAGAACTGCTTTCCACATTCGAGGAGATGCTTGTGTCAA 1521
QY 501 ArgLysMetAsnValAspValSerSerThr 510
DB 1522 AGAAAAATGAATGTTGATGTGAGTAGTACG 1551

```

RESULT 10

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; US-09-620-405B-463
; Sequence 463, Application US/09620405B
; Patent No.: 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 463
; LENGTH: 3681
; TYPE: DNA

```

ORGANISM: Homo sapiens  
US-09-620-405B-463

Alignment Scores:

Pred. No.: 7,83e-232 Length: 3681  
Score: 2224.50 Matches: 446  
Percent Similarity: 87.45% Conservative: 0  
Best Local Similarity: 87.45% Mismatches: 3  
Query Match: 85.59% Indels: 62  
DB: 4 Gaps: 1

US-09-451-739H-16 (1-512) x US-09-620-405B-463 (1-3681)

```

QY 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20
DB 1563 ATGAAGTTTCTATTCACACTTAAGCCTTAGAATTGATGGACATGCAAACTTTCAAGCA 1622
QY 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
DB 1623 GAGCCTCCGAGAGACCATCTGCCTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTC 1682
QY 41 AsnLysAlaLeuGluLysAsnGlnThrLeuArgAlaAspGluIleLeuProSer 60
DB 1683 AATAAGCCTTGGAAATTAAGATGAACAACATTTGAGACAGATGAGATCTCCCATCA 1742
QY 61 GluSerLysGlnLysAspTyrGluLysSerTrpAspSerGluSerLeuCysGluThr 80
DB 1743 GAATCCAAACAAAAGGACTATGAAGAAAGTTCTTGGGATTTCTGAGAGTCTCTGTG 1802
QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100
DB 1803 GTTTCACAGAGAGGATGTGTGTTTACCAGGCTRCRCATCAAAAGAAATAGATAAATA 1862
QY 101 AsnGlyLysLeuGluLysProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
DB 1863 AATGGAAATTTAGAAGAGTCTCTGTATGATGTTTCTGAGAGGCTCCCTGAGAGATG 1922
QY 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140
DB 1923 AAAGTTTCTATTCCAACTAAAGCCTTAGAATGTGATGACATGCAAACTTTCAAGC 1982
QY 141 ProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
DB 1983 CTTCCCGAGAGACCATCTGCCTTCGAGCCTGCCATTGAATGCAAAAGTCTGTTC 2042
QY 161 LysAlaLeuGluLysAsnGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
DB 2043 AAAGCCTTGGAAATTAAGAAATGAACAACATTTGAGACAGATCAGATGTTCCCTTC 2102
QY 181 SerLysGlnLysValGluLysSerTrpAspSerGluSerLeuArgGluThrVal 200
DB 2103 TCATAACAAGAAAGAGTGAAGAAATTTCTGGGATTTCTGAGAGTCTCCGTGAGACT 2162
QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
DB 2163 TCACAGAGAGTGTGTGTGTACCCAGGCTACACATCAAAAGAAATGAGATAAATAAGT 2222
QY 221 GlyLysLeuGluAspSerThrSerLysIleLeuAspThrValHisSerCysGlu 240
DB 2223 GGAATTTAGAAGATTCACATGACCTATCAAAATCTTGGATACAGATTCATTTGTGAA 2282
QY 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluIleMet 260
DB 2283 AGAGCAAGGGAACCTTCAAAAGATCACTGTGAACAACCTACAGGAAAAATGGAACAAATG 2342
QY 261 LysLysLysPheCysValLeuLysValLysLeuSerGluAlaLysGluIleLysSerGln 280
DB 2343 AAAAAAGAGTTTGTGTACTGAAAAAGAACTGTGAGAGCAAGAAATAAATCAACAG 2402
QY 281 LeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuThrLeuAsn 300
DB 2403 TTAGAGAACCAAAAGCTTAAATGGGAAACAGAGCTCTGCAGTGTGAGGTT----- 2452

```







```
Db 2453 -----TCTCAC 2458
Qy 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysGluLeuAla 380
Db 2459 ACTCATGAAATGAAATATATCTTACATGAAATTTGCATGTTGAAAGGAAATGGCC 2518
Qy 381 MetLeuLysLeuGluLeuAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400
Db 2519 ATGCTAAATCTGGAATAGCCACACGAAACACCAATACACGAAAGGAAAGAAATAATATAC 2578
Qy 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
Db 2579 TTTGAGGACATTAAGATTTTAAAGAAAGAAAGCTCAACTTCAGATGACCCCTAAAGACTG 2638
Qy 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle 440
Db 2639 AAAGAGGAATCAATTAATAAGGGCATCTCAATATAGTGGGAGCTTTAAGTTCTGATA 2698
Qy 441 AlaGluAsnThrMetLeuThrSerLysLeuLysGlnLysGlnAspLysGluLeuLeuGlu 460
Db 2699 GCTGAGAACACAACTGCTCACTTCTTAATTTGAAGGAAAGAAACAGACAAAGAAATACTAGAG 2758
Qy 461 AlaGluLeuGluSerHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
Db 2759 GCAGAAATGGAATCACACCATCTTAGACTGGCTTCTGCTGTACAGACCATGATCAAAAT 2818
Qy 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
Db 2819 GTGACATCAAGAAAGCTCAAGACCTGCTTCCACATTCGAGGAGATGCTTGTGTCGA 2878
Qy 501 ArgLysMetAsnValAspValSerThr 510
Db 2879 AGAAATGAAATGTTGATGTGAGTAGTAGC 2908
```

## RESULT 12

```
US-09-604-287A-463
; Sequence 463, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 463
; LENGTH: 3681
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-604-287A-463
```

```
Alignment Scores:
Pred. No.: 7,836-232 .Length: 3681
Score: 2224.50 Matches: 446
Percent Similarity: 87.45% Conservative: 0
Best Local Similarity: 87.45% Mismatches: 3
Query Match: 85.59% Indels: 62
DB: 4 Gaps: 1
```

US-09-451-739H-16 (1-512) x US-09-604-287A-463 (1-3681)

```
Qy 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20
Db 1563 ATGAAAGTTTCTATTCCAACTTAAGCCTTAGAATTTGATGGACATGCAAACTTTCAAAGCA 1622
```

```
Qy 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
Db 1523 GAGCCTCCGAGAGCCATCTGCTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTCCA 1682
Qy 41 AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluLeuLeuProSer 60
Db 1683 AATAAGCCTTGGAAATGAAAGATGAACAAACATTTAGAGCAGATGAGATCTCCCATCA 1742
Qy 61 GluSerLysGlnLysAspTyrGluGluSerSerTyrAspSerGluSerLeuCysGluThr 80
Db 1743 GAATCCAAACAAAGAGCTATGAAGAAAGTTCTTGGATTTCTGAGAGTCTCTGTGAGACT 1802
Qy 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLeuAspLysIle 100
Db 1803 GTTTCCAGAGAGTGTGTGTTTACCACAGGCTTCRCATCAAAAGAAATAGATAAATA 1862
Qy 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120
Db 1863 AATGGAAATTTGAAGAGTCTCTCTGATATGATGTTTCTGAAGGCTCCCTGCAGAAATG 1922
Qy 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140
Db 1923 AAAGTTTCTATTCCAACTTAAAGCCTTAGAATTTGATGACATGCAAACTTTCAAAGCAGAG 1982
Qy 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160
Db 1983 CTCCCGAGAGCCATCTGCTTCGAGCCTGCCATTGAATGCAAAAGTCTGTTCCTCAAAAT 2042
Qy 161 LysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
Db 2043 AAAGCCTTGAATTTGAAGATGAACAAACATTTGAGAGCAGATCAGATGTTTCCCTTCGAA 2102
Qy 181 SerLysGlnLysValGluGluAsnSerTyrAspSerGluSerLeuArgGluThrVal 200
Db 2103 TCAAAACAAAGAGAGTTGAAGAAATTTCTTGGATTTCTGAGAGTCTCCGTGAGACTGTT 2162
Qy 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220
Db 2163 TCACAGAGAGGATGTGTGTACCCAGGCTACACATCAAAAGAAATGGAATAAATAGT 2222
Qy 221 GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu 240
Db 2223 GGAATAATTAGAGATTCACATAGCCTATCAAAATTTCTTGGATACAGTTCATCTTGTGAA 2282
Qy 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260
Db 2283 AGAGCAGGAGACTTCAAAAGATCAGCTGCAACAGCTACAGGAAATGGAACAAATG 2342
Qy 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluLysSerGln 280
Db 2343 AAAAAAGAGTTTGTGTACTGAAAAAGAACTGTGAGAGCAAGAAAGAAATTAATATCAG 2402
Qy 281 LeuGluAsnGlnLysValLysTyrGluGlnLeuCysSerValArgLeuThrLeuAsn 300
Db 2403 TTAGAGAACCAAAAGTTAATTTGGAACAAGAGCTCTGAGTGTGAGGTT----- 2452
Qy 301 GlnGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320
Db 2452 ----- 2452
Qy 321 GlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGlnAla 340
Db 2452 ----- 2452
Qy 341 LeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis 360
Db 2453 -----TCTCAC 2458
Qy 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluLeuAla 380
Db 2459 ACTCATGAAATGAAATATATCTTACATGAAATTTGCAATGTTGAAAAAGAAATGGCC 2518
Qy 381 MetLeuLysLeuGluLeuAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400
```

Db 2519 ATGCTAAACCTGGAAATAGCCACACTGAAACACCAATACCAAGGAAAGGAAATTAATATAC 2578  
Qy 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420  
Db 2579 TTTGAGGACATTAAGATTATAAAGAAAGAAAGTGTGAACCTTCAGATGACCTAAAACCTG 2638  
Qy 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuLe 440  
Db 2639 AAAGAGGAATCATTAACATAAAGGCACTCAATATAGTGGCAGCTTAAGTCTGATA 2698  
Qy 441 AlaGluAsnThrMetLeuThrSerLysLeuLysGlnLysGlnAspLysGluLeuGlu 460  
Db 2699 GCTGAGACACAATGCTCATTCTTAATTTGAAGAAACCAAGCAAAAGAAATACTAGAG 2758  
Qy 461 AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480  
Db 2759 GCAGAAATGGAATCACCATCTAGACTGGCTTCTGCTGTACAGACCATGATCAATTT 2818  
Qy 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500  
Db 2819 GTGACATCAAGAAAGTCAAGAACCTGCTTCCACATTCGAGGAGATGCTTGTTCGAA 2878  
Qy 501 ArgLysMetAsnValAspValSerSerThr 510  
Db 2879 AGAAAAATGAATGTTGATGTGAGTAGTAGC 2908

## RESULT 13

US-09-834-759-463

; Sequence 463, Application US/09834759

; Patent No. 6680197

## GENERAL INFORMATION:

; APPLICANT: Jiang, Yuqiu

; APPLICANT: Dillon, David C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Xu, Jiangchun

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Hepner, William T.

; APPLICANT: Henderson, Robert A.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.470C9

; CURRENT APPLICATION NUMBER: US/09/834,759

; NUMBER OF SEQ ID NOS: 547

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 463

; TYPE: DNA

; LENGTH: 3681

; ORGANISM: Homo sapiens

US-09-834-759-463

Alignment Scores:

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Score:	2224.50	Matches:	446
Percent Similarity:	87.45%	Conservative:	0
Best Local Similarity:	87.45%	Mismatches:	3
Query Match:	85.59%	Indels:	62
DB:	4	Gaps:	1

US-09-451-739H-16 (1-512) x US-09-834-759-463 (1-3681)

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Qy 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40  
Db 1623 GAGCCTCCCGAGAGCCATCTGCTTCGAGCTGCTGCAATGAAATGCAAAAGTCTGTTCCA 1682  
Qy 41 AsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 60  
Db 1683 AATAAAGCCTTGAATTTGAAGATGAACAAACATTCGAGAGCAGATGAGATCTCCCA 1742

Qy 61 GluSerLysGlnLysAspTyrGluSerSerTrpAspSerGluSerLeuCysGluThr 80  
Db 1743 GAATCCAAACAAAGAGACTATGAGAAAGTCTTCGGATTCTGAGAGTCTCTGTGAGACT 1802  
Qy 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100  
Db 1803 GTTTCACAGAGGATGTGTGTTTACCCCAAGGCTRCRCATCAAAAAGAAATAGATAAATA 1862  
Qy 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120  
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Qy 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140  
Db 1923 AAAGTTTCTATTCCAACTTAAGCCTTAGAATTTAGATGTCGACATGCAAACTTTCAAGCAGAG 1982  
Qy 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160  
Db 1983 COTCCCGAAGGCCATCTGCCCTTCGAGCCTGCATTTGAAATGCAAAAGTCTGTTCCAAAT 2042  
Qy 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180  
Db 2043 AAAGCCTTCGAATTTGAAGATGAACAAACATTCAGAGCAGATCAGATGTTCCCTTCAGAA 2102  
Qy 181 SerLysGlnLysValGluLysAsnSerTrpAspSerGluSerLeuArgGluThrVal 200  
Db 2103 TCAAAACAAAGAAAGTTCGAGAAATTTCTGGGATTCGAGAGTCTCGTGAGACTGTT 2162  
Qy 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220  
Db 2163 TCACAGAGATGTGTGTGTACCAAGCTACACATCAAAAGAAATGATGATAAATAAGT 2222  
Qy 221 GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu 240  
Db 2223 CGAAATTTAGAAATTCACCTATCAAAATCTTGGATACACATTCATTTCTGTGTGAA 2282  
Qy 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260  
Db 2283 AGAGCAAGGAACTTCAAAAGATCTGTGACACACGTCAGGAAAGAAATGAAACAATG 2342  
Qy 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluIleLysSerGln 280  
Db 2343 AAAAGAAAGTTTGTCTACTGAAAAAGAACTGTGAGAAAGCAAAAGAAATAAATCAGAG 2402  
Qy 281 LeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuThrLeuAsn 300  
Db 2403 TTAGAGACCAAAAGTTAAATGGGAACAGAGCTCTGCAAGTGTGAGGTT----- 2452  
Qy 301 GlnGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320  
Db 2452 ----- 2452  
Qy 321 GlyArgIleGluGlnHisArgLysGluLeuValLysGlnGlnLeuGluGlnAla 340  
Db 2452 ----- 2452  
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Qy 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380  
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Qy 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420  
Db 2579 TTTGAGGACATTAAGATTTTAAAGAAAGAAATGCTGAACTTCAGATGCCCTTAAACTG 2638

QY 421 LysGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuile 440  
 Db 2639 AAAGAGATCATTAATAAGGGCACTCAATATAGTGGCAGCTTAAGATTCAGTA 2698  
 QY 441 AlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLysGluLeuGlu 460  
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 Db 2759 GCAGAAATTAAGTACACACATCTAGACTGGCTTCTGCTGTACAGACCATGATCAAT 2818  
 QY 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500  
 Db 2819 GTGACATCAAGAAAAAGTCAAGAACCTGCTTCCACATTCGAGGAGATGCTGTTTGCAA 2878  
 QY 501 ArgLysMetAsnValAspValSerThr 510  
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 US-09-620-405B-467  
 ; Sequence 467, Application US/09620405B  
 ; Patent No. 6528054  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jiang, Yugu  
 ; APPLICANT: Dillon, Davin C.  
 ; APPLICANT: Mitcham, Jennifer L.  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Harlocker, Susan L.  
 ; APPLICANT: Hepler, William T.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 ; FILE OF INVENTION: DIAGNOSIS OF BREAST CANCER  
 ; FILE REFERENCE: 210121.470C8  
 ; CURRENT APPLICATION NUMBER: US/09/620.405B  
 ; CURRENT FILING DATE: 2000-07-20  
 ; NUMBER OF SEQ ID NOS: 495  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 467  
 ; LENGTH: 1337  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-620-405B-467  
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 Pred. No.: 1,13e-221 Length: 1337  
 Score: 2125.00 Matches: 416  
 Percent Similarity: 99.76% Conservative: 0  
 Best Local Similarity: 99.76% Mismatches: 1  
 Query Match: 81.76% Indels: 0  
 DB: 4 Gaps: 0  
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 Db 78 ATGAAGATTTCTATTCCAACTAAAGCCCTTAGAATGTAGTGGACATGCCAACTTTCAAAGCA 137  
 QY 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40  
 Db 138 GAGCTCCCGAGAGCCATCTGCTTCGAGCTGCTTGAATGCAAAAGTCTGTTCCA 197  
 QY 41 AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluLeuProSer 60  
 Db 198 AATAAAGCCCTTGAATTTGAAGATGAACAAACATTTGAGAGCAGATGAGATCTCCCATCA 257  
 QY 61 GluSerLysGlnLysAspTyrGluGluSerSerTyrAspSerGluSerLeuLysGluThr 80  
 Db 258 GAATCCAAACAAAGGACTATGAGAAAGTCTTGGGATTCGAGAGTCTCTGTGAGACT 317  
 QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLeuAspLysIle 100  
 Db 318 GTTTCAGAGAGATGTGTTTTCACCAAGGCTGGCCTCAAAAGAAATAGATAAAATA 377

QY 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120  
 Db 378 AATGGAATAATTAGAGAGTCTCTGATAATATGATGGTTTCTGAAGGCTCCCTCGCAATG 437  
 QY 121 LysValSerIleProThrLysAlaLeuMetAspMetGlnThrPheLysAlaGlu 140  
 Db 438 AAAGTTTCTATTCCAACTTAAGCCTTAAGATTCATGAGCATGCACAACTTCAAAGCAGAG 497  
 QY 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160  
 Db 498 CTTCCCGAGAGCCATCTGCTTCGAGCCTGCAATTCGAATGCAAAAGTCTGTCTCAAT 557  
 QY 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180  
 Db 558 AAAGCCTTGAATTTGAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 617  
 QY 181 SerLysGlnLysValGluGluAsnSerTyrAspSerGluSerLeuArgGluThrVal 200  
 Db 618 TCAAAACAAAGAGGTTGAAGAAATTTCTGGATTTCTGAGAGTCTCCGTGAGACTGTT 677  
 QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220  
 Db 678 TCACAGAGGATGTGTGTACCCAGGCTACACATCAAAAGAAATGGTAAATTAAGT 737  
 QY 221 GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu 240  
 Db 738 GGAATTTAGAGATTCACCTATCAAAATCTTGGATACAGTTCATCTCTGTGAA 797  
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 QY 261 LysLysLysPheCysValLeuLysLysLysSerGluAlaLysGluIleLysSerGln 280  
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 Db 918 TTAGAGAACCAAAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 977  
 QY 301 GlnGluGluGluLysArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320  
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 ; Sequence 467, Application US/09433826B  
 ; Patent No. 6579973  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jiang, Yugu  
 ; APPLICANT: Dillon, Davin C.  
 ; APPLICANT: Mitcham, Jennifer L.

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; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433.826B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 467
; LENGTH: 1337
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-433-826B-467

Alignment Scores:
Pred. No.: 1,13e-221 Length: 1337
Score: 2125.00 Matches: 416
Percent Similarity: 99.76% Conservative: 0
Best Local Similarity: 99.76% Mismatches: 1
Query Match: 81.76% Indels: 0
DB: 4 Gaps: 0

US-09-451-739H-16 (1-512) x US-09-433-826B-467 (1-1337)

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QY 21 GluProGluLysProSerAlaPheGluProAlaLeuMetGlnLysSerValPro 40
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QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLysLeuLysLys 100
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QY 101 AsnGlyLysLeuGluLysSerProAsnAspGlyPheLeuLysAlaProCysArgMet 120
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Db 438 AAAGTTTCTATTCCAACTAAAGCCTTAGAATTGATGGACATGCCAATCTTCAAGCAGAG 497

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QY 161 LysAlaLeuGluLysAsnGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180
Db 558 AAAGCCTTGAATTGAAGATGAACAAACATTTGAGAGCAGATCAGATGTTCCCTTCAGAA 617

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Db 618 TCAAAACAAAGAGTTGAGAAATTTCTTGGGATTCGAGAGTCTCCGTGAGACTGTT 677

QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysLysSer 220
Db 678 TCACAGAGGATGTGTGTGTACCCAGGCTACACATCAAAAGAAATGATGATATAAAT 737

QY 221 GlyLysLeuGluAspSerThrSerLeuSerLysLysLeuAspThrValHisSerCysGlu 240
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QY 261 LysLysLysPheCysValLeuLysLysLysSerGluLysLysGluLysSerGln 280
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QY 281 LeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuThrLeuAsn 300
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Db 978 CAAGAAGAAGAGAGAGAGAAATGCCGATATATTAATGAAAAAATTTAGGGAGAAATTA 1037

QY 321 GlyArgLysGluGlnGlnHisArgLysGluLeuValLysGlnGlnLeuGluGlnAla 340
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QY 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluLysAla 380
Db 1158 ACTCATGAAATGAAAAATTTATCTTACATGAAATTTGCAATTTGAAAAAGAAATTTGCC 1217

QY 381 MetLeuLysLeuGluLysAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400
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Search completed: May 6, 2004, 17:03:37  
Job time : 138 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 6, 2004, 11:48:58 ; Search time 586 Seconds  
(without alignments)  
3711.736 Million cell updates/sec

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Perfect score: 2599  
Sequence: 1 MKVSIPTKALELMDQTFKA.....IAGDAQLQRKNVVDVSTDI 512

Scoring table: BLOSUM62  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-DB=N Geneseq 29Jan04 -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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-USER=US09451739@cgn.1.1.470 @runat.05052004.101644.18682 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq 29Jan04:.\*  
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8: Geneseqn2003bs:.\*  
9: Geneseqn2003cs:.\*  
10: Geneseqn2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2589	99.6	4458	6 ABt07694	ABt07694 Breast ca
4	2589	99.6	4458	7 ABt33271	ABt33271 Human tum
5	2589	99.6	4458	7 ACC50246	ACC50246 Breast ca
6	2578	99.2	3288	4 AAs47421	AAs47421 Human CDN
7	2578	99.2	3288	6 AAs64022	AAs64022 Human bre
8	2578	99.2	3288	7 ABt33234	ABt33234 Human tum

9	2578	99.2	3865	4 AAs47411	AAs47411 Human CDN
10	2578	99.2	3865	6 AAs64012	AAs64012 Human bre
11	2578	99.2	3865	7 ABt33224	ABt33224 Human tum
12	2578	99.2	3865	10 ADE44426	ADE44426 Human CDN
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17	2227.5	85.7	2307	4 AAs47410	AAs47410 Human CDN
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30	2125	81.8	1337	4 AAs47409	AAs47409 Human CDN
31	2125	81.8	1337	6 AAs64010	AAs64010 Human bre
32	2125	81.8	1337	7 ABt33222	ABt33222 Human tum
33	2125	81.8	1337	10 ADE44419	ADE44419 Human CDN
34	2077.5	79.9	2043	8 ADB33986	ADb33986 Human bre
35	1781	68.5	3883	7 ACC50245	ACC50245 Breast ca
36	1775	68.3	3720	7 ABt33378	ABt33378 Human tum
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39	1556.5	59.9	2232	7 ABt33235	ABt33235 Human tum
40	1554.5	59.8	1953	7 ABt33259	ABt33259 Human tum
41	1542	59.3	3673	4 AAh28497	AAh28497 Nucleotid
42	1532.5	59.0	1665	4 AAF17692	AAf17692 Human bre
43	1532.5	59.0	1665	4 AAF17692	AAf17692 Human bre
44	1532.5	59.0	1665	4 AAs47122	AAs47122 Human CDN
45	1532.5	59.0	1665	6 ABt08777	ABt08777 Human bre

ALIGNMENTS

RESULT 1  
AAH28489  
ID AAh28489 standard; cDNA; 2030 BP.  
XX  
AC AAh28489;  
XX  
AC  
XX  
DT 17-SEP-2001 (first entry)  
XX  
DE Nucleotide sequence of a human cancer associated antigen.  
XX  
KW Cancer associated antigen; INGI; tumour suppressor; cancer; vaccine; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 42..1580  
FT /\*tag= a  
FT /product= "cancer associated antigen"  
XX  
FN WO200147959-A2.  
XX  
PD 05-JUL-2001.  
XX  
PF 29-NOV-2000; 2000WC-US042334.  
XX  
PR 30-NOV-1999; 99US-00451739.  
XX  
PR 24-OCT-2000; 2000US-00602362.  
XX  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (SLOK) SLOAN KETTERING INST CANCER RES.  
PA (CORR) CORNELL RES FOUND INC.  
XX

Jager D, Stockert E, Scanlan M, Knuth A, Old L, Gure A, Chen Y;  
 WPI; 2001-441706/47.  
 P-PSDB; AAB84701.  
 Isolated cancer associated nucleic acid molecule identified by SPREX  
 (serological identification of antigens by recombinant expression  
 cloning) technique, useful in nucleic acid based therapies to treat  
 cancer.  
 Claim 1; Page 49-50; 62pp; English.  
 The present sequence encodes a human cancer associated antigen. The  
 sequence was identified using probes derived from the INGI gene. The INGI  
 gene is a tumour suppressor candidate gene. The cancer associated antigen  
 polypeptides and polypeptides are useful for screening for the  
 possible presence of a pathological condition in a subject such as  
 cancer. The cancer associated antigen polypeptides are useful for  
 producing vaccines  
 Sequence 2030 BP; 827 A; 334 C; 397 G; 460 T; 0 U; 12 Other;  
 Alignment Scores:  
 Pred. No.: 1,2e-196 Length: 2030  
 Score: 2599,00 Matches: 512  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 4 Gaps: 0  
 US-09-451-739H-16 (1-512) x AAH28489 (1-2030)  
 QY 1 MetLysValSerIleProThrLysAlaLeuMetAspMetGlnThrPheLysAla 20  
 DB 42 ATGAAGGTTCTATTCCAACTTAAGCCCTTAGAATTGATGGACATGCAACTTCCAAAGCA 101  
 QY 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40  
 DB 102 GAGCCTCCGAGAGCCATCTGCCTTCGAGCCTGCCATTGAATGCAAAAGCTGTGTTCCA 161  
 QY 41 AsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluLysLeuProSer 60  
 DB 162 AATAAGCCTTGAATTAAGAAATGAACAACATTGAGACGATGATGACTCCCATCA 221  
 QY 61 GluSerLysGlnLysAspTyrGluLysSerTyrAspSerGluSerLysLeuCysGluThr 80  
 DB 222 GAATCCAAACAAAGAGACTATGAAGAAAGTTCTTGGGATTCGAGAGTCTCTGTGAGACT 281  
 QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLysAspLysTle 100  
 DB 282 GTTTCACAGAGGATGTGTTTACCCAGGCTACACATCAAAAGAAATAGATAAATA 341  
 QY 101 AsnGlyLysLeuGluLysProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120  
 DB 342 AATGGAAANTTAGAAGAGTCTCTGATATATGATGTTTCTGAAGGCTCCCTGCAGAAATG 401  
 QY 121 LysValSerIleProThrLysAlaLeuGluMetAspMetGlnThrPheLysAlaGlu 140  
 DB 402 AAGATTCTATTCCAACTTAAGCCCTTAGAATTGATGGACATCAAACTTTCAGACAGAG 461  
 QY 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160  
 DB 462 CTTCCCGAGAGCCATCTGCCTTCGAGCCTGCCATTGAATGCAAAAGTCTGTTCCAAAT 521  
 QY 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180  
 DB 522 AAAGCCTTGAATTAAGAAATGAACAACATTGAGACGATGATGATGTTCCCTTCAGAA 581  
 QY 181 SerLysGlnLysLysValGluGluAsnSerTyrAspSerGluSerLeuArgGluThrVal 200  
 DB 582 TCAAAACAAAGAGGTTGAAGAAATTTCTTGGATTTCTGAGAGTCTCGTGAGACTGTT 641  
 QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysLysSer 220

DB 642 TCACAGAGGAGTGTGTGTACCCAGGCTACACATCAAAAGAAATGGATAAAATAGT 701  
 QY 221 GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu 240  
 DB 702 GGAAATTTAGAAGATTCAACTAGCCTATCAAAATCTTGGATACAGTTCATTCTGTGAA 761  
 QY 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260  
 DB 762 AGAGCAGGGAACTTCAAAAGATCACTGTGACACAGCTACAGGAAATATGGACAAATG 821  
 QY 261 LysLysLysPheCysValLeuLysLysLysSerGluAlaLysGluLysSerGln 280  
 DB 822 AAAAGAAAGTTTGTGTACTGAAAAGAAAGTGTGAGAGCAAAAGAAATATAATCAAG 881  
 QY 281 LeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuThrLeuAsn 300  
 DB 882 TTAGAGAACCAAAAGTTTAAATGGAACACAGAGCTCTGCAGTGTGAGATTGACTTTAAAC 941  
 QY 301 GlnGluGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320  
 DB 942 CAAAGAAAGAGAGAGAGAAATGCCGATATATTAAATGAAAAAATAGGAGAAATTA 1001  
 QY 321 GlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnLeuGluAla 340  
 DB 1002 GGAAGAAATCGAAGACAGCAGTAGGAAAGAGTTAGAAGTGAACACAACTTGAACAGCT 1061  
 QY 341 LeuArgIleGlnAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360  
 DB 1062 CTCAGAAATACAGATATAGATTGAAGAGTGTAGAAAGTAATTTGAATCAGGTTTCTCAC 1121  
 QY 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluLeuAla 380  
 DB 1122 ACTCATGAAATGAAATTTATCTTACATGAAATTCATGTTGAAAAGGAAATTTGCC 1181  
 QY 381 MetLeuLysLeuGluLysIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400  
 DB 1182 ATGCTAAACTGGAAATAGCCACACTGAAACACCAATACCAGGAAAGGAAATATAATAC 1241  
 QY 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420  
 DB 1242 TTTGAGCAGCATTAAGATTTTAAAGAAAGAAATGCTGAACCTTCAGATGACCCATAAATCTG 1301  
 QY 421 LysGluLysSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLysValLeuIle 440  
 DB 1302 AAAGAGAAATCAATTAATAAGGGCACTCAATATATAGTGGCAGCTTAAAGTCTGATA 1361  
 QY 441 AlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLysGluLeuGlu 460  
 DB 1362 GCTGAGAACACAAATGCTCACTTCTAAATTAAGGAAAGAAACAAAGACAAAGAAATCTAGAG 1421  
 QY 461 AlaGluLysSerHisIleProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480  
 DB 1422 GCAGAAATTAATCAACACCATCTCTAGACCTGCTTCTGCTGTACAGACCATGATCAAT 1481  
 QY 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500  
 DB 1482 GTGACATCAAGAAAGAAAGTCAAGAACTGCTTCCCATTTCCAGATTCAGGAGATGCTTTGTTGCAA 1541  
 QY 501 ArgLysMetAsnValAspValSerSerThrAspIle 512  
 DB 1542 AGAAATTAATGATGTTGATGTAGTAGTAGCATATA 1577

RESULT 2  
 ABT33272  
 ID ABT33272 standard; DNA, 4047 BP.  
 XX  
 AC ABT33272;  
 XX  
 DT 15-MAY-2003 (first entry)  
 XX  
 DE Human tumour-related DNA sequence - SEQ ID No 566.  
 XX

KW Human; ds; vaccine; gene therapy; T cell stimulation; T cell expansion;  
 XW tumour; breast cancer; cancer; immune response stimulation.  
 XX Homo sapiens.  
 XX WO200283956-A1.  
 XX 24-OCT-2002.  
 XX 15-APR-2002; 2002WO-US012378.  
 XX 13-APR-2001; 2001US-00834759.  
 XX 07-DEC-2001; 2001US-00007805.  
 XX 13-FEB-2002; 2002US-00076622.  
 XX (CORI-) CORIXA CORP.  
 XX Houghton RL, Sleath PR, Persing DH, Jiang Y, Dillon DC;  
 PI Mitcham JL, Xu J, Harlocker SL, Repler WT, Henderson RA, Fanger GR;  
 PI Vedvick TS, McNeill PD, Durham M;  
 XX WPI; 2003-103376/09.  
 XX New polypeptide and polynucleotide useful for stimulating and/or  
 PT expanding T cells specific for a tumor protein and treating breast  
 PT cancer.  
 XX Example 12; Page 346-347; 375pp; English.  
 XX The invention comprises a method of stimulating and/or expanding T cells  
 CC specific for a tumor protein. The invention further comprises human  
 CC nucleic acids and proteins that are associated with tumours (e.g. breast  
 CC cancer). The method and sequences of the invention are useful for  
 CC stimulating and/or expanding T cells specific for a tumor protein,  
 CC detecting the presence of cancer, stimulating an immune response in a  
 CC patient and treating breast cancer. The present DNA sequence represents a  
 CC human tumour-related DNA sequence  
 XX  
 SQ Sequence 4047 BP; 1563 A; 716 C; 850 G; 918 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1,66e-195 Length: 4047  
 Score: 2589.00 Matches: 510  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.62% Indels: 0  
 DB: 7 Gaps: 0

US-09-451-739H-16 (1-512) x ABT33272 (1-4047)

QY 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetMetGlnThrPheLysAla 20  
 DB 2053 ATGAAAGTTCTATTCCAACTTAAGCCTTGAATTTGATGGACATGCAAACTTTCAAAGCA 2112  
 QY 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40  
 DB 2113 GAGCTCCGAGAGCCATCTGCTTCGAGCCTGCCATTTGAATGCAAAAGTCTGTCCA 2172  
 QY 41 AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluLeuLeuProSer 60  
 DB 2173 AATAAGCCTTGGAAATTCAGAAATGAACAAACATTCGAGCAGATGATACATCCCATCA 2232  
 QY 61 GluSerLysGlnLysAspTyrGluLysSerTrpAspSerGluSerLeuGluThr 80  
 DB 2233 GAATCCCAACAAAGGACTATGAAGAAGTTCTGGGATTTCTGAGAGTCTCTGTGAGACT 2292  
 QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLeuAspLysIle 100  
 DB 2293 GTTTTCAGAGAGGATGTGTGTTTACCACCAAGCTACACATCAAAAGAAATAGATAAATA 2352  
 QY 101 AsnGlyLysLeuGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120  
 DB 2353 AATGAAATTTAGAGAGTCTCTCTGTAATATGATGGTTTCTGAGAGGCTCCCTGCAGATG 2412

QY 121 LysValSerIleProThrLysAlaLeuGluLeuMetMetGlnThrPheLysAlaGlu 140  
 DB 2413 AAAAGTTCTATTCCAACTTAAGCCTTGAATTTGATGGACATGCAAACTTTCAAAGCAGAG 2472  
 QY 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160  
 DB 2473 CTTCCCGAGAGCCATCTGCTTCGAGCCTGCCATTTGAATGCAAAAGTCTGTTCCTCAAT 2532  
 QY 161 LysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180  
 DB 2533 AAAGCCTTGGAAATTTGAAGAAATGAACAAACATTCGAGCAGATCAGATGTTCCCTTCAGAA 2592  
 QY 181 SerLysGlnLysLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200  
 DB 2593 TCAAAACAAAGAGGTTTGAAGAAATTTCTTGGATTTCTGAGAGTCTCCGTGAGACTGTT 2652  
 QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220  
 DB 2653 TCACAGAGGATGTGTGTGTACCAAGGCTACACATCAAAAGAAATGAATAAATAAAT 2712  
 QY 221 GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu 240  
 DB 2713 GGAATAATTAGAGATTTCAACTAGCCTATCAAAATCTTGGATACAGTTCACTTCTGTGAA 2772  
 QY 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260  
 DB 2773 AGAGCAAGGAACTTCAAAAGATCACTGTGAACACGTACAGCAAAATGGAACAAATG 2832  
 QY 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluLysSerGln 280  
 DB 2833 AAAAAGAGTTTGTGTGTACTGAAAAGAAACTGTGAGAACAAAGAAATATAAATCACAG 2892  
 QY 281 LeuGluAsnGlnLysValLysTrpGluGlnGluLysCysSerValArgLeuThrLeuAsn 300  
 DB 2893 TTACAGAACCAAAAGTTAAATGGAAACAGAGCTCTGCAGTGTGAGATTTGACTTTTAAC 2952  
 QY 301 GlnGluGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320  
 DB 2953 CAAGAAGAGAGAGAGAGAAATGCCATATATTAATGAATAAATTAGGGAGAAATTA 3012  
 QY 321 GlyArgIleGluGluGlnHisArgLysGluLeuValLysGlnGlnLeuGluGlnAla 340  
 DB 3013 GGAAGATCGAAGAGCAGCATAGCAAGAGTTAGAGTGAACCAACAACTTGAACAGCT 3072  
 QY 341 LeuArgIleGlnAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360  
 DB 3073 CTCGAATACAGATATAGAAATTCAGAGTGTAGAAAGTAAATTTGAATTCAGTTTCTCAC 3132  
 QY 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380  
 DB 3133 ACTCATGAATGAATTAATCTCTTACATGAATTTGCAATTTGAAAAAGAAATTTGCC 3192  
 QY 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGlnLysGluAsnLysTyr 400  
 DB 3193 ATGCTAAACTCGAAATAGCCACACTGAACACCAATACCAGGAAAGGAAATAAATATAC 3252  
 QY 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420  
 DB 3253 TTTGAGGACATTAAGATTTTAAAGAAAGAAATGCTGAACTTCAGATGACCTTAAACTG 3312  
 QY 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle 440  
 DB 3313 AAAGAGGAATCATTAACCTAAAGGCGCATCTCAATATATAGTGGGCGAGCTTAAAGTTCTGATA 3372  
 QY 441 AlaGluAsnThrMetLeuThrSerLysLysLysGluLysGlnAspLysGluIleLeuGlu 460  
 DB 3373 GCTGAGAACACATGCTCACTTCTAAATTTGAAGAAACCAAGCAAGAAATATCTAGAG 3432  
 QY 461 AlaGluIleGluSerHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480  
 DB 3433 GCAGAAATTTGAATCACACCATCTAGACTGGCTTCTGTGTACAAGACCATGATCAAT 3492



QY 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500  
 Db 3493 GTGACATCAAGAAAAAGTCAAGACCTGCTTCCACATTCGAGGAGATGCTGTGTTGCAA 3552  
 QY 501 AtcLysMetAsnValAspValSerSerThr 510  
 Db 3553 AGAAAAATGAATGTTGATGTAGTAGTACG 3582

## RESULT 3

ABT07694  
 ID ABT07694 standard; DNA; 4458 BP.

XX AC ABT07694;

XX DT 14-NOV-2002 (first entry)

XX DE Breast cancer-associated gene sequence 2.

XX KW Gene; ds; breast cancer; breast cancer-associated gene sequence;  
 drug development; pharmacogenetics; biosensor development.

XX OS Unidentified.

XX PN W0200259377-A2.

XX PD 01-AUG-2002.

XX PF 24-JAN-2002; 2002W0-US002242.

XX PR 24-JAN-2001; 2001US-0263956P.

XX PR 02-FEB-2001; 2001US-0265328P.

XX PR 09-APR-2001; 2001US-00829472.

XX PR 09-APR-2001; 2001US-0282898P.

XX PR 04-MAY-2001; 2001US-0288590P.

XX PR 29-MAY-2001; 2001US-0294443P.

XX PA (FOSB-) FOS BIOTECHNOLOGY INC.

XX PI Mack DH, Gish KC, Afar D;

XX DR WFI; 2002-583738/62.

XX DR N-FSDB; ABJ05537.

PT Detecting a breast cancer-associated transcript in a patient's cell,  
 useful for diagnosing breast cancer, comprises contacting a biological  
 sample with a polynucleotide that selectively hybridizes with breast  
 cancer nucleic acids.

PS Claim 9; Page 347-348; 414pp; English.

CC The invention comprises a method of detecting a breast cancer-associated  
 transcript in a cell from a patient. The method of the invention involves  
 contacting a biological sample from the patient with a nucleotide that  
 hybridizes to one of the 69 breast cancer-associated gene sequences shown  
 in the specification. The method of the invention is useful in the  
 diagnosis or prognosis of breast cancer, and for detecting genes that are  
 up or down-regulated in breast cancer cells. Genes identified by the  
 method of the invention can be used in diagnostic purposes and also as  
 targets for screening for therapeutic compounds that modulate breast  
 cancer (e.g. hormones or antibodies). Identification of genes that are  
 over or under expressed in breast cancer can additionally provide high-  
 resolution, high-sensitivity datasets which can be used in the areas of  
 diagnostics, therapeutics, drug development, pharmacogenetics, protein  
 structure and biosensor development. DNA sequences ABT07693 - ABT07761  
 represent the 69 breast cancer-associated gene sequences of the invention

SQ Sequence 4458 BP; 1698 A; 812 C; 931 G; 1017 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.86e-195 Length: 4458  
 Score: 2589.00 Matches: 510  
 Percent Similarity: 100.00% Conservativeness: 0  
 Best Local Similarity: 100.00% Mismatches: 0

Query Match: 99.62% Indels: 0  
 DB: 6 Gaps: 0  
 US-09-451-739H-16 (1-512) x ABT07694 (1-4458)  
 QY 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20  
 Db 2128 ATGAAAGTTTCTATTCCAACTTAAAGCCTTGAATTTGATGGACATGCAAACTTTCAAGCA 2187  
 QY 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40  
 Db 2188 GAGCCTCCGAGAGGCCATCTGCTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTGCA 2247  
 QY 41 AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 60  
 Db 2248 AATAAAGCCTTGGAAATGAAGATGAACAACATTGAGACGACATGATGATCTCCATCA 2307  
 QY 61 GluSerLysGlnLysAspTyrGluLysSerSerTrpAspSerGluSerLeuCysGluThr 80  
 Db 2308 GAATCCAAACAAAGGACTATGAAGAAAGTTCTTGGGATTCGAGAGTCTCTGTGAGCT 2367  
 QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100  
 Db 2368 GTTTCACAGAGGATGTGTGTTTACCAGGCTACACATCAAAAGAAATAGATAAATA 2427  
 QY 101 AsnGlyLysLeuGluLysSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120  
 Db 2428 AATGGAATAATTAGAAGAGTCTCTCTGATATGATGCTTTCTGAAGGCTCCCTGCAGATG 2487  
 QY 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140  
 Db 2488 AAAGTTTCTATTCCAACTTAAAGCCTTGAATTTGATGGACATGCAAACTTTCAAGCAGAG 2547  
 QY 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160  
 Db 2548 CCTCCGAGAGGCCATCTGCTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTGCAAAAT 2607  
 QY 161 LysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180  
 Db 2608 AAAGCCTTGGAAATTCAGAGATGAACAACATTGAGACGACATGAGATGTTCCCTTCAGAA 2667  
 QY 181 SerLysGlnLysValGluGluLysSerTrpAspSerGluSerLeuArgGluThrVal 200  
 Db 2668 TCAAAACAAAGAGAGTTTGAAGAAAAATCTTGGGATTCGAGAGTCTCCGTGAGACTGTT 2727  
 QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220  
 Db 2728 TCACAGAGGATGTGTGTACCCAGGCTACACATCAAAAGAAATGGATTAATAAGT 2787  
 QY 221 GlyLysLeuGluAspSerThrSerLysSerLysIleLeuAspThrValHisSerCysGlu 240  
 Db 2788 GGAATAATTAGAAGATTCAACTAGCCTATCAAAAATCTTGGATACAGTTCAATCTTGTGAA 2847  
 QY 241 ArgAlaArgGluLeuGluLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260  
 Db 2848 AGAGCAGAGGAACTTCAAAAAGATCACTGTGACACAGCTACAGAAAAAATGGACAAATG 2907  
 QY 261 LysLysLysPheCysValLeuLysLysLysSerGluAlaLysSerGluIleLysSerGln 280  
 Db 2908 AAAAAAGAGTTTGTGTACTGAAAGAAAGAACTGTCAAGAGCAAAAGAAATAAATAATCACAG 2967  
 QY 281 LeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuThrLeuAsn 300  
 Db 2968 TTAGAGAACCCAAAAGTTTAATGGACACAGAGCTCTGCACTGTGAGATGACTTTAAAC 3027  
 QY 301 GlnGluGluLysArgArgAsnAlaAspIleLeuAsnGlnLysIleArgGluGluLeu 320  
 Db 3028 CAAGAAGAGAGAGAGAGAAATGCCGATATTAATAAGAAAAAATTTAGGAGAAATTA 3087  
 QY 321 GlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGlnAla 340  
 Db 3088 GGAAGAAATCGAGAGAGCAGCAGTATGAAAGAGTTAGAGTGAACCAACAACTTGACAGGCT 3147



QY 341 LeuArgileGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis 360  
 Db 3148 CTGAGATACAGATATAGAAATTTGAAGAGTGTAGAAGTAATTTGAATCAGTTCTTCAC 3207  
 QY 361 ThrHisGluAsnGlnAsnIleLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380  
 Db 3208 ACTCATGAAATGAAATATATCTTACATGAAATTTGCATTTTGAAGAAGGAATTC 3267  
 QY 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400  
 Db 3268 ATGCTAAATCTGGAATATAGCACACTGAAACACCAATACCGAAGAAAGGAATTAATAC 3327  
 QY 401 PheGluAspIleLysLysLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420  
 Db 3328 TTTGAGGACATTAAGATTTTAAAGAAAGAAATGCTGAACCTTCAGATGACCTTAAACTG 3387  
 QY 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle 440  
 Db 3388 AAGAGGAAATCATTAATTAAGGGCATCTCAATATAGTGGCAGCTTAAAGTTCTGATA 3447  
 QY 441 AlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLysGluIleLeuGlu 460  
 Db 3448 GCTGAGAACACAATGCTCACTTCTAAATTTGAAGAAACAAAGACAAAGAAATACTAGAG 3507  
 QY 461 AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480  
 Db 3508 GCAGAAATTTGAATCACACCATCTAGACTGGCTTCTGCTGTACAGACCATGATCAAAAT 3567  
 QY 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500  
 Db 3568 GTGACATCAAGAAAAAGTCAAGAACCTGCTTCCACATTCGAGGAGATGCTTGTGTGCAA 3627  
 QY 501 ArgLysMetAsnValAspValSerSerThr 510  
 Db 3628 AGAAAAATGATGTTGATGTAGTAGTACG 3657  
 RESULT 4  
 ABT33271  
 ID ABT33271 standard; DNA; 4458 BP.  
 AC ABT33271;  
 XX  
 DT 15-MAY-2003 (first entry)  
 XX  
 DE Human tumour-related DNA sequence - SEQ ID No 564.  
 XX  
 KW Human; ss; vaccine; gene therapy; T cell stimulation; T cell expansion;  
 KW tumour; breast cancer; cancer; immune response stimulation; PCR; primer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200283956-A1.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 15-APR-2002; 2002WO-US012378.  
 XX  
 PR 13-APR-2001; 2001US-00834759.  
 PR 07-DEC-2001; 2001US-00007805.  
 PR 13-FEB-2002; 2002US-00075622.  
 XX  
 XX (CORI-) CORIXA CORP.  
 PA  
 XX Houghton RL, Sleath PR, Persing DH, Jiang Y, Dillon DC;  
 PI Mitcham JL, Xu J, Harlocker SL, Hepler WT, Henderson RA, Fanger GR;  
 PI Vedvick TS, McNeill PD, Durham M,  
 XX WPI; 2003-103376/09.  
 DR  
 XX New polypeptide and polynucleotide useful for stimulating and/or  
 PT expanding T cells specific for a tumor protein and treating breast  
 PT cancer.

PS Example 9; Page 340-341; 375pp; English.

XX The invention comprises a method of stimulating and/or expanding T cells  
 CC specific for a tumor protein. The invention further comprises human  
 CC nucleic acids and proteins that are associated with tumors (e.g. breast  
 CC cancer). The method and sequences of the invention are useful for  
 CC stimulating and/or expanding T cells specific for a tumor protein,  
 CC detecting the presence of cancer, stimulating an immune response in a  
 CC patient and treating breast cancer. The present DNA sequence represents a  
 CC human tumour-related PCR primer  
 XX

SQ Sequence 4458 BP; 1698 A; 812 C; 931 G; 1017 T; 0 U; 0 Other;

# Alignment Scores:

Pred. No.: 1-866-195 Length: 4458  
 Score: 2589.00 Matches: 510  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.62% Indels: 0  
 DB: 7 Gaps: 0

US-09-451-739H-16 (1-512) x ABT33271 (1-4458)

QY 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20  
 Db 2128 ATGAAAGTTTCTATTCCAACTAAAGCCTTAGAATTTGATGGACATGCCAACTTTTCAAGCA 2187  
 QY 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40  
 Db 2188 GAGCCTCCCGAGAGACCATCTGCCTTCGAGCTGCCATTGAAATGCAAAAGTCTGTTCCA 2247  
 QY 41 AsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 60  
 Db 2248 AATAAAGCCTTGGAATTCAGAAATGAACAAACATTTGAGAGCAGATGATCTCCCAATCA 2307  
 QY 61 GluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGluSerLeuLysGluThr 80  
 Db 2308 GAATCCAAACAAAGAGCATATGAGAAAGTTCTTGGGATTTCTGAGAGTCTCTGTGAGACT 2367  
 QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100  
 Db 2368 GTTTCACAGAGAGATGTGTGTTTACCAAGGCTACACATCAAAAGAAATAGATAAAATA 2427  
 QY 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120  
 Db 2428 AATGGAATTTAGAGAGTCTCTGATAATGATGTTTCTGGAAGGCTCCCTGCAGAAATG 2487  
 QY 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140  
 Db 2488 AAGTTTCTATTCCAACTAAAGCCTTAGAATTTGATGGACATGCAAACTTTCAAGCAGAG 2547  
 QY 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160  
 Db 2548 CCTCCCGAGAGACCATCTGCCTTCGAGCTGCCATTGAAATGCAAAAGTCTGTTCCTCAAT 2607  
 QY 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180  
 Db 2608 AAAGCCTTGGAATTTGAGAAATGAACAAACATTTGAGAGCAGATCAGATGTTTCCCTTCAGAA 2667  
 QY 181 SerLysGlnLysLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200  
 Db 2668 TCAAAACAAAGAGAGTTTGAAGAAATTTCTTGGGATTTCTGAGAGTCTCTCCGTGAGACTGTT 2727  
 QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220  
 Db 2728 TCACAGAGAGATGTGTGTACCAAGCCTACACATCAAAAGAAATTCGATAAATTAAT 2787  
 QY 221 GlyLysLeuGluAspSerThrSerLysIleLeuAspThrValHisSerCysGlu 240  
 Db 2788 GGAAATTTAGAGATTTCACTAGCCTATCAAAATTTTGGATACAGTTTCAATCTTGTGAA 2847  
 QY 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260



Qy 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140  
 Db 2488 AARSTTTCTTCAACTAAGGCTTAGAATTGATGACATGCACAACTTTCAAGCAGAG 2547  
 Qy 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160  
 Db 2548 CCTCCGAGAGCCATCGCTCGAGCCGCGCCATTGAAATGCAAAAGTCTGTTCAAAT 2607  
 Qy 161 LysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180  
 Db 2608 AAGCCCTTGAATTGAAGATGAACAAACATTGAGAGCAGATCAGATGTTCCCTTCAGAA 2667  
 Qy 181 SerLysGlnLysLysValGluGluLysSerTrpAspSerGluSerLeuArgGluThrVal 200  
 Db 2668 TCAAAACAAAAGAGGTGAAGAAATTCCTGGGATTCAGAGCTCCCGTGAGACGT 2727  
 Qy 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220  
 Db 2728 TCACAGAAGGATGTGTGTGATCCCAAGCTACACATCAAAAGAAATGGATAAATAAGT 2787  
 Qy 221 GlyLysLeuGluAspSerThrSerLysSerLysIleLeuAspThrValHisSerCysGlu 240  
 Db 2788 GGAATATTAGAAGATTCACATAGGCTATCAAAATCTTGGATACAGTTCATCTTTGTGAA 2847  
 Qy 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260  
 Db 2848 AGAGCAAGGACCTTCAAAAGATCACCTGTGACACCTACAGGAAAAATGGACAAATG 2907  
 Qy 261 LysLysLysPheCysValLeuLysLysLysLysSerGluAlaLysGluLysLysSerGln 280  
 Db 2908 AAAAAGAAAGTTTGTGTACTGAAAAAGAACTGTGAGAGCAAGAAAGAAATAAATCAAG 2967  
 Qy 281 LeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuThrLeuAsn 300  
 Db 2968 TTAGAGAACCAAAAGTTAAATGGGAACAGAGCTCTGCAGTGTGAGATTGACTTTAAAC 3027  
 Qy 301 GlnGluGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysLysLysLysLys 320  
 Db 3028 CAAGAAGAGAGAGAGAGAAATGCCGATATATTAATGAAAAATTTAGGGAAGAATTA 3087  
 Qy 321 GlyArgIleGluGlnHisArgLysGluLeuGluValLysGlnLeuGluGlnAla 340  
 Db 3088 GGAGAATCGAAGAGCAGATAGGAAGAGTTAGAAAGTGAACAACTTGAACAGGCT 3147  
 Qy 341 LeuArgIleGlnAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360  
 Db 3148 CTCAGAAATCAAGATATAGATTGAAGAGCTGTAGAAAGTAATTTGAATCAGGCTTCTCAC 3207  
 Qy 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380  
 Db 3208 ACTCATGAAATGAAATATCTCTTACATGAAATTTGCATGTTGAAAGGAATTCGCC 3267  
 Qy 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400  
 Db 3268 ATGCTAAACTGGAAATAGCCACCTGAAACACCAATACAGGAAAGGAAATAAATAC 3327  
 Qy 401 PheGluAspIleLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 420  
 Db 3328 TTTGAGGACATTAAAGATTTAAAGAAAGAAATGCTGGAATTCAGATGCCCTTAAACATG 3387  
 Qy 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLysValLeuIle 440  
 Db 3388 AAAGAGGAATCATTAATAAGAGGATCTCATATATAGTGGCAGCTTAAAGTTCTGATA 3447  
 Qy 441 AlaGluAsnThrMetLeuThrSerLysLysLysGluLysGlnAspLysGluIleLeuGlu 460  
 Db 3448 GCTGAGAACCAATGCTCACTTCTAAATTTGAAGGAAAAACAGACAAAGAAATACATAGAG 3507  
 Qy 461 AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480  
 Db 3508 GCAGAAATTTGAATCACCACTCTAGACTGCTTCTGCTGTACAGACCATCATCAAT 3567  
 Qy 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500

Db 3568 GTGACATCAAGAAAAGTCAAGAACCTGCTTTCACATTCAGGAGATGCTTGTTCGAA 3627  
 Qy 501 ArgLysMetAsnValAspValSerSerThr 510  
 Db 3628 AGAAAATGAATGTTGATGTGAGTAGTACG 3657  
 RESULT 6  
 AAS47421  
 ID AAS47421 standard; cDNA; 3288 BP.  
 AC AAS47421;  
 XX 18-DEC-2001 (first entry)  
 DT  
 XX Human cDNA encoding breast cancer protein B726P fusion protein #1.  
 DE  
 XX Human; ss; breast cancer protein; tumour; cancer; cytostatic;  
 KW Gene therapy.  
 XX Homo sapiens.  
 OS  
 XX WO200179286-A2.  
 PN  
 XX 25-OCT-2001.  
 PD  
 XX 12-APR-2001; 2001WO-US012164.  
 PF  
 XX 17-APR-2000; 2000US-00551621.  
 XX 08-JUN-2000; 2000US-00590751.  
 PR 22-JUN-2000; 2000US-00604287.  
 PR 20-JUL-2000; 2000US-00620405.  
 XX  
 XX (CORI-) CORIXA CORP.  
 PA  
 PI Jiang Y, Dillon DC, Mitcham JL, Xu J, Harlocker SL, Hepler WT;  
 XX WPI; 2001-611721/70.  
 DR P-PSDB; AAU33357.  
 XX  
 PT Breast Tumor Proteins and nucleic acids useful for the prevention,  
 XX diagnosis and treatment of breast cancer.  
 PS Claim 37; Page 290-291; 297pp; English.  
 CC The invention relates to isolated breast tumour proteins and nucleic  
 CC acids that encode them, including immunogenic fragments of the proteins.  
 CC Also included are expression vectors expressing the proteins, transformed  
 CC cells and antibodies raised against the proteins or an antigen presenting  
 CC cell expressing the protein. The proteins and nucleic acids may be used  
 CC in the prevention, diagnosis and treatment of diseases associated with  
 CC inappropriate breast tumour protein expression, i.e. breast tumours and  
 CC breast cancer e.g. by gene therapy. The nucleic acids and their  
 CC complements may also be used as DNA probes in diagnostic assays to detect  
 CC and quantitate the presence of similar nucleic acids in samples, and  
 CC therefore which patients may be in need of restorative therapy. The  
 CC proteins, nucleic acids and antibodies may be used in assays to identify  
 CC modulators (e.g. antagonists) of breast tumour protein expression and  
 CC activity. The antibodies and antagonists may also be used to down  
 CC regulate expression and activity. The antibodies may also be used as  
 CC diagnostic agents for detecting the presence of the proteins in samples  
 CC (e.g. by enzyme linked immunosorbent assay (ELISA)) and in other immuno-  
 CC purification diagnostic techniques. The present sequence is a cDNA from a  
 CC breast tumour cDNA library isolated by subtractive hybridisation against  
 CC a normal breast cDNA library and encodes a breast tumour protein of the  
 CC invention  
 XX  
 SQ Sequence 3288 BP; 1293 A; 564 C; 664 G; 761 T; 0 U; 6 Other;

Alignment Scores:  
 Pred. No.: 9,71e-195 Length: 3288  
 Score: 2578.00 Matches: 508  
 Percent Similarity: 99.61% Conservative: 0

Best Local Similarity: 99.61%			Mismatches: 2		
Query Match: 99.19%			Indels: 0		
DB: 4			Gaps: 0		
US-09-451-739H-16 (1-512) x AAS47421 (1-3288)					
QY	1	MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20	QY	341	LeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis 360
DB	1291	ATGAAGATTCTATTCCAACTAAGCCTTAGAATTGATGACATGCACAACTTTCAAGCA 1350	DB	2311	CTCAGAAATACAAAGATATAGAAATTCAGAGTGTAGAAAGTAATTTGATCAGGTTTCTCAC 2370
QY	21	GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40	QY	361	ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380
DB	1351	GAGCTCCCGAGAAGCCATCTGCCCTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTC 1410	DB	2371	ACTCATGAAATGAAATTAATCTCTTACATGAAATTCATGTTGAAAAAGGAAATGGCC 2430
QY	41	AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 60	QY	381	MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400
DB	1411	AATAAGCCCTTGAATTGAGAAATGACAAACATTGAGAGCAGATGAGATCTCCCATCA 1470	DB	2431	ATGCTAAAACCTGGAATAGCCACACTGAAACACCAATACCAGGAAAAAGGAAATAAATAC 2490
QY	61	GluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGluSerLeuCysGluThr 80	QY	401	PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420
DB	1471	GAATCCAAACAAAGAGGACTATGAAGAAAGTTCTTTGGGATTTCTGAGACTCTCTG 1530	DB	2491	TTTGAGGACATTAGAAATTTAAAGAAAGAAATGCTGAATCTCAGATGACCCCTAAACTG 2550
QY	81	ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100	QY	421	LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle 440
DB	1531	GTTTCACAGAAGGATGTGTGTTTACCCAGGCTRCRCATCAAAAGAAATAGATAAATA 1590	DB	2551	AAAGAGGAATCATTAACATAAAGGCGCATCTCAATATAGTGGCAGCTTAAAGTTCTGATA 2610
QY	101	AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120	QY	441	AlaGluAsnThrMetLeuThrSerLysLysLeuLysGluLysGlnAspLysGluIleLeuGlu 460
DB	1591	AATGGAAATTTAGAGAGCTCTCTGATAATGATGGTTTCTGCAAGGCTCCCTGCAAGATG 1650	DB	2611	GCTGAGAACACAATGCTCATTCTTAATTTGAAGGAAAAACAAGACAAAGAAATACTAGAG 2670
QY	121	LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140	QY	461	AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480
DB	1651	AAAGTTTCTATTCCAACTTAAGCCTTAGAATTGATGGACATGCCAACTTTCAAGCAGAG 1710	DB	2671	GCAGAAATTTGAATCACACCATCTAGACTGGCTTCTGCTGTACAGACCATGATCAAAAT 2730
QY	141	ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160	QY	481	ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500
DB	1711	CTCTCCGAGAGCCATCTGCCCTTCGAGCCTGCCATTGAAATGCAAAAGCTGTGTCCAAAT 1770	DB	2731	GTGACATCAAGAAAAAGTCAAGAACCTGCTTTCCACATTGCAGGAGATGCTTTGTTCCAA 2790
QY	161	LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180	QY	501	ArgLysMetAsnValAspValSerSerThr 510
DB	1771	AAAGCCTTTGGAATTGAAGAAATGAACAAACATTGAGAGCAGATCAGATGTTCCCTTCAGAA 1830	DB	2791	AGAAAAATGAATGTTGATGTGAGTAGTAGC 2820
QY	181	SerLysGlnLysLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200	RESULT 7		
DB	1831	TCAAAACAAAGAAAGTGTGAAGAAATTTCTGGGATTTCTGAGAGTCTCCGTGAGAGCTGT 1890	ABS64022		
QY	201	SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220	ID	ABS64022 standard; DNA; 3288 BP.	
DB	1891	TCACAGAAGGATGTGTGTATCCCAAGGCTACACATCAAAAGAAATGATGATATAATAAGT 1950	XX		
QY	221	GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu 240	AC	ABS64022;	
DB	1951	GGAAAAATTAGAAGATTTCACTAGCCTATCAAAAAATCTTGGATACAGTTCATTTCTGTGAA 2010	XX		
QY	241	ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260	XX	15-NOV-2002 (first entry)	
DB	2011	AGAGCAAGGGAATCTCAAAAAATCACTGTGAAACACGTACAGGAAAAATGGAACAATG 2070	DE	Human breast tumour polynucleotide #471.	
QY	261	LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluIleLysSerGln 280	XX	Human; breast tumour protein; gene; ds; breast cancer; cytostatic;	
DB	2071	AAAAAGAGTTTGTGTACTGAAAGAAAGAACTGTGAGAGCAAAAGAAATAAATACACAG 2130	KW	vaccine.	
QY	281	LeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuThrLeuAsn 300	XX	Homo sapiens.	
DB	2131	TTAGAGAACCAAAAGTTAAATGGGAACAGAGCTCTGCAGTGTGAGATTTGACTTTAAAC 2190	OS	US2002085998-A1.	
QY	301	GlnGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320	XX	04-JUL-2002.	
DB	2191	CAAGAGAGAGAGAGAGAGAAATGCCGATATATTAAATGAAAAAATTAGGGAAGAAATTA 2250	XX	13-APR-2001; 2001US-00834759.	
QY	321	GlyArgIleGluGlnGlnHisArgLysGluLeuGluValLysGlnGlnLeuGluGlnAla 340	XX	28-DEC-1998; 98US-00222575.	
DB	2251	GGAAGAATCGAAGCAGCAGCATAGAAAGAGTTAGAAAGTGAACAAACAACTTGACAGGCT 2310	PR	02-APR-1999; 99US-00285480.	
			PR	23-JUN-1999; 99US-00339338.	
			PR	02-SEP-1999; 99US-00389681.	
			PR	03-NOV-1999; 98US-00433826.	
			PR	17-APR-2000; 2000US-00551621.	
			PR	08-JUN-2000; 2000US-00590751.	
			PR	22-JUN-2000; 2000US-00604287.	
			PR	20-JUL-2000; 2000US-00620405.	
			XX	(CORI-) CORIXA CORP.	
			XX	Jiang Y, Dillon DC, Mitcham JL, Xu J, Harlocker SL, Hepler WT;	
			PI	Henderson RA;	
			XX		



XX Human; ds; vaccine; gene therapy; T cell stimulation; T cell expansion;  
 KW tumour; breast cancer; cancer; immune response stimulation.  
 XX Homo sapiens.  
 XX W0200283956-A1.  
 XX PD 24-OCT-2002.  
 XX PF 15-APR-2002; 2002WO-US012378.  
 XX PR 13-APR-2001; 2001US-00834759.  
 XX PR 07-DEC-2001; 2001US-00007805.  
 XX PR 13-FEB-2002; 2002US-00076622.  
 XX PA (CORI-) CORIXA CORP.  
 XX PI Houghton RL, Sleath PR, Persing DH, Jiang Y, Dillon DC;  
 PI Mitcham JL, Xu J, Harlocker SL, Hepler WT, Henderson RA, Fanger GR;  
 PI Vedvick TS, McNeill PD, Durham M;  
 XX WI: 2003-103376/09.  
 XX New polypeptide and polynucleotide useful for stimulating and/or  
 PT expanding T cells specific for a tumor protein and treating breast  
 PT cancer.  
 XX Disclosure; Page 307-308; 375pp; English.  
 XX The invention comprises a method of stimulating and/or expanding T cells  
 CC specific for a tumor protein. The invention further comprises human  
 CC nucleic acids and proteins that are associated with tumours (e.g. breast  
 CC cancer). The method and sequences of the invention are useful for  
 CC stimulating and/or expanding T cells specific for a tumour protein,  
 CC detecting the presence of cancer, stimulating an immune response in a  
 CC patient and treating breast cancer. The present DNA sequence represents a  
 CC human tumour-related DNA sequence  
 XX SQ Sequence 3288 BP; 1293 A; 564 C; 664 G; 761 T; 0 U; 6 Other;

Alignment Scores:  
 Pred. No.: 9,71e-195 Length: 3288  
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 Query Match: 99.19% Indels: 0  
 DB: 7 Gaps: 0

US-09-451-739H-16 (1-512) x ABT33234 (1-3288)

QY 1 MetLysValSerIleProThrLysAlaLeuMetAspMetGlnThrPheLysAla 20  
 DB 1291 ATGAAGTTTCTATCCAACTAAAGCCTTAGATTGATGGACATGCCAACTTTCAGACA 1350  
 QY 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40  
 DB 1351 GAGCCTCCCGAGAAGCCATCGCTTCGAGCCTGCCATGAAATGCAAAAGCTCTGTCCA 1410  
 QY 41 AsnLysAlaLeuGluLysAsnGlnThrLeuArgAlaAspGluIleLeuProSer 60  
 DB 1411 AATAAGCCTTGAATTGAAGATGAACAAACATTGAGAGCAGATGAGATCTCCATCA 1470  
 QY 61 GluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGluSerLysCysGluThr 80  
 DB 1471 GAATCCAAACAAAGGACATATGAAGAAAGTCTCTGGATTCTGAGAGTCTCTGTGAGACT 1530  
 QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100  
 DB 1531 GTTTCACAGAAGATGTGTGTTTACCAGGCTTCACATCAAAAGAAATAGATATAATA 1590  
 QY 101 AsnGlyLysLeuGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120

DB 1591 AATGGAAANTAGAGAGTCTCTGATATGATGTTTCTGAGGCTCCCTGCAGATG 1650  
 QY 121 LysValSerIleProThrLysAlaLeuMetAspMetGlnThrPheLysAlaGlu 140  
 DB 1651 AAGTTTCTATTCCAACTAAAGCCTTAGAATTGATGCACATGCAACTTTTCAAGCAGAG 1710  
 QY 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160  
 DB 1711 CTTCCCGAGAAGCCATCTGCCITTCGAGCCTGCCATGAAATGCAAAAGTCTGTCCCAAT 1770  
 QY 161 LysAlaLeuGluLysAsnGluInThrLeuArgAlaAspGlnMetPheProSerGlu 180  
 DB 1771 AAGCCTTGGATTGAAGATGAACAAACATTGAGAGCAGATCAGATGTTCCCTTCAGAA 1830  
 QY 181 SerLysGlnLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200  
 DB 1831 TCAAAACAAAGAGAGTGTGAAGAAATTTCTGGATTCTGAGAGTCTCCGTGAGACTGTT 1890  
 QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220  
 DB 1891 TCACAGAGGAGTGTGTGTGTACCAAGCCTACACATCAAAAGAAATGGATAAAATAAGT 1950  
 QY 221 GlyLysLeuGluAspSerThrSerLysSerLysIleLeuAspThrValHisSerCysGlu 240  
 DB 1951 GGAATTTAGAGATTCACCTAGCCTATCAAAATCTTGGATTACAGTTCAATCTTGTGAA 2010  
 QY 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260  
 DB 2011 AGCAGAGGAGACTTCAAAAGATCACTGTGAACACAGTACAGGAAATGGACAAATG 2070  
 QY 261 LysLysLysPheCysValLeuLysLysLysSerGluLysAlaLysGluIleLysSerGln 280  
 DB 2071 AAAAGAAAGTTTGTGTACTGAAAAGAAACTGTGACAGCAAAAGAAATAAATTCACAG 2130  
 QY 281 LeuGluAsnGlnLysValLysValLysValLysValLysValLysValLysValLysVal 300  
 DB 2131 TTAGAGAACCAAAAGTTTAAATGGACACAGAGCTCTGCAGTGTGAGATTGACTTTAAAC 2190  
 QY 301 GlnGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320  
 DB 2191 CAAGAAGAAGAGAGAGAGAGAAATGCCGATATATTAATGAAATAATTTAGGGAAGAAATTA 2250  
 QY 321 GlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGluGlnAla 340  
 DB 2251 GGAAGAAATCGAAGACAGCAGCATTAGGAAGAGTTAGAGTGAACACAACTTTGAACAGCT 2310  
 QY 341 LeuArgIleGlnAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360  
 DB 2311 CTCAGAAATCAAGATATAGAAATGAAGAGTGTAGAAGATTAATTTGAATCAGGTTTCTCAC 2370  
 QY 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380  
 DB 2371 ACTCATGAAATAATGAAATAATTTATCTCTTACATGAAATTTGCATGTTGAAAAGGAAATTC 2430  
 QY 381 MetLysLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400  
 DB 2431 ATGCTAAACTGGAAATAGCCACACTGAAACACCAATACCAGAAAGGAAATAAATATAC 2490  
 QY 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLysLysLeu 420  
 DB 2491 TTTGAGGACATTAAGATTTTAAAGAAAGAAATGCTGAACTTCAGATGACCCCTTAAACTG 2550  
 QY 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLysValLeuIle 440  
 DB 2551 AAAGAGGAATCATTAACCTAAAGGGCATCTCAATATAGTGGGCGAGCTTAAAGTCTTGATA 2610  
 QY 441 AlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLysGluIleLeuGlu 460  
 DB 2611 GCTGAGAACCAATGCTCACTTCTAAATTCAGAGGAAACCAAGACAAAGAAATACTAGAG 2670  
 QY 461 AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480  
 DB 2671 GCAGAAATTCAGATCACCACCTCTAGACTGGCTTCTGCTGTACAGACCATGATCAAAAT 2730



Qy 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500  
Db 2731 GTGACATCAAGAAAGTCAAGAACCTGCTTCCACATTCAGAGATGCTTGTTCGAA 2790

Qy 501 ArgLysMetAsnValAspValSerSerThr 510  
Db 2791 AGAAAAATGAATGTTGATGTGAGTAGTACG 2820

RESULT 9

ID AAS47411 standard; cDNA; 3865 BP.

AC AAS47411;

DT 18-DEC-2001 (first entry)

XX Human cDNA encoding breast cancer protein B726P alternative splice form.

KW Human; ss; breast cancer protein; tumour; cancer; cytostatic;

KX gene therapy.

XX Homo sapiens.

XX WO200179286-A2.

XX 25-OCT-2001.

XX 12-APR-2001; 2001WO-US01.2164.

XX 17-APR-2000; 2000US-00551621.

PR 08-JUN-2000; 2000US-00590751.

PR 22-JUN-2000; 2000US-00604287.

XX 20-JUL-2000; 2000US-00620405.

XX (CORI-) CORIXA CORP.

XX Jiang Y, Dillon DC, Mitcham JL, Xu J, Harlocker SL, Hepler WT;

DR WPI; 2001-611721/70.

DR P-PSDB; AAU33351.

XX Breast Tumor Proteins and nucleic acids useful for the prevention,

PT diagnosis and treatment of breast cancer.

XX Claim 1; Page 280-281; 297pp; English.

XX The invention relates to isolated breast tumour proteins and nucleic acids that encode them, including immunogenic fragments of the proteins. Also included are expression vectors expressing the proteins, transformed cells and antibodies raised against the proteins or an antigen presenting cell expressing the protein. The proteins and nucleic acids may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate breast tumour protein expression, i.e. breast tumours and breast cancer e.g. by gene therapy. The nucleic acids and their complements may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The proteins, nucleic acids and antibodies may be used in assays to identify modulators (e.g. antagonists) of breast tumour protein expression and activity. The antibodies and antagonists may also be used to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the proteins in samples (e.g. by enzyme linked immunosorbant assay (ELISA)) and in other immunopurification diagnostic techniques. The present sequence is a cDNA from a breast tumour cDNA library isolated by subtractive hybridisation against a normal breast cDNA library and encodes a breast tumour protein of the invention. The present sequence is also a splice variant

SQ Sequence 3865 BP; 1499 A; 697 C; 801 G; 862 T; 0 U; 6 Other;

Alignment Scores:

Pred. No.: 1.17e-194 Length: 3865

Score: 2578.00 Matches: 508  
Percent Similarity: 99.61% Conservativeness: 0  
Best Local Similarity: 99.61% Mismatches: 2  
Query Match: 99.19% Indels: 0  
DB: 4 Gaps: 0

US-09-451-739H-16 (1-512) x AAS47411 (1-3865)

Qy 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20  
Db 1563 ATGAAAGTTTCTATTCCAACTAAAGCCTTAGAAATGATGGACATGCAAACTTTCAAGCA 1622  
Qy 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40  
Db 1623 GAGCCTCCGAGAGCCATCTGCCCTTCGAGCCTGCCATTGAAATGCAAAAGTCTCTTCA 1682  
Qy 41 AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 60  
Db 1683 ATTAAGCTTTGGATTGAGATGAAACAACATTGAGAGCAGATGAGATACCTCCATCA 1742  
Qy 61 GluSerLysGlnLysAspTyrGluLysSerSerTrpAspSerGluSerLysGluThr 80  
Db 1743 GAATCCAAACAAAGGACTATGAGAAAGTTCTTGGGATTTCTGAGAGTCTCTGTGAGACT 1802  
Qy 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100  
Db 1803 GTTTCACAGAGGATGTGTGTTTACCCAGGCTRCATCAAAAGAAATAGATAAATA 1862  
Qy 101 AsnGlyLysLeuGluLysProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120  
Db 1863 AATGGAATAATTAGAGAGTCTCTGATAATGATGTTTCTGAGGCTCCCTGCAAGATG 1922  
Qy 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140  
Db 1923 AAAAGTTTCTATTCCAACTAAAGCCTTAGAAATGATGGACATGCAAACTTTCAAGCAGAG 1982  
Qy 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160  
Db 1983 CTTCCCGAGAGGCACTCTGCCCTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTCAAAT 2042  
Qy 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180  
Db 2043 AAAAGCCTTGGAAATGGAATGAACAACATTTGAGAGCAGATGAGATGCTCCCTCAGAA 2102  
Qy 181 SerLysGlnLysLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200  
Db 2103 TCAAAACAAAGAAAGSGTTGAAGAAATTTCTGGGATTTCTGAGAGTCTCGGTGAGACTGT 2162  
Qy 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220  
Db 2163 TCACAGAGGATGTGTGTACCAAGGCTACACATCAAAAGAAATGGAATAAATAGT 2222  
Qy 221 GlyLysLeuGluLysAspSerThrSerLysLysIleLeuAspThrValHisSerCysGlu 240  
Db 2223 GGAATAATTAGAGATTCACTAGCCTATCAAAATCTTGATACAGTTCATTTCTGTGAA 2282  
Qy 241 ArgAlaArgGluLeuGlnLysAspHisCysGluArgThrGlyLysMetGluGlnMet 260  
Db 2283 AGAGCAAGGGAACCTTCAAAAGATCACTGTGAACAACGTCACGGAATAATGGAAACAATG 2342  
Qy 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluLysSerGln 280  
Db 2343 AAAAGAAAGTTTTGTGTACTGAAAAGAAACTGTCAAGACCAAAAGAAATAAATCACAG 2402  
Qy 281 LeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuThrLeuAsn 300  
Db 2403 TTAGAGAACCAAAAGTTAAATGGGAACAAGAGCTCTGCAGTGTGAGATTGACTTTAAAC 2462  
Qy 301 GlnGluGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320  
Db 2463 CAAGAGAGAGAGAGAGAGAAATGCCGATATATTAATGAAAAAATTAGGAGAAATTA 2522  
Qy 321 GlyArgIleGluGluGlnHisArgLysGluLeuValLysGlnGlnLeuGluGlnAla 340

DB 2523 GGAGAGATCGAGGAGCGATAGAGACAGTTTACAGTGAACACAACTTGAACAGGCT 2582  
 QY LeuArgilleGlnAspilleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis 360  
 DB 2593 CTCAGATACAGATATAGATTGAGAGATGTAGAAAGTAATTTGAATCAGGTTTCTCAC 2642  
 QY ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluLeuAla 380  
 DB 2643 ACTCATGAATAATGAATAATATCTCTTACATGAAATTCATGTTTGAAGAGAAATGCC 2702  
 QY MetLeuLysLeuGluLeuAlaThrLeuLysHisGlnTyrGlnGlnLysGluLeuLysTyr 400  
 DB 2703 ATGCTAAACCTGGAATATAGCCACTGAACACCAATACCCAGGAAAGGAAATTAATAC 2762  
 QY PheGluAspilleLysLysLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420  
 DB 2763 TTTGAGGACATTAAGATTTTAAAGAAAGAAAGTCTGAATTCAGATGACCTTAAACTG 2822  
 QY LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuLeu 440  
 DB 2823 AAAGAGGAATCAATTAACCTAAAGGCGCATCTCAATATAGTGGCAGCTTAAAGTTCTGATA 2882  
 QY AlaGluAsnThrMetLeuThrSerLysLeuLysGlnAspLysGluLysLeuGlu 460  
 DB 2883 GCTGAGAACACATGCTCACTTCTTAATTCAGAGGAAACACAGACAAAGAAATACAGAG 2942  
 QY AlaGluLeuGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisGlnLeu 480  
 DB 2943 GCAGAAATTTGAATCACACCATCTAGACTGGCTTCTGCTGTACAGACCATGATCAAAAT 3002  
 QY ValThrSerArgLysSerGlnGluProAlaPheHisLeuAlaGlyAspAlaCysLeuGln 500  
 DB 3003 CTGACATCAAGAAAAAGTCAAGAACCTGCTTCCACATTCAGAGAGATGCTTTTGCAA 3062  
 QY ArgLysMetAsnValAspValSerSerThr 510  
 DB 3063 AGAAAAATGAATGATGTAGTAGACG 3092  
 RESULT 10  
 ID ABS64012 standard; cDNA; 3865 BP.  
 XX  
 AC ABS64012;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE Human breast tumour polynucleotide #464.  
 XX  
 KW Human; breast tumour protein; gene; ss; breast cancer; cytostatic;  
 KW vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002085998-A1.  
 XX  
 PD 04-JUL-2002.  
 XX  
 PF 13-APR-2001; 2001US-00834759.  
 XX  
 PR 28-DEC-1998; 9AUS-00222575.  
 PR 02-APR-1999; 9AUS-00285480.  
 PR 23-JUN-1999; 9AUS-00339338.  
 PR 02-SEP-1999; 9AUS-00389681.  
 PR 03-NOV-1999; 9AUS-00433826.  
 PR 17-APR-2000; 2000US-00551621.  
 PR 08-JUN-2000; 2000US-00590751.  
 PR 22-JUN-2000; 2000US-00604287.  
 PR 20-JUL-2000; 2000US-00620405.  
 XX  
 PA (CORI-) COREIXA CORP.  
 XX  
 PI Jiang Y, Dillon DC, Mitcham JL, Xu J, Harlocker SL, Hepler WT;

PI Henderson RA;  
 DR WPI; 2002-635657/68.  
 DR P-PSDB; ABG78918.  
 XX  
 PT Novel breast cancer polynucleotides and polypeptides encoded by the  
 PT polynucleotides, useful for detecting the presence of breast cancer in a  
 PT patient, and in pharmaceutical compositions, for treating breast cancer.  
 XX  
 PS Claim 1; Page 207-208; 247pp; English.  
 XX  
 CC The invention relates to an isolated breast tumour polynucleotide and the  
 CC polypeptide it encodes. The polynucleotide and polypeptide are useful for  
 CC detecting the presence of breast cancer in a patient, and in  
 CC pharmaceutical compositions for treating breast cancer. The sequences are  
 CC useful for stimulating an immune response in a patient and can therefore  
 CC be used in production of vaccines. The sequences are also useful for  
 CC detecting the presence of a cancer in a patient, by obtaining a  
 CC biological sample from the patient, contacting the biological sample with  
 CC a composition of the invention and detecting the amount of polynucleotide  
 CC that hybridizes to the sample. This sequence represents a human breast  
 CC tumour polynucleotide of the invention  
 XX  
 SQ Sequence 3865 BP; 1499 A; 697 C; 801 G; 862 T; 0 U; 6 Other;  
 Alignment Scores:  
 Pred. No.: 1,17e-194 Length: 3865  
 Score: 2578.00 Matches: 508  
 Percent Similarity: 99.61% Conservative: 0  
 Best Local Similarity: 99.61% Mismatches: 2  
 Query Match: 99.19% Indels: 0  
 DB: 6 Gaps: 0  
 US-09-451-739H-16 (1-512) x ABS64012 (1-3865)  
 QY 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20  
 DB 1563 ATGAAAGTTTCTATTCCAACTAAAGCCTTAGAATTTGATGGACATGCAAACTTTCAAAGCA 1622  
 QY 21 GluProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40  
 DB 1623 GAGCCTCCCGAGAGAGCCATCTGCTTCGAGCGTCCCATTTGAATGCAAAAGTCTGTTCCTCA 1682  
 QY 41 AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluLeuLeuProSer 60  
 DB 1683 AATAAGCCTTGGATTTGAAGAAATGAACAAACATTTGAGAGAGATGAGATCTCCCATCA 1742  
 QY 61 GluSerLysGlnLysAspTyrGluLysSerSerTyrAspSerGluSerLeuLysGluThr 80  
 DB 1743 GAATCCAAACAAAGAGGACTATGAGAAAGTTCTTGGGATTTCTGAGAGTCTCTGTGAGACT 1802  
 QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLeuLeuAspLysTle 100  
 DB 1803 GTTTCACAGAGGATGTGTGTTTACCAAGGCTRCRCATCAAAAGAAAGAAATAGATAAATA 1862  
 QY 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120  
 DB 1863 AATGGAAATTTAGAGAGTCTCTGATAATGATGTTTCTCAAGGCTCTCTGAGAGATG 1922  
 QY 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140  
 DB 1923 AAAAGTTTCTATTCCAACTAAAGCCTTAGAATTTGATGGACATGCAAACTTTCAAAGCAGAG 1982  
 QY 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160  
 DB 1983 CCTCCCGAGAGAGCATCTGCTTCGAGCGTCCCATTTGAATGCAAAAGTCTGTTCCTCAAA 2042  
 QY 161 LysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180  
 DB 2043 AAAGCCTTGGATTTGAAGAAATGAACAAACATTTGAGAGAGATGAGATGTTCCCTTCAGAA 2102  
 QY 181 SerLysGlnLysLysValGluGluAsnSerTyrAspSerGluSerLeuArgGluThrVal 200





101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120  
1863 AATGGAAATTTAGAGAGTCTCTGATAATGATGGTTTCTGAAGCTCCCTGCGAATG 1922  
121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140  
1923 AAAGTTTCTAATTCATTAAGCTTTAGAAATGATGACATGCAAACTTTCAAGCAGAG 1982  
141 ProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160  
1983 CCTCCGAGAGGCAATCTGCTTCGAGCTGCCATTCGAAATGCANAAGTCTGTTCACAAT 2042  
161 LysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180  
2043 AAAGCTTGGAAATGGAATGGAATGAACAAACATGAGAGCAGATCGAATGCCCTTCAGAA 2102  
181 SerLysGlnLysLysValGluGluAsnSerTyrAspSerGluSerLeuArgGluThrVal 200  
2103 TCAAAACAAAGAAAGTGAAGAAATCTTGGATTCGAGAGTCTCGTGAGACTGTT 2162  
201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220  
2163 TCACAGAGGATGTGTGTACCAAGGCTACACATCAAAAGAAATGGAATGGAATTAAT 2222  
221 GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu 240  
2223 GGAATTTAGAGATTCAACTAGCTATCAAAATCTTGATACAGTTCAATCTCTGTGAA 2282  
241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260  
2283 AGACCAAGGGAACCTTCAAAAGATCACTGTGAACAGTACGGAAGAAATGGAACAAATG 2342  
261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluLysLysSerGln 280  
2343 AAAAGAAGTTTCTGTACTGAAAGAACTGTGACAGCAAAAGAAATTAATACAG 2402  
281 LeuGluAsnGlnLysValLysTyrGluGlnLeuCysSerValArgLeuThrLeuAsn 300  
2403 TTAGAGAACCAAAAGTTAAATGGGAACAGAGCTCTGAGTGTGAGATTGACTTTAAAC 2462  
301 GlnGluGluGluLysArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320  
2463 CAAAGAGAGAGAGAGAGAGAGATGCCGATATTAATGAAATTAATGAGGAATTA 2522  
321 GlyArgIleGluGluGlnHisArgLysGluLeuValLysGlnGlnLeuGluGlnAla 340  
2523 GGAAGAATCGAAGAGCAGCATAGGAAGAGTTAGAGTGAACAACTTGAACAGGCT 2582  
341 LeuArgIleGlnAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360  
2583 CTCAGATACAGATATAGATTAAGAGTGTAGAGTGAATTAATGATCAGGTTCTCAC 2642  
361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380  
2643 ACTCATGAAATGAAATTTATCTTCAATCAAAATTCATGTTGAAAGAAAGAAATTCGC 2702  
381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400  
2703 ATGCTAAACTGGAATGAAATGACCACTGAAACCAATACCAAGGAAAGAAATTAATAC 2762  
401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420  
2763 TTTGAGGACATTAAGATTTAAAGAAAGAAATGCTGAATTCAGATCACTCACTAAACTG 2822  
421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle 440  
2823 AAAGAGGAATCATTAACATAAGGAGCATCTCAATATAGTGGGCGCTTAAAGTTCTGATA 2882  
441 AlaGluAsnThrMetLeuThrSerLysLysGluLysGlnAspLysGluIleLeuGlu 460  
2883 GCTGAGACACAACTCTCACTTCTAAATTTAGGAAAGAAACAAAGAAATTAATCTAGAG 2942  
461 AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480

2943 GCAGAAATTTGAATCACACCATCTCTAGACTGGCTTCGTGTACAGCCATGATCAAT 3002  
481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500  
3003 GTGACATCAAGAAAAAGTCAAGAACCTGCTTCCACATTCGAGAGATGCTTCTTGGCA 3062  
501 ArgLysMetAsnValAspValSerSerThr 510  
3063 AGAAAAATGAATGTTGATGTCAGTAGTACG 3092  
RESULT 12  
ADE44426  
ID ADE44426 standard; cDNA; 3865 BP.  
XX ADE44426;  
AC ADE44426;  
XX  
DT 29-JAN-2004 (first entry)  
XX Human cDNA associated with breast cancer #464.  
DE human; ss; gene; breast tumour; cancer; vaccine; T cell stimulator;  
KW T cell expander.  
XX Homo sapiens.  
OS  
XX  
XX  
XX US2003104366-A1.  
XX  
XX 05-JUN-2003.  
XX 17-APR-2000; 2000US-00551621.  
XX 28-DEC-1998; 98US-00222575.  
PR 02-APR-1999; 99US-00285480.  
PR 23-JUN-1999; 99US-00339338.  
PR 02-SEP-1999; 99US-00389681.  
PR 03-NOV-1999; 99US-00433826.  
XX  
XX (JIAN/) JIANG Y.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (XUJU/) XU J.  
PA (HASL/) HARLOCKER S L.  
XX  
PI Jiang Y, Dillon DC, Mitcham JL, Xu J, Harlocker SL;  
XX  
XX WPI; 2004-020270/02.  
DR P-PSDB; ADE44427.  
XX  
XX Novel isolated polypeptide comprising immunogenic portion of breast tumor protein or its variant, useful for formulating vaccines for inhibiting cancer development in a patient.  
PT  
PT  
XX  
PS Claim 5; SEQ ID NO 474; 217pp; English.  
XX  
XX The invention relates to an isolated polypeptide comprising at least an immunogenic portion of a breast tumour protein. The polynucleotide, its polypeptide, its antibody, a pharmaceutical composition comprising the fusion protein or the polynucleotide encoding it, a vaccine comprising the fusion protein or the polynucleotide encoding it, an isolated T cell population comprising T cells specific for a breast tumour protein, and a method for removing tumour cells from a biological sample is useful for inhibiting the development of a cancer in a patient. The polypeptide is useful for stimulating and/or expanding T cells specific for a breast tumour protein. Stimulating and/or expanding T cells specific for a breast tumour protein is useful for inhibiting the development of a cancer in a patient. The method additionally involves the step of cloning at least one proliferated cell and then administering the cloned T cells to the patient. The present sequence represents a cDNA associated with breast cancer.  
XX  
XX Sequence 3865 BP; 1499 A; 697 C; 801 G; 862 T; 0 U; 6 Other;

Alignment Scores:

Pred. No.: 1.17e-194 Length: 3865  
 Score: 2578.00 Matches: 508  
 Percent Similarity: 99.61% Conservative: 0  
 Best Local Similarity: 99.61% Mismatches: 2  
 Query Match: 99.19% Indels: 0  
 DB: 10 Gaps: 0

US-09-451-739H-16 (1-512) x ADE44426 (1-3865)

Qy	1	MetLysValSerIleProThrLysAlaLeuGluMetAspMetGlnThrPheLysAla	20
Db	1563	ATGAAGTTTCTATTCCAACTTAAAGCCTTAGAATTGATGACATGCAAACTTTCAAAGCA	1622
Qy	21	GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro	40
Db	1623	GAGCCTCCGAGAGCCTATGCTTCGAGCTGCCATTGAAATGCAAAAGTCTGTTC	1682
Qy	41	AsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer	60
Db	1683	AATRAAGCCTTGGAAATGGAAGATGAAACAAATGAGAGCAGATGAGATCTCCCATCA	1742
Qy	61	GluSerLysGlnLysAspTyrGluLysSerTrpAspSerGluSerLeuCysGluThr	80
Db	1743	GAATCCAAACAAAGGAGCTATGAAGAAAGTTCTTGGGATCTGAGAGTCTCTGTGAGACT	1802
Qy	81	ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle	100
Db	1803	GTTCACAGAGGATGTGTGTTTACCCCAAGCTRCRCATCAAAAGAAATAGATAAAATA	1862
Qy	101	AsnGlyLysLeuGluLysProAspAsnAspGlyPheLeuLysAlaProCysArgMet	120
Db	1863	AATGAAATATAGAAAGTCTCTGATATATGATGTTTCTGAAGGCTCCCTGAGAAATG	1922
Qy	121	LysValSerIleProThrLysAlaLeuGluMetAspMetGlnThrPheLysAlaGlu	140
Db	1923	AAAGTTTCTATTCCAACTTAAGCCTTAGAATTGATGAGATGCAAACTTTCAAGCAGAG	1982
Qy	141	ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn	160
Db	1983	CCTCCGAGAGCCTATGCTGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTT	2042
Qy	161	LysAlaLeuGluLysAsnGluGlnThrLysAlaAspGlnMetPheProSerGlu	180
Db	2043	AAAGCCTTGGAAATGGAAGATGAAACAAATGAGAGCAGATGATGTTCCCTTCAGAA	2102
Qy	181	SerLysGlnLysValGluLysAsnSerTrpAspSerGluSerLeuArgGluThrVal	200
Db	2103	TCAAAACAAAGAGAGTGGTGAAGAAATTTCTGGGATTTCTGAGAGTCTCCGTGAGACTGT	2162
Qy	201	SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer	220
Db	2163	TACAGAGAGGATGTGTGTATCCCAAGGCTACACATCAAAAGAAATGGAATAAATAGT	2222
Qy	221	GlyLysLeuGluAspSerThrSerLysSerLysIleLeuAspThrValHisSerCysGlu	240
Db	2223	GGAAATATTAGAGATTCAACTAGCCTATCAAAATCTTGGATACAGTTCACTTCTGTGAA	2282
Qy	241	ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetClnGlnMet	260
Db	2283	AGAGCAAGGAACTTCAAAAGATCACTGTGAACACGACGACGAGAAATGGAACAAATG	2342
Qy	261	LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluIleLysSerGln	280
Db	2343	AAAAAGAGTTTGTCTACTGAAAGAAAGAACTGTGAGAGCAAAAGAAATATAAATACAG	2402
Qy	281	LeuGluAsnGlnLysValLysTrpGluGlnGluLysSerValArgGluThrLeuAsn	300
Db	2403	TTAGAGAACCAAAAGCTTAAATGGGAACCAAGAGCTCTGAGTGTGAGATTTGATTAAC	2462
Qy	301	GlnGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu	320
Db	2463	CAGAGAGAGAGAGAGAGAGAGATGCGGATATATTAAATGAAATAATAGGAGAGATTA	2522

Qy	321	GlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnLeuGluGlnAla	340
Db	2523	GGAGAAATCGAAGACGACCATAGGAAGAGTTAGAGTGAACAACTTTGAACAGCT	2582
Qy	341	LeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis	360
Db	2583	CTCAGATACAAGATATAGAATTGAAGAGTGTAGAAAATTAATTTGAATCAGTTTCTCAC	2642
Qy	361	ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla	380
Db	2643	ACTCATGAATAATGAATAATTAATCTCTTACATGAATAATGCACTTTGAAAAGGAAATGCC	2702
Qy	381	MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr	400
Db	2703	ATGCTAAATTCGAAATAGCCACACTGAAACACCAATACCAGGAAAGGAAATAAATAC	2762
Qy	401	PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu	420
Db	2763	TTTGAGGACATTAAAGATTTTAAAGAAAGAAATGCTGAACTTCAGATGACCTTAAACTG	2822
Qy	421	LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle	440
Db	2823	AAAGAGGAATCATTAACATAAAGGCGCATCTCAATATAGTGGCGAGCTTAAAGTTCTGATA	2882
Qy	441	AlaGluAsnThrMetLeuThrSerLysLysLysGlnLysGlnAspLysGluIleLeuGlu	460
Db	2883	GCTGAGAACACAAATGCTCACITCTAAATTTGAAGGAAACAAAGACAAAGAAATACAGAG	2942
Qy	461	AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle	480
Db	2943	GCAGAAATTTGAATCACACCATCTAGACTGGCTTCTGTGTACAAGACCATGATCAAAAT	3002
Qy	481	ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln	500
Db	3003	GTGACATCAAGAAAGTCAAGAACCTGCTTTCCACATTCAGAGAGATGCTTGTTCGAA	3062
Qy	501	ArgLysMetAsnValAspValSerSerThr	510
Db	3063	AGAAATAATGAATGTTGATGTGAGTAGTAGC	3092

RESULT 13

ABT33258  
 ID ABT33258 standard; DNA; 3045 BP.

XX AC ABT33258;

XX AC 15-MAY-2003 (first entry)

Human tumour-related DNA sequence - SEQ ID No 548.

Human; ds; vaccine; gene therapy; T cell stimulation; T cell expansion;  
 tumour; breast cancer; cancer; immune response stimulation.

XX Homo sapiens.

OS WO200283956-A1.

XX PD 24-OCT-2002.

XX PF 15-APR-2002; 2002WO-US012378.

XX PR 13-APR-2001; 2001US-00834759.

XX PR 07-DEC-2001; 2001US-00007805.

XX PR 13-FEB-2002; 2002US-00076522.

XX PA (CORI-) CORIXA CORP.

XX PI Houghton RL, Sleath PR, Persing DH, Jiang Y, Dillon DC;

XX PI Mitcham JL, Xu J, Harlocker SL, Hepler WT, Henderson RA, Fanger GR;

XX PI Vedwick TS, McNeill PD, Durham M;

XX DR WPI; 2003-103376/09.

XX New polypeptide and polynucleotide useful for stimulating and/or  
 PT expanding T cells specific for a tumor protein and treating breast  
 PT cancer.  
 XX Example 8; Page 329-330; 375pp; English.  
 CC The invention comprises a method of stimulating and/or expanding T cells  
 CC specific for a tumor protein. The invention further comprises human  
 CC nucleic acids and proteins that are associated with tumors (e.g. breast  
 CC cancer). The method and sequences of the invention are useful for  
 CC stimulating and/or expanding T cells specific for a tumor protein,  
 CC detecting the presence of cancer, stimulating an immune response in a  
 CC patient and treating breast cancer. The present DNA sequence represents a  
 CC human tumor-related DNA sequence.  
 XX  
 SQ Sequence 3045 BP; 1222 A; 521 C; 613 G; 689 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. NO.: 1.28e-194 Length: 3045  
 Score: 2576.00 Matches: 507  
 Percent Similarity: 99.61% Conservative: 1  
 Best Local Similarity: 99.41% Mismatches: 2  
 Query Match: 99.12% Indels: 0  
 Gaps: 7

US-09-451-739H-16 (1-512) x ABT33258 (1-3045)

QY 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20  
 DB 1045 ATGAAGATTTCTATTCAACCTAAAGCCTTAGAATGTGACATGCAACCTTTCAAGCA 1104  
 QY 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40  
 DB 1105 GAGCCTCCGAGAGCCATCTGCTTCGAGCTGCCATTGAAATGCAAAAGTCTGTCCA 1164  
 QY 41 AsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 60  
 DB 1165 AATAAGCCTTGGAAATTCAGAAATCAACAAACATTCAGAGCAGATGATCTCCCATCA 1224  
 QY 61 GluSerLysGlnLysAspTyrGluLysSerTrpAspSerGluSerLeuGluThr 80  
 DB 1225 GAATCCCAACAAAGAGCATATGAAGAAAGTCTTGGGATTCAGAGCTCTGTGAGACT 1284  
 QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100  
 DB 1285 GTTTCACAGAGGATGTGTGTTTACCCAAAGCTGGCCATCAAAAGAAATAGATAAATA 1344  
 QY 101 AsnGlyLysLeuGluLysSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120  
 DB 1345 AATGGAAATTTAGAAGAGTCTCTGATATGATGTTTCTGAAGTCTCCCTGCGAATG 1404  
 QY 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140  
 DB 1405 AAAGTTCTATTCCCACTAAAGCCTTAGAATTCAGAGCATGCAAACTTTCAAGCAGAG 1464  
 QY 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160  
 DB 1465 CCTCCGAGAGCCATCTCCCTCGAGCCTGCAATGAAATGCAAAAGTCTGTTCCTCAAT 1524  
 QY 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180  
 DB 1525 AAAGCCTTGGAAATTCAGAAATGAACAAACATTCAGAGCAGATCAGATGTTCCCTTCAGAA 1584  
 QY 181 SerLysGlnLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200  
 DB 1585 TCAAAACAAAGAACCTTGAAGAAATCTTGGATTCAGAGTCTCCGTGAGACTGTT 1644  
 QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220  
 DB 1645 TCACAGAGGATGTGTGTACCCAGAGGCTACACATCAAAAGAAATGATTAATAAGT 1704  
 QY 221 GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu 240

DB 1705 GGAAATATAGAGATTCACATAGCTATCAAAATCTTGATACAGTTCATTCTTGAA 1764  
 QY 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260  
 DB 1765 AGAGCAAGGGAATCTTCAAAAGATCACTGTGAACAACAGTACAGGAAATATGGAAACAATG 1824  
 QY 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluLysSerGln 280  
 DB 1825 AAAAAGAGTTTGTGTACTGAAAGAAAGTCTCAGAGCAAAAGAAATAAATACACAG 1884  
 QY 281 LeuGluAsnGlnLysValLysTyrGluGlnGluLeuCysSerValArgLeuThrLeuAsn 300  
 DB 1885 TTAGAGAACCAAAAGTTAAATGGGAACAAGAGCTCTGCAGTGTGAGATTGATTTAAAC 1944  
 QY 301 GlnGluGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320  
 DB 1945 CAAGAAGAGAGAGAGAGAAATGCCGATATATTAAATCAAAATATGGGAAGAAATTA 2004  
 QY 321 GlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnGlnGluGlnAla 340  
 DB 2005 GGAAGATCGAAGAGCAGCATAGGAAAGAGTGTAGAGTGAACCAACACTTGACAGGCT 2064  
 QY 341 LeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis 360  
 DB 2065 CTCAGATACAGATATAGAAATTCAGAGTGTAGAAAGTATTTAAATCAGTTTCTCAC 2124  
 QY 361 ThrHisGluAsnGluAsnTyrLeuHisGluAsnCysMetLeuLysLysGluIleAla 380  
 DB 2125 ACTCATGAAATGAAATATATCTCTTACATGAAATTCATGTTGAAAGGAAATTCGCC 2184  
 QY 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400  
 DB 2185 ATGCTTAAACCTGGAATAGCCACACTGAAACCAACATACCAGGAAAGGAAATTAATATC 2244  
 QY 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420  
 DB 2245 TTTGAGGACATTAAGATTTTAAAGAAAGAAATGCTGAATTCAGATGACCTTAAACTG 2304  
 QY 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle 440  
 DB 2305 AAAGAGGATCAATTAACATAAAGGCGCATCTCATATAGTGGCAGCTTAAAGTCTGATA 2364  
 QY 441 AlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLysGluLeuGlu 460  
 DB 2365 GCTGAGAACACATGCTCACTTCTTAAATTTGAAGGAAACCAAGACAAAGAAATACTAGAG 2424  
 QY 461 AlaGluIleGluSerHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480  
 DB 2425 GCAGAAATTTGAATTCACACCATCTAGACTGGCTTCTGTGTACAAGACCATGATCAAT 2484  
 QY 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500  
 DB 2485 GTGACATCAAGAAATAAGTCAAGAACCTGCTTCCACATTCAGAGGAGATGCTTGTTCGAA 2544  
 QY 501 ArgLysMetAsnValAspValSerSerThr 510  
 DB 2545 AGAAATGAATGTTGATGTGAGTAGTACG 2574

# RESULT 14

AAS47405

ID AAS47405 standard; cDNA; 3681 BP.

XX AC AAS47405;

XX AC AAS47405;

DT 18-DEC-2001 (first entry)

DE Human cDNA cloneB726P-spliced\_seq\_B726P encoding a breast cancer protein.

XX Human; ss; breast cancer protein; tumour; cancer; cytostatic;

XX gene therapy.

OS Homo sapiens.

XX W0200179286-A2.  
 XX PD 25-OCT-2001.  
 XX 12-APR-2001; 2001WO-US012164.  
 XX 17-APR-2000; 2000US-00551621.  
 XX 08-JUN-2000; 2000US-00590751.  
 XX 22-JUN-2000; 2000US-00604287.  
 XX 20-JUL-2000; 2000US-00620405.  
 XX (CORI-) CORIXA CORP.  
 XX Jjiang Y, Dillon DC, Mitcham JL, Xu J, Harlocker SL, Hepler WT;  
 XX P-PSDB; AAU33346.  
 XX WPI; 2001-611721/70.  
 XX DR P-PSDB; AAU33346.  
 XX PT Breast Tumor Proteins and nucleic acids useful for the prevention,  
 XX diagnosis and treatment of breast cancer.  
 XX FS Claim 1; Page 271-272; 297pp; English.  
 XX The invention relates to isolated breast tumour proteins and nucleic  
 CC acids that encode them, including immunogenic fragments of the proteins.  
 CC Also included are expression vectors expressing the proteins, transformed  
 CC cells and antibodies raised against the proteins or an antigen presenting  
 CC cell expressing the protein. The proteins and nucleic acids may be used  
 CC in the prevention, diagnosis and treatment of diseases associated with  
 CC inappropriate breast tumour protein expression, i.e. breast tumours and  
 CC breast cancer e.g by gene therapy. The nucleic acids and their  
 CC complements may also be used as DNA probes in diagnostic assays to detect  
 CC and quantitate the presence of similar nucleic acids in samples. The  
 CC therefore which patients may be in need of restorative therapy. The  
 CC proteins, nucleic acids and antibodies may be used in assays to identify  
 CC modulators (e.g. antagonists) of breast tumour protein expression and  
 CC activity. The antibodies and antagonists may also be used to down  
 CC regulate expression and activity. The antibodies may also be used as  
 CC diagnostic agents for detecting the presence of the proteins in samples  
 CC (e.g. by enzyme linked immunosorbent assay (ELISA)) and in other immuno-  
 CC purification diagnostic techniques. The present sequence is a cDNA from a  
 CC breast tumour cDNA library isolated by subtractive hybridisation against  
 CC a normal breast cDNA library and encodes a breast tumour protein of the  
 CC invention. The present sequence is also a splice variant  
 XX SQ Sequence 3681 BP; 1412 A; 680 C; 758 G; 826 T; 0 U; 5 Other;

Alignment Scores:  
 Pred. No.: 3,88e-167 Length: 3681  
 Score: 2230.50 Matches: 447  
 Percent Similarity: 87.65% Conservative: 0  
 Best Local Similarity: 87.65% Mismatches: 2  
 Query Match: 85.62% Indels: 62  
 DB: 4 Gaps: 1

US-09-451-739H-16 (1-512) x AAS47405 (1-3681)  
 QY 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20  
 DB 1563 ATGAAGTTTCTATTCCAACTTAAAGCCCTTGAATGATGGACATGCAAACTTTCCAAAGCA 1622  
 QY 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40  
 DB 1623 GAGCCTCCGAGAGCCATCTGCCTTCGAGCTGCCATTGAAATGCAAAAGTCTGTCCA 1682  
 QY 41 AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 60  
 DB 1683 AATAAAGCCTTGGAAATGGAATGAACAACATTTGAGAGCAGATGATATCTCCCATCA 1742  
 QY 61 GluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGluSerLeuLysGluThr 80  
 DB 1743 GAATCCAAACAAAGGACTATGAAAGAGTCTTGGGATTTCTGAGACTCTCTGTGAGACT 1802

QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysAla 100  
 DB 1803 GTTTCACAGAGGATGTGTGTTTACCCAGGCTRCRCATCAAAAAGAAATAGATAAATA 1862  
 QY 101 AsnGlyLysLeuGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120  
 DB 1863 AATGGAAATTTAGAAGAGTCTCTGTGATAATGATGTTTCTGAAGGCTCCCTGCAGAAATG 1922  
 QY 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140  
 DB 1923 AAAGTTTCTATTCCAACTTAAAGCCTTAGAATTTAGATGACATGCAAACTTTCAAGACGAG 1982  
 QY 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160  
 DB 1983 CCTCCGAGAGCCATCTGCCTTCGAGCTGCCATTGAAATGCAAAAGTCTGTTCCAAAT 2042  
 QY 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180  
 DB 2043 AAAGCCTTGGAAATTTGAAGATGAACAACATTTGAGACGATCAGATGTTCCCTTCAGAA 2102  
 QY 181 SerLysGlnLysLysValGluGluAsnSerTrpAspSerGluSerLeuArgGluThrVal 200  
 DB 2103 TCNAACAAAGAAAGTTGAAGAAAATCTTGGGATTCCTGAGAGTCTCCGTGAGACTGTT 2162  
 QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220  
 DB 2163 TCACAGAGGATGTGTGTGTACCAAGGCTACACATCAAAAAGAAATGGATAAAATAGT 2222  
 QY 221 GlyLysLeuGluAspSerThrSerLysSerLysIleLeuAspThrValHisSerCysGlu 240  
 DB 2223 GGAAATTTAGAGATTCACCTAGCTATCAAAATCTTGGATACAGTTCATTCITGTGAA 2282  
 QY 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260  
 DB 2283 AGAGCAAGGAACTTCAAAAAGATCACTGTGACACACGTACAGAAAATGGAAACAAATG 2342  
 QY 261 LysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluIleLysSerGln 280  
 DB 2343 AAAAAGAGATTTGTGTACTGAAAAGAAATCTGACAGAGCAAAAAGAAATAAATACAG 2402  
 QY 281 LeuGluAsnGlnLysValLysTrpGluGlnGluLysCysSerValArgLeuThrLeuAsn 300  
 DB 2403 TTAGAGAACCAAAAAGTTAAATGGAAACACAGAGCTCTGCAGTGTGAGGTT----- 2452  
 QY 301 GlnGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320  
 DB 2452 ----- 2452  
 QY 321 GlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGlnAla 340  
 DB 2452 ----- 2452  
 QY 341 LeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis 360  
 DB 2453 -----TCTCAC 2458  
 QY 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380  
 DB 2459 ACTCATGAAATGAAATTTATCTTACATGAAATTTGCATGTTGAAAAGGAAATTCGC 2518  
 QY 381 MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400  
 DB 2519 ATGCTAAAACCTGGAATAGCCACCTGAAACACCAATACCAAGGAAAGGAAATAAATAC 2578  
 QY 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420  
 DB 2579 TTTGAGACATTTAGATTTTAAAGAAAGAAATGCTGAATTCAGATCCCTCAAACTG 2638  
 QY 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle 440  
 DB 2639 AAAGAGGAATCATTAACATAAAGGGCATCTCAATATAGTGGGCAGCTTAAAGTCTTGATA 2698

QY 441 AlaGluAsnThrVetLeuThrSerIysLeuLysGluLysGlnAspIysGluIleLeuGlu 460  
 Db 2699 GCTGAGAACACAAATGCTCACTTCTAAATTAAGGAAAAACAAGACAAAGAAATCTAGAG 2759  
 QY 461 AlaGluIleGluSerHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480  
 Db 2759 GCAGAAATTAATCAACACCACTCTAGACTGGCTTCTGCTGTACAGACCAATCAAT 2819  
 QY 481 ValThrSerArgIysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500  
 Db 2819 GTGACATCAAGAAAAAGTCAAGAACCTGCTTCCACATTCAGGAGATGCTTTGTCGAA 2878  
 QY 501 ArgLysMetAsnValAspValSerThr 510  
 Db 2879 AGAAAAATGAATGTTGATGTGAGTAGTAGC 2908

RESULT 15  
 AAF17980  
 ID AAF17980 standard; cDNA; 2307 BP.  
 XX  
 AC AAF17980;  
 DT 13-MAR-2001 (first entry)  
 XX  
 DE Human breast cancer associated B72P splice sequence #5.  
 XX  
 KW Human; breast cancer associated gene; vaccine; diagnosis; therapy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200060076-A2.  
 XX  
 PD 12-OCT-2000.  
 XX  
 PF 15-FEB-2000; 2000WO-US003308.  
 XX  
 PR 02-APR-1999; 99US-00285480.  
 PR 23-JUN-1999; 99US-00339338.  
 PR 02-SEP-1999; 99US-00389681.  
 PR 03-NOV-1999; 99US-00433826.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Yuqiu J, Dillon DC, Mitcham JL, Xu J, Harlocker SL;  
 XX  
 DR WPI, 2001-122627/13.  
 XX  
 PT An isolated polypeptide useful for the treatment and diagnosis of tumors  
 PT e.g. breast cancer comprises at least an immunogenic portion of a breast  
 PT tumor protein.  
 XX  
 PS Claim 6; Page 229-230; 238pp; English.  
 XX  
 CC The present invention provides the coding sequences and some protein  
 CC sequences of proteins associated with breast cancer in humans. These  
 CC sequences can be used in the diagnosis and treatment of cancers,  
 CC particularly breast tumours  
 XX  
 SQ Sequence 2307 BP; 919 A; 409 C; 439 G; 540 T; 0 U; 0 Other;  
 XX

Alignment Scores:  
 Pred. NO.: 3.9e-167 Length: 2307  
 Score: 2227.50 Matches: 446  
 Percent Similarity: 87.65% Conservative: 1  
 Best Local Similarity: 87.45% Mismatches: 2  
 Query Match: 85.71% Indels: 62  
 DB: 4 Gaps: 1

US-09-451-739H-16 (1-512) x AAF17980 (1-2307)

QY 1 MetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAla 20  
 Db 206 ATGAAGATTCTATCTCACTAAGCCTTAGAATTGATGACATGCAACTTTCAAAGCA 265

QY 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40  
 Db 266 GAGCCTCCCGAAGGCCATCTGCCTTCGAGCCTGCCATTTGAATATGAAAAGICTGTTC 325  
 QY 41 AsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 60  
 Db 326 AATAAAGCCTTGAAATTAAGAAATGAACAAACATTCAGAGCAGATCAGATCTCCCATCA 385  
 QY 61 GluSerLysGlnLysAspTyrGluLysSerSerTyrAspSerGlnSerLysLeuGluThr 80  
 Db 386 GAATCCAAAACAAAGACATATGAAGAAAGTCTTGGATTCAGAGTCTCTGTGAGACT 445  
 QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100  
 Db 446 GTTTCACAGAGGATGTGTGTTTACCACAGGCTACACATCAAAAAGAAATAGATAAATA 505  
 QY 101 AsnGlyLysLeuGluLysProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120  
 Db 506 AATGAAAAATTAGAAGAGTCTCTGATAATGATGGTTCCTGAGTCTCCCTCGAAGT 565  
 QY 121 LysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGlu 140  
 Db 566 AAGTTTCTATTCACACTAAGCCTTAGAATTCAGACATGCAACTTTCAAAGCAGAG 625  
 QY 141 ProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160  
 Db 626 CTTCCCGAAGGCCATCTGCCTTCGAGCCTGCCATTTGAAATGCAAAAGTCTGTCCAAAT 685  
 QY 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180  
 Db 686 AAGCCTTGGAATTAAGAAATGAACAAACATTCAGAGCAGATCAGATGTCCTTCAGAA 745  
 QY 181 SerLysGlnLysValGluGluAsnSerTyrAspSerGluSerLeuArgGluThrVal 200  
 Db 746 TCAAAACAAAAGACGTTGAAGAAATCTTGGATTCAGAGTCTCCCTGAGACTGT 805  
 QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220  
 Db 806 TCACAGAGGATGTGTGTGTACCCAGCCTACACATCAAAAAGAAATGGAATTAAGT 865  
 QY 221 GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu 240  
 Db 866 GGAATAATTAGAAGATTCACTAGCTATCAAAATCTTGATACAGTTCACTTCTTGTA 925  
 QY 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGluArgThrGlyLysMetGluGlnMet 260  
 Db 926 AGACCAAGGGAACTTCAAAAAGATCACTGTGAACACGTCAGAAAAATGGAACAAATG 985  
 QY 261 LysLysLysPheCysValLeuLysLysLeuSerGluAlaLysGluIleLysSerGln 280  
 Db 986 AAAAAGAGTTTGTGTACTGMAAAAGAACTGTCAAGACAAAAGAAATAAATCAG 1045  
 QY 281 LeuGluAsnGlnLysValLysTyrGluGlnGluLeuCysSerValArgLeuThrLeuAsn 300  
 Db 1046 TTAGAACCAAAAAGTTAAATGGGAACAAGAGCTCTGAGTGTGAGTT----- 1095  
 QY 301 GlnGluGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeu 320  
 Db 1095 ----- 1095  
 QY 321 GlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGluGlnAla 340  
 Db 1095 ----- 1095  
 QY 341 LeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis 360  
 Db 1096 -----TCTCAC 1101  
 QY 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380  
 Db 1102 ACTCATGAAATGAAATTAATCTCTTACATGAAATTCATGTTGAAAAAGGAAATGCC 1161

Qy	381	MetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr	400
Db	1162	ATGCTAAAACTGGAAATAGCCACACTGAACACCAATACCAGGAAAGGAAATATAATAC	1221
Qy	401	PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu	420
Db	1222	TTTGAGGACATTAAAGATTTTAAAGAAAGAAATGCTGAACCTTCAGATGACCCCTAAACTG	1281
Qy	421	LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle	440
Db	1282	AAAGAGGAATCATTAACCTAAAGGGCATCTCAATATAGTGGGCGACTTAAAGTTCGATA	1341
Qy	441	AlaGluAsnThrMetLeuThrSerLysLeuLysGlnAspLysGluIleLeuGlu	460
Db	1342	GCTGAGACACATGCTCACTTCTAAATTGAAGGAAACAAAGACAAAGAAATACTAGAG	1401
Qy	461	AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle	480
Db	1402	GCAGAAATTGAATCACACATCCTAGACTGGCTTCTGCTGTACAGACCATGATCAATT	1461
Qy	481	ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln	500
Db	1462	GTGACATCAAGAAAAAGTCAAGAACCTGCTTTCCACATTGCAGGAGATGCTTGTGTCAA	1521
Qy	501	ArgLysMetAsnValAspValSerSerThr	510
Db	1522	AGAAAAATGATGTGATGTGAGTAGTACG	1551

Search completed: May 6, 2004, 14:16:21  
Job time : 623 secs



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 6, 2004, 11:51:33 ; Search time 6047 Seconds  
(without alignments)  
3669.858 Million cell updates/sec

Title: US-09-451-739H-16

Perfect score: 2599  
Sequence: 1 MKVSIPTKALEMDMOTFFA.....IAGDACLRQKMNVDVSSDTI 512

Scoring table: BLOSUM62  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.\*

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2: gb.btg.\*

3: gb.in.\*

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7: gb.ph.\*

8: gb.pl.\*

9: gb.pr.\*

10: gb.ro.\*

11: gb.sts.\*

12: gb.sy.\*

13: gb.un.\*

14: gb.vi.\*

15: em.ba.\*

16: em.fun.\*

17: em.hum.\*

18: em.in.\*

19: em.mu.\*

20: em.om.\*

21: em.or.\*

22: em.ov.\*

23: em.pat.\*

24: em.ph.\*

25: em.pl.\*

26: em.ro.\*

27: em.sts.\*

28: em.un.\*

29: em.vi.\*  
30: em.htg.hum.\*  
31: em.htg.inv.\*  
32: em.htg.other.\*  
33: em.htg.mus.\*  
34: em.htg.pln.\*  
35: em.htg.rodi.\*  
36: em.htg.mam.\*  
37: em.htg.vrt.\*  
38: em.sy.\*  
39: em.htgo.hum.\*  
40: em.htgo.mus.\*  
41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	2589	99.6	4458	6	AX829110	Sequence
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# ALIGNMENTS

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 AX367056.1 GI:18855278  
 VERSION  
 KEYWORDS Homo sapiens (human)  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 Jager,D., Stockert,E., Scanlan,M., Knuth,A., Old,L., Gure,A. and  
 Chen,Y.T.  
 TITLE Isolated nucleic acid molecules encoding cancer associated  
 antigens, the antigens per se, and uses thereof  
 JOURNAL Patent: WO 0147959-A 15 05-JUL-2001;  
 LUDWIG INSTITUTE FOR CANCER RESEARCH (US); MEMORIAL  
 SLOAN-KETTERING CANCER CENTER (US); Cornell Research Foundation  
 (US)  
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 AX829110.1 GI:39838904  
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 Sequence 3 from Patent WO02059377.  
 AX829110  
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 AX829110.1 GI:39838904

KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 Mack, D.H., Gish, K.C. and Afar, D.  
 Methods of diagnosis of breast cancer, compositions and methods of  
 screening for modulators of breast cancer  
 Patent: WO 02059377-A 3 01-AUG-2002;  
 JOURNAL EOS Biotechnology, Inc. (US)  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 4458)  
 Jager, D., Stockert, E., Gure, A.O., Scanlan, M.J., Karbach, J.,  
 Jager, E., Knuth, A., Old, L.J. and Chen, Y.T.

TITLE Identification of a tissue-specific putative transcription factor in breast tissue by serological screening of a breast cancer library  
 JOURNAL Cancer Res. 61 (5), 2055-2061 (2001)  
 MEDLINE 21174979  
 PUBMED 11280766  
 REFERENCE 2 (bases 1 to 4458)  
 AUTHORS Jaeger, D., Stockert, E., Guere, A.O., Scanlan, M.J., Karbach, J., Jaeger, E., Knuth, A., Old, L.J. and Chen, Y.T.  
 TITLE Direct Submission  
 JOURNAL Submitted (18-MAY-2000) Pathology, Cornell Medical Center, 1300 York Avenue, New York, NY 10021, USA

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QY 421 LysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIle 440  
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 DEFINITION Sequence 490 from patent US 6528054.  
 ACCESSION AR283467  
 VERSION AR283467.1 GI:29720294  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 1 (bases 1 to 3288)  
 REFERENCE Jiang,Y., Dillon,D.C., Mitcham,J.L., Xu,J., Harlocker,S.L. and Hepler,W.T.  
 AUTHORS  
 TITLE Compositions and methods for the therapy and diagnosis of breast cancer  
 JOURNAL Patent: US 6528054-A 490 04-MAR-2003;  
 FEATURES Location/Qualifiers  
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 /organism="unknown"  
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 Best Local Similarity: 99.61% Mismatches: 2  
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US-09-451-739H-16 (1-512) x AR283467 (1-3288)

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LOCUS AX303170  
DEFINITION Sequence 490 from Patent WO0179286.  
ACCESSION AX303170  
VERSION AX303170.1 GI:17383660  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 Jiang,Y., Dillon,D.C., Mitcham,J.L., Xu,J., Harlocker,S.L. and Hepler,W.T.  
AUTHORS Compositions and methods for the therapy and diagnosis of breast cancer  
TITLE Patent: WO 0179286-A 490 25-OCT-2001;  
JOURNAL CORIXA CORPORATION (US)  
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VERSION
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KEYWORDS
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ORGANISM
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REFERENCE
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AUTHORS
Jiang, Y., Dillon, D.C., Mitcham, J.L., Xu, J., Harlocker, S.L. and
Hepler, W.T.
TITLE
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cancer
JOURNAL
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VERSION
AR351426.1      GI:33753105
KEYWORDS
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SOURCE
Unknown.
ORGANISM
Unclassified.
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 JIANG, Y., DILLON, D.C., MITCHAM, J.L., XU, J., HARLOCKER, S.L. and  
 HEPLER, W.T.  
 TITLE Compositions and methods for the therapy and diagnosis of breast  
 JOURNAL Cancer  
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 Db 1923 AAGTTTCTATTCCAACTTAAGCCTTAGAATTGATGGACATGCAAACTTTCAAAGCAGAG 1982

QY 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160  
 Db 1983 CCTCCGAGAGGACCATCTGCTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTCAAAT 2042

QY 161 LysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180  
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QY 241 ArgAlaGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260  
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QY 301 GlnGluGluGluLysArgAsnAlaAspIleLeuGlnGluLysIleArgGluGluLeu 320  
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QY 321 GlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGlnGlnLeuGlnAla 340  
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QY 341 LeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis 360  
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QY 361 ThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluLeuAla 380  
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QY 381 MetLeuLysLeuGluLeuAlaThrLeuLysHisGlnTyrGlnGluLysGluAsnLysTyr 400  
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QY 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420  
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QY 461 AlaGluIleGluSerHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480  
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 VERSION AX303154.1 GI:17383650  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1  
 AUTHORS Jiang, Y., Dillon, D.C., Mitcham, J.L., Xu, J., Harlocker, S.L. and  
 Hepler, W.T.  
 TITLE Compositions and methods for the therapy and diagnosis of breast  
 JOURNAL Cancer  
 PATENT WO 0179286-A 474 25-OCT-2001;  
 CORIXA CORPORATION (US)  
 FEATURES Location/Qualifiers  
 1. 3865  
 source

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ORIGIN

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Query Match: 99.19% Indels: 0
DB: 6 Gaps: 0

US-09-451-739H-16 (1-512) x AX303154 (1-3865)

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QY 61 GluSerLysGlnLysAspPyrGluGluSerSerTrpAspSerGluSerLeuGluThr 80
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QY 281 LeuGluAsnGlnLysValLysTyrPglGlnGluLeuCysSerValArgLeuThrLeuAsn 300  
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LOCUS AR344224  
DEFINITION Sequence 468 from patent US 6579973.  
ACCESSION AR344224  
VERSION AR344224.1 GI:33740124  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 2307)  
AUTHORS Yudiu,J., Dillon,D.C., Mitcham,J.L., Xu,J. and Harlocker,S.L.  
TITLE Compositions for the treatment and diagnosis of breast cancer and methods for their use  
JOURNAL Patent: US 6579973-A 468 17-JUN-2003;  
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Pred. No.: 2227.50 Matches: 446  
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Percent Similarity: 87.65% Conservative: 1  
Best Local Similarity: 87.45% Mismatches: 2  
Query Match: 85.71% Indels: 62  
DB: 6 Gaps: 1

US-09-451-739H-16 (1-512) x AR344224 (1-2307)

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 ACCESSION AR351425  
 VERSION AR351425.1 GI:33753104  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE  
 1 (bases 1 to 2307)  
 AUTHORS Jiang, Y., Dillon, D.C., Mitcham, J.L., Xu, J., Harlocker, S.L. and Hepler, W.T.  
 TITLE Compositions and methods for the therapy and diagnosis of breast cancer  
 JOURNAL Patent: US 6586572-A 468 01-JUL-2003;  
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 Qy 61 GluSerLysGlnLysAspTyrGluGluSerSerTTPAspSerGluSerLeuCysGluThr 80  
 Db 386 GAATCCAAACAAAGAGCTATGAAGAAAGTCTTGGATCTCGAGAGTCTCTGTGAGACT 445

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Db 1095 ----- 1095  
QY 321 GlyArgIleGluGluGlnHisArgLysGluLeuValLysGlnGlnLeuGluGlnAla 340  
Db 1095 ----- 1095  
QY 341 LeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHis 360  
Db 1096 -----TCTCAC 1101  
QY 361 ThrHisGluAsnGluAsnTrpLeuLeuHisGluAsnCysMetLeuLysLysGluLeuAla 380  
Db 1102 ACTCATGAAATGAAATATCTCTACATGAAATTTGCATGTAATGCTGTAATGAAAGAAATGCCC 1161  
QY 381 MetLeuLysLeuGluLeuAlaThrLeuLysHisGlnTrpGlnGluLysGluAsnLysTrp 400  
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QY 401 PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeu 420  
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QY 461 AlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIle 480  
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QY 481 ValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCysLeuGln 500  
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Db 1522 AGAAAAATGAATGTTGATGCTGAGTAGTAG 1551  
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LOCUS AX282975 2307 bp DNA linear PAT 02-NOV-2001  
DEFINITION Sequence 24 from Patent WO0175171.  
ACCESSION AX282975  
VERSION AX282975.1 GI:15609908  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 Houghton,R.L., Dillion,D.C., Molesh,D.A., Xu,J., Zehentner,B. and  
AUTHORS Persing,D.H.  
TITLE Methods, compositions and kits for the detection and monitoring of  
breast cancer  
JOURNAL Patent: WO 0175171-A 24 11-OCT-2001;  
CORIXA CORPORATION (US)  
FEATURES  
source  
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Db 266 GAGCCTCCCGAGAGAGCCATCTGCTTCGAGCTGCCATTTGAATGCAAAAGTCTGTTCGA 325  
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Db 326 AATAAGCCTTGGAAATGAAGAAATGAACAAACATTTGAGAGCAGATGAGATATCCCATCA 385  
QY 61 GluSerLysGlnLysAspTrpGluGluSerSerTrpAspSerGluSerLeuCysGluThr 80  
Db 386 GAATCCAAACAAAGGACTATGAGAAAGTTCTTGGATCTGAGAGTCTCTGTGAGACT 445  
QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLeuLysLysIle 100  
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QY 201 SerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMetAspLysIleSer 220  
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 QY 221 GlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCysGlu 240  
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 QY 241 ArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMet 260  
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 QY 281 LeuGlnAsnGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuThrLeuAsn 300  
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 DB 2452 ----- 2452  
 QY 321 GlyArgIleGluGluGlnHisArgLysGluLeuValLysGlnGlnLeuGlnAla 340  
 DB 2452 ----- 2452  
 QY 341 LeuArgIleGlnAspIleGluLysSerValGluSerAsnLeuAsnGlnValSerHis 360  
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 QY 361 ThrHisGluAsnGluAsnTrpLeuLeuHisGluAsnCysMetLeuLysLysGluIleAla 380  
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RESULT 15  
 AR344219  
 LOCUS AR344219 3681 bp DNA linear PAT 17-AUG-2003  
 DEFINITION Sequence 463 from patent US 6579973.  
 ACCESSION AR344219  
 VERSION AR344219.1 GI:33740119  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.

REFERENCE  
 AUTHORS Yudin,J., Dillon,D.C., Mitcham,J.L., Xu,J. and Harlocker,S.L.  
 TITLE Compositions for the treatment and diagnosis of breast cancer and methods for their use  
 JOURNAL Patent: US 6579973-A 463 17-JUN-2003;  
 FEATURES Location/Qualifiers  
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 /organism="unknown"  
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Unclassified.  
 1 (bases 1 to 3681)

Alignment Scores:  
 Pred. No.: 8.51e-140 Length: 3681  
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 Percent Similarity: 87.45% Conservative: 0  
 Best Local Similarity: 87.45% Mismatches: 3  
 Query Match: 85.59% Indels: 62  
 DB: 6 Gaps: 1

US-09-451-739H-16 (1-512) x AR344219 (1-3681)

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 QY 41 AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 60  
 DB 1683 AATAAGCCTTGGAATTGAAGATGAACAACATTTGAGCAGATGAGATATCTCCATCA 1742  
 QY 61 GluSerLysGlnLysAspTrpGluLysSerTrpAspSerGluSerLeuCysGluThr 80  
 DB 1743 GAATCAAAACAAAGAGACTATGAAGAAAGTTCTTGGGATCTGAGAGTCTCTGTGAGACT 1802  
 QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluIleAspLysIle 100  
 DB 1803 GTTTCAGAGAGATGTGTGTTTACCAGGCTCCRCATCAAAAGAAATAGATAAATA 1862  
 QY 101 AsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLysAlaProCysArgMet 120  
 DB 1863 AATGGAATATTAGAAGAGTCTCCTGATATGATGTTTCTGAGGCTCCCTGCAAGATG 1922  
 QY 121 LysValSerIleProThrLysAlaLeuMetAspMetGlnThrPheLysAlaGlu 140  
 DB 1923 AAAGTTTCTATTCCAACCTTAAGCCTTAGAATTGATGGACATGCAAACTTCAAGCAGAG 1982  
 QY 141 ProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValProAsn 160  
 DB 1983 CCTCCCGAGAGCCATCTGCTTCGAGCTGCCATTGAAATGCAAAAGTCTGTCCAAT 2042  
 QY 161 LysAlaLeuLysLysAsnGluGlnThrLeuArgAlaAspGlnMetPheProSerGlu 180  
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Search completed: May 6, 2004, 15:57:13  
Job time : 6078 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 06:27:28 ; Search time 2575.23 Seconds  
(without alignments)  
8952.060 Million cell updates/sec

Title: US-09-451-739H-8  
Perfect score: 772  
Sequence: 1 aaagcttctcggcggcagc.....cagagcagactccatctta 772

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

- 1: em\_estba:\*\*
- 2: em\_esthum:\*\*
- 3: em\_estin:\*\*
- 4: em\_estmv:\*\*
- 5: em\_estov:\*\*
- 6: em\_estpl:\*\*
- 7: em\_estro:\*\*
- 8: em\_hcc:\*\*
- 9: gb\_est1:\*\*
- 10: gb\_est2:\*\*
- 11: gb\_hcc:\*\*
- 12: gb\_est3:\*\*
- 13: gb\_est4:\*\*
- 14: gb\_est5:\*\*
- 15: em\_estfun:\*\*
- 16: em\_estom:\*\*
- 17: em\_gss\_hum:\*\*
- 18: em\_gss\_inv:\*\*
- 19: em\_gss\_pln:\*\*
- 20: em\_gss\_prt:\*\*
- 21: em\_gss\_fun:\*\*
- 22: em\_gss\_lam:\*\*
- 23: em\_gss\_mus:\*\*
- 24: em\_gss\_pro:\*\*
- 25: em\_gss\_rod:\*\*
- 26: em\_gss\_phg:\*\*
- 27: em\_gss\_vri:\*\*
- 28: gb\_gss1:\*\*
- 29: gb\_gss2:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	276	35.8	794	12	BM976892 UI-CF-EN1
C 2	274.4	35.5	729	13	BU622930 UI-H-FL1-
C 3	268	34.7	673	10	BF057660 7K51e08.x
C 4	265	34.3	761	12	BM042700 60361e058

5	260.8	33.8	503	28	AQ877998	HS_2160_A
6	258.2	33.4	822	12	BG249643	602319736
C 7	255	33.0	592	28	AQ351424	BQ351424
C 8	255	33.0	701	13	BU615970	UI-H-DF0-
9	254.2	32.9	458	28	B80438	B80438
C 10	253.4	32.8	613	28	AQ074754	CIT-HSP-2
C 11	253	32.8	689	29	AG158054	AG158054
C 12	252.8	32.7	731	28	AQ35280	RPC111-10
C 13	252.4	32.7	587	13	EX486697	EX486697
C 14	252.2	32.7	662	29	AG144106	Pan trogl
15	252.2	32.7	1073	28	BZ601227	BZ601227
16	252	32.6	349	13	BU963522	AGENCOURT
17	251.6	32.6	1201	13	EX461522	EX461522
18	251.4	32.6	515	28	AQ019249	CIT-HSP-2
C 19	251.2	32.5	447	10	AW276817	AW276817
C 20	251.2	32.5	716	13	BU617628	UI-H-DF0-
C 21	250.6	32.5	517	9	AL046409	AL046409
22	250.4	32.4	807	28	BZ606304	BZ606304
C 23	250	32.4	498	28	AQ540219	RPCI-11-3
C 24	250	32.4	669	29	AG155696	Pan trogl
C 25	250	32.4	706	14	CA416075	CA416075
C 26	249.8	32.4	396	13	EX478578	EX478578
27	249.8	32.4	591	9	AL704268	AL704268
C 28	249.8	32.4	773	12	BI087460	BI087460
29	249.8	32.4	877	28	AQ740209	AQ740209
C 30	249.6	32.3	448	9	A1471481	A1471481
C 31	249.6	32.3	562	14	CA388905	CA388905
C 32	249.6	32.3	564	13	BU860291	BU860291
C 33	249.6	32.3	566	13	BU957747	BU957747
C 34	249.6	32.3	650	29	AG116352	AG116352
C 35	249.4	32.3	455	28	BH367084	BH367084
36	249.2	32.3	444	28	B89781	B89781
C 37	249	32.3	865	13	EX431638	EX431638
C 38	248.8	32.2	380	9	A1151261	A1151261
C 39	248.8	32.2	664	28	AQ343449	AQ343449
40	248.6	32.2	541	14	CA437967	CA437967
C 41	248.6	32.2	721	12	EM679639	EM679639
C 42	248.4	32.2	745	29	AG039211	AG039211
C 43	248	32.1	323	13	BU588591	BU588591
C 44	248	32.1	365	10	AW472872	AW472872
C 45	248	32.1	457	28	AQ010278	AQ010278

ALIGNMENTS

RESULT 1	BM976892/c	794 bp	mRNA	linear	EST 21-FEB-2003
LOCUS	UI-CF-EN1-adb-n-01-0-UI.s1	UI-CF-EN1	Homo sapiens	cdna clone	
DEFINITION	UI-CF-EN1-adb-n-01-0-UI 3', mRNA sequence.				
ACCESSION	BM976892				
VERSION	BM976892.1	GI:19594754			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	1 (bases 1 to 794)				
DISCUSSION	Bonaldi,M.F., Lennon,G. and Soares,M.B.				
ABSTRACT	Normalization and subtraction: two approaches to facilitate gene				
GENOME	Genome Res. 6 (9), 791-806 (1996)				
MEDLINE	97044477				
PubMed	889548				
COMMENT	Contact: McCray, PB				
	University of Iowa				
	2024 University of Iowa Med Labs, Iowa City, IA 52242, USA				
	Tel: 319 356 4866				
	Fax: 319 356 7171				
	Email: paul-mccray@uiowa.edu				
	Tissue Procurement: Dr. M. J. Welsh, University of Iowa				

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA sequencing: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researcher may obtain clones from research  
 genetics ([www.resgen.com](http://www.resgen.com)) or from Open Biosystems  
 ([www.openbiosystems.com](http://www.openbiosystems.com)).  
 Seq primer: M13 FORWARD.  
 POLA=Yes.

## FEATURES

Location/Qualifiers  
1. .794  
/organism="Homo sapiens"  
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/clone\_type="Primary Lung Cystic Fibrosis Epithelial Cells"  
/dev\_stage="Adult"  
/lab\_host="PH103 (Life Technologies) (T1 phage resistant)"  
/clone\_lib="UI-CF-EN1"  
/notes="Organ. Lung. Vector: pT7T3-Pac (Pharmacia) with a modified Polylinker; Site\_1: EcoR I; Site\_2: Not I; UI-CF-EN1 is a normalized cDNA library containing the following tissue(s): Primary Lung Cystic Fibrosis Epithelial Cells. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (GT)<sub>18</sub> tail. The sequence tag for this library is CTGCTCAGGT.  
TAG TISSUE=Human Lung Epithelial Cell Lines untreated LPS 6hr to LPS 24h  
TAG LIB=UI-CF-EN1  
TAG\_SEQ=CTGCTCAGGT"

## ORIGIN

Query Match 35.8%; Score 276; DB 12; Length 794;  
Best Local Similarity 80.8%; Pred. No. 1.7e-46;  
Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;

Qy	2	AAGCGTTCTCGCGCGCAGCGCAACAACTAGAACCGTGAGAACGCGTCCAGCAACCGCGAC	61
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Qy	62	CCACGACGCGTCACTTCGGSCACGCCCCNAGGAGAGAAAGCCAGACCTCTAGAGAA	121
Db	597	CCACGACGACGGCGCCTTCGGGCAACCCAAAGAGAGAGGCCAAGACCTCCNAGAGAA	538
Qy	122	GCAGGGTCTCATGTGCAAGGCGTAGCGCAGCGGTCCGCCGACAGACCTCCCATCTGACCC	181
Db	537	GAAGCGCTCCAGGCGCAAGGCGGAGGAGCGGTCCCTCCGACCTCCCATCTGACCC	478
Qy	182	CAGCGAGCC-----CTCTACTGGGAGATGATCGGTGCGA	217
Db	477	CAACGAACCCACGTACTGTCTGTGCAACAGGTCTCTATGGGAGATGATCGGTGCGA	418
Qy	218	CA---ACGAATGCCCATCGAGTGGTTCGGTTTCGTGTGTGAGTCTCAACCATAAACC	274
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Db	357	CAAGGGCAAGTGATCTCTCCCAAGTGCCTGGGGGAGAACGAGACCATGGACAAAGC	298
Qy	327	CTTTGAGAAGTCCAGAAAAAAGGGCTTATACAGGTAGTTTGGGGACATGGCTCTA	386
Db	297	CCTGGAGAAATCC--AAAAAGAGAGGGCTTACAACAGGTAGTTTGTGTGACAGGGCCCTG	240
Qy	387	ATAGTGAGGAGAAACAAAATAAGCCAGTGTGTTGATTACATTGCCACCTTTCGTGAGGTGC	446

239 GT -GTGAGGAGGACAAATAACC -GTGTATTATTACATTCTGCTCCCTTTGTGTGAGTGC 182 Db

447 AGGAAGTGTAAATGTATATCTTTTAAAGAAATCTTGTTAGAGG 488 QY

181 AAGGAGTGTAAATGTATATCTTTTAAAGAAATCTTGAAGAAGG 140 Db

RESULT 2  
BU622930/c

BU622930/c	729 bp	mRNA	linear	EST 23-SEP-2002
LOCUS	729 bp	mRNA	linear	EST 23-SEP-2002
DEFINITION	UI-H-FU1-bgb-f-08-0-UI.s1 NCI CGAP_FU1 Homo sapiens CDNA clone			
	UI-H-FU1-bgb-f-08-0-UI 3', mRNA sequence.			
ACCESSION	BU622930			
VERSION	BU622930.1	GI:23289145		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 729)			
AUTHORS	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .			
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),			
	Tumor Gene Index.			
JOURNAL	Unpublished (1997)			
COMMENT	Contact: Robert Strausberg, Ph.D.			
	Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a>			
	Tissue Procurement: James Martin			
	cDNA Library preparation: Dr. M. Bento Soares, University of Iowa			
	cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa			
	DNA Sequencing by: Dr. M. Bento Soares, University of Iowa			
	Clone Distribution: Clone distribution information can be obtained			
	from Dr. M. Bento Soares, <a href="mailto:bento-soares@uiowa.edu">bento-soares@uiowa.edu</a>			
	Seq primer: M13 FORWARD			
	POLYA=Yes.			

## FEATURES

```

1. 729
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FL1-bgp-f-08-0-J1"
/tissue_type="Cell lines"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_Flu1"
/note="Organ: Chondrosarcoma; Vector: pRTT3-Pac
(Pharmacia) with a modified polylinker; Site 1: Ecor I;
Site 2: Not I; NCI CGAP Flu1 is a normalized cDNA library
derived from a pool of mRNA obtained from 4 cell lines
from grade III chondrosarcoma tissues. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an Ecor I
adaptor, digested with Not I, and cloned directionally
into pRTT3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
PvuII site. The sequence tag for this library is
GAGGTCCGGT. The cell lines were provided by Dr. James
Martin from the University of Iowa.
TAG TISSUE=Human Chondrosarcoma Grade 3 cell line mix
TAG LIB=UI-H-FL1
TAG_SEQ=GAGGTCCGGT"

```

ORIGIN

Query Match	35.5%	Score 274.4	DB 13	Length 729
Best Local Similarity	80.7%	Pred. No. 3.6e-46		
Matches 421	Conservative	0	Mismatches 61	Indels 40
Gaps				
Qy	2	AAGCGTCTTCGGCGGCAGCGCAACAACTAGAAACGGTGAAGACCGCTCCAGCAACCGCGAC	61	
Db	659	AAGCGTTCAGCGGCAGCGCAACAAAGAGAAACGGTGAAGACCGCTCCAGCAACCGCGAC	601	

polylinker; Site\_1: Not I; Site\_2: Eco RI; Plasmid DNA from the normalized library NCI\_GAP\_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones IDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. "

	ORIGIN	Query Match	Best Local Similarity	Score 268;	DB 10;	Length 673;
		Matches 417;	Conservative	0;	Mismatches 65;	Indels 40; Gaps 7;
Qy	2	AAGCGTTCTCGGCGCAGCGCAACAACTPAGAACCGTGAGAACGGGTCCAGCAACCGCGAC	61			
Db	649	AAGCGCTACGTGCGCAGCGCAACAAACGAGATCGTGAGACGGTCCATCAACTCGA-	591			
Qy	62	CCACGACGACGTTCACCTCGGGCAGCCCAAGAGAGAAAGCCACGACCTCTAAGAGAA	121			
Db	590	CCTGACGACGGCGCTCTGGGCAACACCAAGGAGAAAGGCCAAGACCTCCAAGAGAA	531			
Qy	122	CGAGGGTCCATGGCCCAAGGGGTACGCGCAGCGTCCCGCCGACACCTCCCGATCGACC	181			
Db	530	GAAGCGCTCCAAAGGCCAAGCGGAGCGAGCGGTCCCTCGGACCTCCCATCGACC	471			
Qy	182	CAGCGAGCC-----CTCTACTGGGAGATGATCCGCTGGGA	217			
Db	470	CAACGAACCCAGTACTGTGTGCAACCAAGGTCTCTCTATGGGAGATGATCGGTGGGA	411			
Qy	218	CA---ACGATCGCCATCGAGTGTTCGGTCTCTCGTGTGTGAGTCTCAACCATAAACC	274			

275	AAAGCGCAAGTGGTACTGTTCCAGATGCCGGGGAAGAAGC-----ATGGGCAAAAGC	326	
Db	350	CARGGCAAGTGGTACTGTTCCAGTCCGGGGGGAACGAGAGACCATGGACAAAGC	291
Qy	327	CCTGTGAAGTCCAGAAAAAACAAGCGGCTTATAACAGGTAGTTTGGGACATCGGTCTA	386
Db	290	CCTGGAGAAATCC-AAAAAAGAGAGGGGCTTACAACAGTAGTTTGTGCACAGGCGCCTG	233
Qy	387	ATAGTGAGGAGAACAAAATAAGCCAGTGTGTTGATTACATTCGCCACCTTTGCTGAGGTGC	446
Db	232	GT-GTGAGGAGGACAAAATAAACC-GTGTATTATTACATTCTGCTCCTTTGTGTGAGGTGC	175
Qy	447	AGGAAGTGTAAAATGTATATTTTAAAGAATGTGTGTAGAGG	488
Db	174	AAGSAGTGTAAAATGTATATTTTAAAGAATGTAGAAAAGG	133

BM042700/c  
 LOCUS  
 DEFINITION  
 761 bp mRNA linear EST 07-NOV-2001  
 603616058t1 NIH\_MGC\_112 Homo sapiens cDNA clone IMAGE:5420510 3',  
 mRNA sequence.  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 EST.  
 BM042700.1 GI:16771967  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 761)  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-x@mail.nih.gov](mailto:cgapbs-x@mail.nih.gov)  
 Tissue Procurement: DCTD/DTP  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)  
 DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a>	
Plate: LLCW1875	row: d column: 15
High quality sequence start: 2	
High quality sequence stop: 754	
Location/Qualifiers	
1..761	
/organism="Homo sapiens"	
/mol_type="mRNA"	
/db_xref="taxon:9606"	
/clone="IMAGE:5420510"	
/tissue_type="melanotic melanoma, cell line"	
/lab_host="DH10B (phage-resistant)"	
/clone_lib="NIH MGC 112"	
/note="Organ: skin; Vector: pOTB7; Site: 1; XhoI; Site 2: EcoRI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."	
ORIGIN	
Query Match	34.3%; Score 265; DB 12; Length 761;
Best Local Similarity	80.7%; Pred. No. 3.1e-44;
Matches	422; Conservative 0; Mismatches 60; Indels 41; Gaps 8;
QY	2 AAGCGTCTCGGGGCGGACGACACTAGACCGTGTGAGACCGTCCAGACACCGCAC 61
DB	
QY	566 AAGCGTCTACGGCGGCGGACGACGACGAGACCGTGTGAGACCGTCCAGACACCGA- 508
DB	
QY	62 CCACGACGACGTCACCTCGGGCAGCCGCCAAGAGAGAAAGCCAGACCTTAAAGAGAA 121
DB	
QY	507 CCACGACGACGCGGCGCTCGGGCAGACCCCAAGAGAGAAAGGCGCAAGCCTCCAGAGAA 448
DB	
QY	122 GCAGGCGCTCATGCGCAAGCGGTAGCGGAGCGGCTCCCGGAGACCTCCCATCGACCC 181
DB	
QY	447 GAAGCGCTCCAGGCCAAGCGGAGCGGCGGCTCCCGGAGACCTCCCATCGACCC 388
DB	
QY	182 CACGAGACCC-----CTCTACTCGGAGATGATCCGTGCGA 217
DB	
QY	387 CACGAGACCCACGTACTGTGTGTGCAACACGAGTCTCTATGGGAGATGATCGGTGCGA 328
DB	
QY	218 CA---ACGATGCCCATCGAGTGTTCGCTCTCGTGTGAGTCTCAACCATAAACC 274
DB	
QY	327 CAACGACGAGTGCCTCCATCGAGTGTTCACCTTCTCGTGGGTGGGCTCAATCAATACC 268
DB	
QY	275 AAAGCGCAAGTGGTA-CTGTTCAGATGCGGGGGAAGAACG-----ATGGGCAAG 325
DB	
QY	326 CCCTTGAGAGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 385
DB	
QY	207 CCCTGGAGAGATCC--AAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 150
DB	
QY	386 AATAGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 445
DB	
QY	149 GGT-GTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 488
DB	
QY	446 CAGAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 49
DB	
QY	91 CAAGAGTGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 49
DB	
RESULT 5	
AQB77998	
LOCUS	
DEFINITION	
HS 2160 A2_C07 MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2160 Col=14 Row=E, genomic survey sequence.	
AQB77998	
ACCESSION	
AQB77998.1 GI:6309465	
GSS	
Homo sapiens (human)	
Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
1 (bases 1 to 503)	
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Kellar,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.	
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome	
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)	
99380589	
10449764	
Contact: Mahairas GG, Wallace JC, Hood L	
High Throughput Sequencing Center	
University of Washington	
401 Queen Anne Avenue North, Seattle, WA 98109, USA	
Tel: (206) 616-3618	
Fax: (206) 616-3887	
Email: jwallace@u.washington.edu	
Clones may be purchased from Research Genetics (info@resgen.com).	
BAC end Web Server: <a href="http://www.htsc.washington.edu">http://www.htsc.washington.edu</a>	
Plate: 2160 row: E column: 14	
Seq Primer: M13 Reverse	
Class: BAC ends	
High quality sequence stop: 503.	
Location/Qualifiers	
1..503	
/organism="Homo sapiens"	
/mol_type="genomic DNA"	
/db_xref="taxon:9606"	
/clone="Plate=2160 Col=14 Row=E"	
/sex="male"	
/clone_lib="CIT Approved Human Genomic Sperm Library D"	
/notes="Organ: Sperm; Vector: pBelOBAcl1; BAC Clones in E-Coli DH10B"	
ORIGIN	
Query Match	33.8%; Score 260.8; DB 28; Length 503;
Best Local Similarity	79.1%; Pred. No. 2.2e-43;
Matches	307; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
QY	385 TAATAGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 444
DB	
QY	80 TAGAACAAGATATGAAAAAGTAATTCATGATATCAGAAAAATAATTCATATCTGAATG 139
DB	
QY	445 GCAGGAGTGTAAATGATATTTTAAAGAAATGTTTAAAGAGCGCGCGCGGTGGCTC 504
DB	
QY	140 AAAAAATCTACAAAGAGATATCATTTAAAAAGAAATATTGGGGCTGGGCGGTGGCTC 199
DB	
QY	505 ACGGCTGTAAATCCAGACATTTGGGAGCGCGAGCGGTCCGATCAGAGGTCAAGAGATC 564
DB	
QY	200 ACGGCTGTAAATCCAGACATTTGGGAGCGCGAGCGGTCCGATCAGAGGTCAAGAGATC 259
DB	
QY	565 GAGACCATCTGGCTACAGGTGAACCCCGCTCTACTTAAATAATTTAAAAAATAATTT 624
DB	
QY	260 GAGACCATCTGGCTACAGGTGAACCCCGCTCTCTATTAATAATAATAATAATAATTT 319
DB	
QY	625 AGCTGGGCGTGGTGGCGGGCGCTGTAGTCCCGAGCTATTCCGAGGCTGAGGAGAGAA 684
DB	
QY	320 AGCGGGCGGTGGTGGCGCGCTGTAGTCCCGAGCTACTCGGAGGCTGAGGAGAGAA 379
DB	
QY	695 TGGGNTGAACTGGGAGGTGGAGCTTCAGTGGAGGCTCGGAGGCTCGGAGGCTCGGAGG 744
DB	
QY	380 TGGGNTGAACTGGGAGGTGGAGCTTCAGTGGAGGCTCGGAGGCTCGGAGGCTCGGAGG 439
DB	
QY	745 CTGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 772
DB	
QY	440 CTGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 467
DB	

RESULT 6	EG249643	602319736F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4414905 5', mRNA sequence.	822 bp	linear	EST 13-FEB-2001
LOCUS	EG249643	mRNA sequence.			
DEFINITION	EG249643	1 GI:12759459			
ACCESSION	EG249643				
VERSION	EG249643				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 822)				
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgapbs-remail.nih.gov">cgapbs-remail.nih.gov</a> Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LLAM10143 row: h column: 10 High quality sequence stop: 546.				
FEATURES	Location/Qualifiers				
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	/organism="Homo sapiens"				
	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/clone="IMAGE:4414905"				
	/tissue_type="hypermephroma, cell line"				
	/lab_host="DH10B (phage-resistant)"				
	/clone_lib="NTH MGC 89"				
	/note="Oran; KIDney; Vector: pCMV-SPORE6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."				
ORIGIN					
	Query Match 33.4%; Score 258.2; DB 12; Length 822;				
	Best Local Similarity 90.8%; Pred. No. 7,8e-43;				
	Matches 286; Conservative 0; Mismatches 25; Indels 4; Gaps 1.				
Qy	458 AATGTATATTTTAAAGAAATGTTGTAGAGCGCGCGGTGCCTACGGCTGTAATCC	517			
Db	178 ACTGAATTTTTTTAAAAATTCAGATATCGCGCGCGCGGTGCCTACGGCTGTAATCC	237			
Qy	518 CAGCACTTTGGAGGCCGAGCGGTTCGGATCAGAGGTGAGGATCGAGACCATCTCG	577			
Db	238 CAGCACTTTGGAGGCCGAGCGCGGTTCAGAGGTGAGGATCGAGACCATCTCG	297			
Qy	578 CTACACGGTGAACCCCGTCTCTACTAAAAATTCAAAAAAAATTAAGTCGGCGTGT	637			
Db	298 CTACACGGTGAACCCCGTCTCTACTAAAAATTCAAAAAAAATTAAGTCGGCGTGT	353			
Qy	638 GCGCGCGCTGTAGTCCAGTATTTCGGAGAGCTGAGGACGAGAAATGCGNTGACCTG	697			
Db	354 AGCGCGCGCTGTAGTCCAGTATTTCGGAGAGCTGAGGACGAGAAATGCGNTGACCTG	413			
Qy	698 GGAGTGGAGCTTGCAATGAGCCAGGTGCGCCACTGCACCTCCAGCTGGGCGGACAG	757			
Db	414 GGAGGCGGAGCTTGCAATGAGCCAGGTGCGCCACTGCACCTCCAGCTGGGCGGACAG	473			
Qy	758 CGAGACTCCATCTTA	772			
Db	474 CGAGACTCCGCTCA	488			

## RESULT 7

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AQ351424/C
LOCUS       592 bp          DNA          linear          GSS 07-MAY-1999
DEFINITION  RPCI11-111K4.TV RPCI-11 Homo sapiens genomic clone RPCI-11-111K4,
              genomic survey sequence.
ACCESSION   AQ351424
VERSION     AQ351424.1
KEYWORDS    GI:4178759
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 592)
Zhao,S., Adams,W.D., Nierman,W., Malek,J., de Jong,P. and
Venter,J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
Unpublished (1997)
Other GSSs: RPCI11-111K4.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbs@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac\_end\_search/bac\_end\_search.html
Seq primer: T7
Class: BAC ends.
FEATURES             Location/Qualifiers
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         /organism="Homo sapiens"
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         /db_xref="GDB:7542483"
         /db_xref="caxon:9608"
         /clone="RPCI-11-111K4"
         /sex="Male"
         /cell_type="Lymphocytes"
         /clone_lib="RPCI-11"
         /note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI;
RPCI11 Human Male BAC library"

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ORIGIN	Query Match	33.0%	Score 255;	DB 28;	Length 592;
	Best Local Similarity	88.2%;	Pred. No. 3.4e-42;		
	Matches 276;	Conservative 0;	Mismatches 37;	Indels 0;	Gaps 0;
QY	459	ATGTATATTTTAAAGAAATGTGTAGAGGCGCGCGTGTCTCAGCGCTGTAACTCC	518		
Db	359	ATTCAGGTTATAAAGTTAGATACCTTTGAGCGGACGCGTGGCTCATGCTGTAACTCC	300		
QY	519	AGCACTTTGGGAGGCCGAGGCGGTCGGATCAGGAGTTCGAGAGATCGAGACCATCTCGC	578		
Db	299	AGCACTTTGGGAGGCCGAGGCGCGGATCAGCGAGTTCAGGAGCTCAAGACCATCTCGC	240		
QY	579	TAAACAGGTGAAACCCCGTCTCTACTAAAAATTCAAAAAAAATTTAGCTGGCGCGTGGTG	638		
Db	239	TAAACATGTTGAAACCCCGTCTCTACTAAAAATACAAAAAAATTTAGCCGGCGTGGTG	180		
QY	639	GGGGCGCGCTGTAGTCCAGATTATCGGGAGGCTGAGGCAGGAGAAATGGNTGAACCTGG	598		
Db	179	GGGGTGTCTGTAGTCCAGCTACTTCGGGAGGCTGAGGCAGGAGAAATGGCGTGAACCTGG	120		
QY	699	GAGGTGGAGCTTGCAATGAGCCAAAGTTCGGCCACTGCATCTCAGAGCTGGGCGACAGAGC	758		
Db	119	GAGGCGGAGCTTGCAGTAGCGCCGAGATTGACCACTGCATCTCCAGCTGGGGACAGAGC	60		
QY	759	GAGACTCCATCTT	771		

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Db      59 AAGACTCTGTCTT 47
RESULT 8
BU615970/c      701 bp mRNA linear EST 23-SEP-2002
LOCUS          UI-H-DF0-ben-c-08-0-UI.s1 NCI CGAP DF0 Homo sapiens cDNA clone
DEFINITION    UI-H-DF0-ben-c-08-0-UI 3', mRNA sequence.
ACCESSION     BU615970
VERSION       BU615970
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE     1 (bases 1 to 701)
AUTHORS      NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE        National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
              Tumor Gene Index
COMMENT       Unpublished (1997)
              Contact: Robert Strausberg, Ph.D.
              Email: cgaps-remail.nih.gov
              Tissue Procurement: Dr. Jose Mercuende
              cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
              DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
              DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
              Clone Distribution: clone distribution information can be obtained
              from Dr. M. Bento Soares, bento-soares@uiowa.edu
              The following repetitive elements were found in this cDNA
              sequence: 11-299, >ALU (matched complement)
              Seq primer: M13 FORWARD
              POLYA=Yes.

FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-DF0-ben-c-08-0-UI"
                     /tissue_type="Subchondral Bone"
                     /dev_stage="Adult"
                     /lab_hosts="DH10B (Life Technologies)"
                     /clone_lib="NCI-CCAP DF0"
                     /note="Organ: Bone; Vector: p773-Pac (Pharmacia) with a
                     modified polylinker; Site: 1: Scor I; Site 2: Not I;
                     NCI CGAP DF0 is a cDNA library containing the following
                     tissue(s): Subchondral Bone. The library was constructed
                     according to Bonaldo, Lennon and Soares, Genome Research,
                     6:791-806, 1996. First strand cDNA synthesis was primed
                     with an oligo-dT primer containing a Not I site. Double
                     stranded cDNA was ligated to an EcoR I adaptor, digested
                     with Not I, and cloned directionally into p773-Pac
                     vector. The oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (d)18 tail. The
                     sequence tag for this library is GTTAAGCGTC.
                     TAG TISSUE=Subchondral bone
                     TAG LIB=UI-H-DF0
                     TAG_SEQ=GTTAAGCGTC"

ORIGIN
Query Match      33.0%; Score 255; DB 13; Length 701;
Best Local Similarity 86.4%; Pred. No. 3.5e-42;
Matches 293; Conservative 0; Mismatches 42; Indels 4; Gaps 1;

QY 434 TTGTGAGTGCAGAGAGTGAATATGATATATTTTAAAGAACTTTTAGAGCGCGG 493
DB 352 TTGGGAGATGTTAATATGTTGAAGACACACATGTTTAAAGATCTGCCATCTGCGCGG 293
QY 494 CGCGGTGGCTCAGCGCTGTAATCCAGCACTTTGGAGAGCGCGAGCGGTCCGATCACGAG 553
DB 292 CGCGGTGGCTCAGCGCTGTAATCCAGCACTTTGGAGAGCGCGAGCGCGGTACGAG 233
QY 554 GTCAGGAGATCGAGACCATCTCGGTCTAACACCGTGAACCCCGTCTCTACTAAAAATCA 613

Db      232 GTCAGGAGATCGAGACCATCTCGGTCTAACACCGTGAACCCCGTCTCTACTAAAT --- 176
QY 614 AAAAAAATTAGCTGGCGCTGCTGGCGCGCGCTGTAGTCCAGCTATTCGGAGGCTG 673
DB 175 -ACAAAAAATTAGCGGGCGTGTAGCGGCGGCTGTAGTCCAGCTACTTCGGAGGCTG 117
QY 674 AGGAGAGAGATGCGNTGACCTCGGAGCTGGAGCTTGCACTGAGCAAGGTGCGGCCAC 733
DB 116 AGGAGAGAGATGCGGTGAACCCCGGAGGCGGAGCTTGAGTGAGCGGAGATCGGCCAC 57
QY 734 TGCACTCCAGCTGGCGGCGAGACGCGAGACTCCATCTTA 772
DB 56 TGCACTCCAGCTGGCGGCGAGACGCGAGACTCCGCTCTCA 18

RESULT 9
B80438
LOCUS          CIT-HSP-2045M21.TR CIT-HSP Homo sapiens genomic clone 2045M21,
DEFINITION    genomic survey sequence.
ACCESSION     B80438
VERSION       B80438
KEYWORDS      GSS.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE     1 (bases 1 to 458)
AUTHORS      Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
              Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
              Simon,K., and Venter,J.C.
              Use of a random BAC End Sequence Database for Sequence-Ready Map
              Building (1998)
              Unpublished (1998)
              Other GSSs: CIT-HSP-2045M21.TF
              Contact: Mark Adams
              Department of Eukaryotic Genomics
              The Institute for Genomic Research
              9712 Medical Center Dr., Rockville, MD 20850, USA
              Tel: 301 838 0200
              Fax: 301 838 0208
              Email: mdadams@tigr.org
              Clones are available from Research Genetics (info@resgen.com). BAC
              end search page:
              http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html
              Seq primer: M13 Reverse
              Class: BAC ends.

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                     /note="Vector: pBelobAC11; Site 1: HindIII; Site 2:
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Best Local Similarity 90.0%; Pred. No. 4.9e-42;
Matches 271; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 472 AAGATGTTTAGAGCGCGCGGTGCTCAGCTGTATCCAGCACTTTGGGAG 531
DB 56 AAAAAATCTTGGGCTCGCGGCGGCGGTGCTCAGCTGTATCCAGCACTTTGGGAG 115
QY 532 GCCAGGCGCGTCCGATCACGAGTCCAGGAGATCGAGACCATCTCGCTTAACACGCTGAA 591
DB 116 GCCAAGCGCGCGGATCACAGGTCCAGGAGATTGAGACCATCTCGCTTAACACGCTGAA 175

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470 TAAAGAAATGTTGTAGAGCGCGCGGTGGCTCAGCGCTGTAATCCAGCACTTTGGG 529  
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527 TTAAGAAAGTATAGGCGCGCGGTGGCTCAGCGCTGTAATCCAGCACTTTGGG 529  
468  
530 AGGCCGAGGCGGTGGCTCAGAGGTCAGAGATCGAGACCATCTGGCTTAACCGGTGA 589  
467 AGGCCGAGGCGGTGGCTCAGAGGTCAGAGATCGAGACCATCTGGCTTAACCGGTGA 408  
590 AACCCCGTCTCTACTAAAAATTCAAAAAATTTAGCTGGCGGTGGCTGGCGCGCTG 649  
407 AACCCCGTCTCTACTAAAAATTCAAAAAATTTAGCTGGCGGTGGCTGGCGCGCTG 348  
650 TAGTCCAGCTATTCGGGAGGTCAGGAGGTCAGAGATCGAGACCATCTGGCTTAACCGGTGA 709  
347 TAGTCCAGCTATTCGGGAGGTCAGGAGGTCAGAGATCGAGACCATCTGGCTTAACCGGTGA 288  
710 TGCANTGAGCAAGTTCGGCGCTCAGCTCCAGCTGGCGGACAGAGCGAGACTCCATC 769  
287 TGCAGTGCAGAGATTGGCGCTCAGCTCCAGCTGGCGGACAGAGTGAGACTCTGTC 228  
770 TTA 772  
227 TCA 225

RESULT 12  
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LOCUS  
DEFINITION  
Genomic survey sequence.  
ACCESSION  
A0315280  
VERSION  
A0315280.1 GI:4046743  
KEYWORDS  
GSS.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens

REFERENCE  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 731)  
AUTHORS  
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,  
Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.  
Use of human BAC End Sequences for Sequence-Ready Map Building  
Unpublished (1998)  
TITLE  
Other GSSs: RPC111-104N24.T1  
JOURNAL  
Contact: Shaying Zhao, William Nierman, Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850  
COMMENT  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: hse@tigr.org  
Clones are derived from the human BAC library RPCI-11. For BAC  
library availability, please contact Pieter de Jong  
(pieter@dejong.med.buffalo.edu). Clones may be purchased from  
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from  
Research Genetics (info@resgen.com). BAC end search page:  
http://www.tigr.org/tldb/humgen/bac\_end\_search/bac\_end\_search.html  
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Class: BAC ends.

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Query Match 32.7%; Score 252.8; DB 28; Length 731;  
Best Local Similarity 87.7%; Pred. No. 1.2e-41;

Best Local Similarity 90.9%; Pred. No. 9.9e-42;  
Matches 280; Conservative 0; Mismatches 24; Indels 4; Gaps 1;  
465 ATTTTAAAGAAATGTTGTAGAGCGCGCGGTGGCTCAGCGCTGTAATCCAGCACT 524  
117 ATTATATAAGAAAGAGGTTTAGCGCGCGGTGGCTCAGCGCTGTAATCCAGCACT 176  
525 TTGGAGGCGCGAGCGGTGGATCAGAGGTAGAGATCGAGACCATCTGGCTTAACAC 584  
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585 GGTGAACCCCGTCTCTACTAAAAATTCAAAAAATTTAGCTGGCGGTGGCTGGCGGGC 644  
237 GGTGAACCCCGTCTCTACTAAAAATTCAAAAAATTTAGCTGGCGGTGGCTGGCGGGC 292  
645 GCCTGTAGTCCAGCTATTCGGGAGGTCAGGAGGTCAGGAGGTCAGGAGGTCAGGAGGTC 704  
293 GCCTGTAGTCCAGCTATTCGGGAGGTCAGGAGGTCAGGAGGTCAGGAGGTCAGGAGGTC 352  
705 GAGCTTGCAAGTGCAGAGGTCGCGCTCAGCTCCAGCTGGCGGACAGAGCGAGACT 764  
353 GAGCTTGCAAGTGCAGAGGTCGCGCTCAGCTCCAGCTGGCGGACAGAGCGAGACT 412  
765 CCATCTTA 772  
413 CCGTCTCA 420

RESULT 13  
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LOCUS  
DEFINITION  
DKFZp686A15253.1 587 (synonym: hlcc3) Homo sapiens cDNA clone  
DKFZp686A15253.5, mRNA sequence.  
ACCESSION  
BX486697  
VERSION  
BX486697.1 GI:31950617  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens

REFERENCE  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 587)  
AUTHORS  
Blöcker,H., Boecker,M., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,  
Fobbe,G., Han,M. and Wiemann,S.  
EST (Blöcker,H., Boecker,M., Mewes,H.W., Weil,B., Amid,C., et al.)  
Unpublished (2003)  
TITLE  
Contact: MIPS  
JOURNAL  
MIPS  
COMMENT  
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by GSF (National Research Centre for Biotechnology Ltd.,  
Braunschweig/Germany) within the cDNA sequencing consortium of the  
German Genome Project.  
No 5' sequence available.  
This clone (DKFZp686A15253) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES  
Location/Qualifiers  
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cDNA-collection"

ORIGIN  
Query Match 32.7%; Score 252.4; DB 13; Length 587;  
Best Local Similarity 87.7%; Pred. No. 1.2e-41;

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 507 GCGTGTATCCAGACACTTTGGAGCGCGAGCGGTGCGATCACAGGTCTAGAGATCGA 566  
 312 GCGTGTATCCAGACACTTTGGAGCGCGAGCGGTGCGATCACAGGTCTAGAGATCGA 253  
 567 GACCATCTGGCTAAACAGCGTGAACCCCGCTCTTACTAAATAATCAAAAAAAATTTAG 626  
 252 GACCATCTGGCTAAACAGCGTGAACCCCGCTCTTACTAAATAATCAAAAAAAATTTAG 195  
 627 CTGGCGGTGGTGGCGCGCGCTGTAGTCCAGACTATTCGGAGGCTGAGGAGGAGATG 686  
 194 CCGGGCGTAGTGGCGCGCGCTGTAGTCCAGACTATTCGGAGGCTGAGGAGGAGATG 135  
 687 GNTGAACTCTGGAGGTGAGCTTGCANTGAGCGAAGTTCGGCGCACTGCTCCAGGCT 746  
 134 GCGTGAACCGGAGCGGAGCTTGCAGTGAAGCGAGATTGCGCCACTGCTCCAGGCT 75  
 747 GCGCGACAGAGGAGACTCCATCTTA 772  
 74 GCGCGACAGAGGAGACTCCGCTCA 49

RESULT 14  
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 LOCUS Pan troglodytes DNA, clone: RP43-005A01.TJ, genomic survey  
 DEFINITION  
 ACCESSION AG144106  
 VERSION AG144106.1 GI:16673784  
 KEYWORDS GSS.  
 SOURCE Pan troglodytes (chimpanzee)  
 ORGANISM Pan troglodytes  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 REFERENCE 1  
 FUJIIYAMA, A., HATTORI, M., TOYODA, A., TAYLOR, T.D., YADA, T.,  
 TOTOKI, Y., WATANABE, H. and SAKAKI, Y.  
 BAC end sequences of Library RPCI-43  
 Unpublished  
 TITLE 2 (bases 1 to 662)  
 JOURNAL  
 REFERENCE  
 FUJIIYAMA, A., HATTORI, M., TOYODA, A., TAYLOR, T.D., YADA, T.,  
 TOTOKI, Y., WATANABE, H. and SAKAKI, Y.  
 Direct Submission  
 TITLE Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical  
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 (E-mail: chimpbes@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,  
 Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
 Clones are derived from the chimpanzee BAC library RPCI-43. This BAC  
 end was generated during the R&D process and may have higher chance  
 of clone tracking errors.  
 PRIMER  
 Sequencing: TJ  
 LIBRARY  
 Vector : pBACe3.6  
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ORIGIN

Query Match 32.7%; Score 252.2; DB 29; Length 662;  
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 532 GCGAGGCGGTGCGATCACAGGTCTAGGAGATCGAGACCATCTGCTTAACACGGTGA 591  
 344 GCGAGGCGCGGTGCGATCACAGGTCTAGGAGATCGAGACCATCTGCTTAACACGGTGA 403  
 592 CCCGCTCTTACTTAAATAATCAAAAAAAATTTAGTGGCGGTGGTGGCGCGCTGTA 651  
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 712 CANTGAGCAAGTTCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 771  
 520 CAGTGAGCGAGATCGCGCACTGCACTCCACCTCGCGCGAGAGAGACTCCGCTCT 579  
 772 A 772  
 580 A 580

RESULT 15  
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 LOCUS WHADC89TR Human MCF7 breast cancer cell line library (MCF7.1) Homo  
 DEFINITION sapiens genomic clone MCF7.1-19P9, genomic survey sequence.  
 ACCESSION BZ601227  
 VERSION BZ601227.1 GI:31509689  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1073)  
 AUTHORS Volik, S., Zhao, S., Chin, K., Brebner, J.H., Herndon, D.R., Tao, O.,  
 Kowbel, D., Huang, G., Lapuk, A., Kuo, W.-L., Magrane, G., de Jong, P.,  
 Gray, J.W. and Collins, C.  
 End-sequence profiling: Sequence-based analysis of aberrant genomes  
 Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7696-7701 (2003)

TITLE  
 JOURNAL  
 MEDLINE  
 22709111  
 PUBMED  
 12788976  
 CONTACT: Volik SV  
 Colin Collins' lab  
 UCSF Comprehensive Cancer Center  
 UCSF Box 0808, San Francisco, CA 94143-0808, USA  
 Tel: 415 502 7066  
 Fax: 415 502 5665  
 Email: svolik@cc.ucsf.edu  
 This clone is available from Amplicon Express  
 http://www.genomex.com  
 Class: BAC ends.  
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 /note="Vector: pECBAC1; Site 1: HindIII; This library was  
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 Express (http://www.genomex.com) using their standard  
 procedure."

ORIGIN

FEATURES  
 source

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Query Match      32.7%; Score 252.2; DB 28; Length 1073;
Best Local Similarity 89.3%; Pred. No. 1.4e-41;
Matches 283; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

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Qy 516 CCCAGCACTTTGGAGGCCGAGCGGTGCGGATCACGAGGTACGAGATCGAGACCATCCT 575
Db 362 CCCAGCACTTTGGAGGCCGAGCGGTGCGGATCACGAGGTACGAGATCGAGACCATCCT 421
Qy 576 GGCTAACACCGTGAAACCCCGTCTCTACTATAAAATTCAAAAAATTTAGTGGCGCTG 635
Db 422 GGCTAAAAACCGTGAAACCCCGTCTCTACTATAAAATAC-----AAAAAATTTAGCGGCGTA 477
Qy 636 GTGCGGGCGCGCTCTAGTCCAGCTATTTCGGGAGGCTGAGGCGAGGAGATGGGNTGAAC 695
Db 478 GTGCGGGCGCGCTCTAGTCCAGCTATTTCGGGAGGCTGAGGCGAGGAGATGGGNTGAAC 537
Qy 696 TGGAGGTGGAGCTTGCAATGAGCCAAAGGTGCGGCCACTGCACTCCAGCCTGGGCGACAG 755
Db 538 CGGAGGCGGAGCTTGCAATGAGCCAAAGGTGCGGCCACTGCACTCCAGCCTGGGCGACAG 597
Qy 756 AGCGAGACTCCATCTTA 772
Db 598 AGCGAGACTCCGCTCA 614

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Search completed: May 6, 2004, 11:48:52  
Job time : 2581.23 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 06:25:29 ; Search time 3361.45 Seconds  
(without alignments)  
9954.293 Million cell updates/sec

Title: US-09-451-739H-8  
Perfect score: 772  
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Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: gb.htg.\*  
3: gb.in.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sy.\*  
13: gb.un.\*  
14: gb.vi.\*  
15: em.ba.\*  
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17: em.hum.\*  
18: em.in.\*  
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22: em.pat.\*  
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25: em.ro.\*  
26: em.sts.\*  
27: em.un.\*  
28: em.vi.\*  
29: em.vt.\*  
30: em.htg.hum.\*  
31: em.htg.inv.\*  
32: em.htg.other.\*  
33: em.htg.mus.\*  
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36: em.htg.man.\*  
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40: em.htgo.mus.\*  
41: em.htgo.other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Length	DB	ID	Description
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3	754.8	97.8	86703	2	AL159989	AL159989 Homo sapi
4	754.8	97.8	248968	9	HSXDPB	AL159763 Homo sapi
5	277.6	36.0	97465	9	AL157820	AL157820 Human DNA
6	277.6	36.0	159983	2	AC013713	AC013713 Homo sapi
7	276	35.8	1074	9	AF149722	AF149722 Homo sapi
8	276	35.8	1143	6	AX367043	AX367043 Sequence
9	276	35.8	1189	9	AF149723	AF149723 Homo sapi
10	276	35.8	1533	6	AX367042	AX367042 Sequence
11	276	35.8	1533	9	AF149721	AF149721 Homo sapi
12	276	35.8	1902	6	AR079046	AR079046 Sequence
13	276	35.8	1902	6	AR087457	AR087457 Sequence
14	276	35.8	1902	6	AR110646	AR110646 Sequence
15	276	35.8	1905	6	AR154563	AR154563 Sequence
16	276	35.8	1905	6	AX839842	AX839842 Sequence
17	276	35.8	1980	9	AB024404	AB024404 Homo sapi
18	276	35.8	2061	6	AR087464	AR087464 Sequence
19	276	35.8	2061	6	AR110653	AR110653 Sequence
20	276	35.8	2061	6	AR154570	AR154570 Sequence
21	276	35.8	2061	6	AR171883	AR171883 Sequence
22	276	35.8	2081	9	AF001954	AF001954 Homo sapi
23	276	35.8	2086	9	HSP33ING2	AF078837 Homo sapi
24	276	35.8	2296	9	BC018348	BC018348 Homo sapi
25	276	35.8	2306	9	AB031269	AB031269 Homo sapi
26	276	35.8	2444	9	AB024401	AB024401 Homo sapi
27	276	35.8	2552	9	HSING3	AF167551 Homo sapi
28	276	35.8	2886	9	AF181849	AF181849 Homo sapi
29	276	35.8	2891	9	AB024402	AB024402 Homo sapi
30	276	35.8	2897	9	AF181850	AF181850 Homo sapi
31	276	35.8	2925	9	AB037386S2	AB037387 Homo sapi
32	276	35.8	163350	6	AX839844	AX839844 Sequence
33	272.8	35.3	2061	6	AR219160	AR219160 Sequence
34	271.4	35.2	167691	9	HS406A7	AL023284 Human DNA
35	270.6	35.1	124615	9	AC006019	AC006019 Homo sapi
36	270.6	35.1	184526	9	AC114969	AC114969 Homo sapi
37	270.4	35.0	61027	9	AC034204	AC034204 Homo sapi
38	270.4	35.0	191308	9	AC034243	AC034243 Homo sapi
39	269.6	34.9	97653	2	AC137570	AC137570 Homo sapi
40	269.6	34.9	149110	9	AP003692	AP003692 Homo sapi
41	269.2	34.9	132433	9	HSJ210B1	AL078593 Human DNA
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43	269	34.8	157834	2	AC022931	AC022931 Homo sapi
44	268.2	34.7	107846	9	AC105030	AC105030 Homo sapi
45	268.2	34.7	154604	2	AC104974	AC104974 Homo sapi

ALIGNMENTS

RESULT 1  
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DEFINITION Sequence 8 from Patent WO0147959.  
ACCESSION AX367049  
VERSION AX367049.1 GI:18855271  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 Jager,D., Stockert,E., Scanlan,M., Knuth,A., Old,L., Gure,A. and  
Chen,Y.T.  
AUTHORS Isolated nucleic acid molecules encoding cancer associated  
TITLE

AX367049 772 bp DNA linear PAT 16-FEB-2002  
Sequence 8 from Patent WO0147959.

Pred. No. is the number of results predicted by chance to have a

antigens, the antigens per se, and uses thereof  
Patent: WO 0147959-A 8 05-JUL-2001;  
LUDWIG INSTITUTE FOR CANCER RESEARCH (US); MEMORIAL  
SLOAN-KETTERING CANCER CENTER (US); Cornell Research Foundation  
(US)

FEATURES  
source Location/Qualifiers  
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Query Match 99.7%; Score 770; DB 6; Length 772;  
Best Local Similarity 100.0%; Pred. No. 4.1e-184;  
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Db 121 AGCAGGCTCCATGGCCAGCGGTAGCGGAGCGTCCCGCGAGACCTCCCATGACC 180  
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Db 181 CCACGAGCGCTCTCTACTGGGAGATGATCCGCTGCGACCAACGAAATGCCCATCGAGTGT 240  
Qy 241 TCCGCTTCTCGTGTGTGAGTCTCAACCATAAACCAAGCGAGTGTGTCTGTTCAGAT 300  
Db 241 TCCGCTTCTCGTGTGTGAGTCTCAACCATAAACCAAGCGAGTGTGTCTGTTCAGAT 300  
Qy 301 GCCGGGAGAAACCAATGGGCAAGCCCTTGAGAGTCCAGAGGAGGAGGAGGAGGAGGAGG 360  
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Qy 361 ACAGGTAGTTGGGAGACATGCGTCTAATAGTGGAGAGAAACAAATAGCCAGTGTGTGA 420  
Db 361 ACAGGTAGTTGGGAGACATGCGTCTAATAGTGGAGAGAAACAAATAGCCAGTGTGTGA 420  
Qy 421 TTACATTGCCACCTTCTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 480  
Db 421 TTACATTGCCACCTTCTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 480  
Qy 481 GTTAGAGCGCGGCGCGGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 540

RESULT 2  
AF149724 772 bp mRNA linear PRI 10-DEC-2001  
LOCUS AF149724  
DEFINITION Homo sapiens INGI-like tumor suppressor protein mRNA, complete cds.

AF149724  
AF149724.1 GI:8131966  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 772)  
Jager,D., Stockert,E., Scanlan,M.J., Gure,A.O., Jager,E., Knuth,A.,  
Old,L.J. and Chen,Y.T.  
Cancer-testis antigens and INGI tumor suppressor gene product are  
transcripts and a homologue gene  
Cancer Res. 59 (24), 6197-6204 (1999) 12/99  
20090239  
PUBMED 10626813  
REFERENCE 2 (bases 1 to 772)  
Jaeger,D.  
Direct Submission  
Submitted (10-MAY-1999) Pathology, Cornell University, 1300 York  
Avenue, New York, NY 10021, USA  
Location/Qualifiers  
1. 772  
/organism="Homo sapiens"  
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204..332  
CDS  
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/protein\_id="AAF73156.1"  
/db\_xref="GI:8131967"  
/translation="MIRCDNECPIEWFRFSCVSLNHKPKWYKWCRCRGRKNDGSP"

Query Match 99.7%; Score 770; DB 9; Length 772;  
Best Local Similarity 100.0%; Pred. No. 4.1e-184;  
Matches 772; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGCGTTCTCGGCGGAGCGGACCACTAGACCGGTGAGACCGCTCCAGCAACCGCGA 60  
Db 1 AAGCGTTCTCGGCGGAGCGGACCACTAGACCGGTGAGACCGCTCCAGCAACCGCGA 60  
Qy 61 CCCACGACGAGTCACTTCGGGCGACCGCCCAAGGAGAGAAAGCCAGACCTCTAAGAAGA 120  
Db 61 CCCACGACGAGTCACTTCGGGCGACCGCCCAAGGAGAGAAAGCCAGACCTCTAAGAAGA 120  
Qy 121 AGCAGGCTCCATGGCCAGCGGTAGCGGAGCGTCCCGCGAGACCTCCCATGACC 180  
Db 121 AGCAGGCTCCATGGCCAGCGGTAGCGGAGCGTCCCGCGAGACCTCCCATGACC 180  
Qy 181 CCACGAGCGCTCTCTACTGGGAGATGATCCGCTGCGACCAACGAAATGCCCATCGAGTGT 240  
Db 181 CCACGAGCGCTCTCTACTGGGAGATGATCCGCTGCGACCAACGAAATGCCCATCGAGTGT 240  
Qy 241 TCCGCTTCTCGTGTGTGAGTCTCAACCATAAACCAAGCGAGTGTGTCTGTTCAGAT 300  
Db 241 TCCGCTTCTCGTGTGTGAGTCTCAACCATAAACCAAGCGAGTGTGTCTGTTCAGAT 300  
Qy 301 GCCGGGAGAAACCAATGGGCAAGCCCTTGAGAGTCCAGAGGAGGAGGAGGAGGAGGAGG 360  
Db 301 GCCGGGAGAAACCAATGGGCAAGCCCTTGAGAGTCCAGAGGAGGAGGAGGAGGAGGAGG 360  
Qy 361 ACAGGTAGTTGGGAGACATGCGTCTAATAGTGGAGAGAAACAAATAGCCAGTGTGTGA 420  
Db 361 ACAGGTAGTTGGGAGACATGCGTCTAATAGTGGAGAGAAACAAATAGCCAGTGTGTGA 420  
Qy 421 TTACATTGCCACCTTCTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 480  
Db 421 TTACATTGCCACCTTCTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 480  
Qy 481 GTTAGAGCGCGGCGCGGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 540



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Db      481 GTTAGAGCGCGGGGGTGGCTCAGCCTGTGTAATCCACGACTTTGGGAGCGCGAGCGG 540
Qy      541 GTCGGATCAGAGGTGAGGATCGAGACCATCTGCTTAACAGGTGAAACCCGCTTC 600
Db      541 GTCGGATCAGAGGTGAGGATCGAGACCATCTGCTTAACAGGTGAAACCCGCTTC 600
Qy      601 TACTAAAAATTCAAAAAATTTAGCTGGCGTGGTGGCGGCGCTGTAGTCCAGCT 660
Db      601 TACTAAAAATTCAAAAAATTTAGCTGGCGTGGTGGCGGCGCTGTAGTCCAGCT 660
Qy      661 ATTGGGAGGCTGAGGAGAGAGATGCGNTGAACCTGGGAGGTGGAGCTTGCAATGAGCC 720
Db      661 ATTGGGAGGCTGAGGAGAGAGATGCGNTGAACCTGGGAGGTGGAGCTTGCAATGAGCC 720
Qy      721 AAGTCCGGCAGCTGCACTCCAGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 772
Db      721 AAGTCCGGCAGCTGCACTCCAGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 772

RESULT 3
LOCUS   AL159989                      86703 bp    DNA        linear    HTG 10-JUL-2001
DEFINITION Homo sapiens chromosome X clone RP4-583H20 map q13.1-13.3, 13
unordered pieces.
ACCESSION AL159989
VERSION   AL159989.5 GI:9926479
KEYWORDS  HTG; HTGS PHASE1; HTGS_CANCELLED.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS   Mclay, K.
TITLE     Direct Submission
JOURNAL   Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
          CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
          requests: clonerequest@sanger.ac.uk
          On Aug 25, 2000 this sequence version replaced gi:9212671.
          ----- Genome Center
          Center: Sanger Centre
          Center code: SC
          Web site: http://www.sanger.ac.uk
          Contact: humquery@sanger.ac.uk
          ----- Project Information
          Center project name: dj583H20
          ----- Summary Statistics
          Sequencing program: XGAP4; version 4.5
          Sequencing vector: plasmid; 108752; 100% of reads
          Chemistry: Dye-terminator Big Dye; 100% of reads
          Consensus quality: 79403 bases at least Q40
          Consensus quality: 82568 bases at least Q30
          Consensus quality: 84293 bases at least Q20
          Insert size: 8503; sum-of-contigs
          Quality coverage: 3.21x in Q20 bases; sum-of-contigs Quality
          coverage: 2.47x in Q20 bases; agarose-fp
          -----
          * NOTE: This is a 'working draft' sequence. It currently
          * consists of 13 contigs. The true order of the pieces
          * is not known and their order in this sequence record is
          * arbitrary. Gaps between the contigs are represented as
          * runs of N, but the exact sizes of the gaps are unknown.
          * This record will be updated with the finished sequence
          * as soon as it is available and the accession number will
          * be preserved.
          *
          * 1 2642: contig of 2642 bp in length
          * 2643 2742: gap of 100 bp
          * 2743 8583: contig of 5841 bp in length
          * 8584 8683: gap of 100 bp
          * 8684 25159: contig of 16476 bp in length
          * 25160 25259: gap of 100 bp
          * 25260 30489: contig of 5230 bp in length
          * 30490 30589: gap of 100 bp

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* 30590 35034: contig of 4445 bp in length
* 35035 35134: gap of 100 bp
* 35135 39882: contig of 4748 bp in length
* 39883 51110: contig of 11128 bp in length
* 51111 51210: gap of 100 bp
* 51211 60581: contig of 9371 bp in length
* 60582 64492: contig of 3811 bp in length
* 64493 66337: contig of 2045 bp in length
* 66338 70822: contig of 4085 bp in length
* 70823 70922: gap of 100 bp
* 70923 83280: contig of 12358 bp in length
* 83281 83380: gap of 100 bp
* 83381 86703: contig of 3323 bp in length.

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                        /mol_type="genomic DNA"
                        /db_xref="taxon:9606"
                        /chromosome="X"
                        /map="q13.1-13.3"
                        /clone="RP4-583H20"
                        /clone_lib="RPCI-4"
     misc_feature      1..2642
                        /note="assembly_fragment:00012"
                        clone_end:SP6
                        vector_side:left
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                        /note="assembly_fragment:00118"
                        fragment_chain:1
     misc_feature      8684..25159
                        /note="assembly_fragment:00314"
                        fragment_chain:1
     misc_feature      25260..30489
                        /note="assembly_fragment:00281"
                        fragment_chain:1
     misc_feature      30590..35034
                        /note="assembly_fragment:00230"
                        fragment_chain:2
     misc_feature      35135..39882
                        /note="assembly_fragment:00673"
                        fragment_chain:2
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                        /note="assembly_fragment:00593"
                        fragment_chain:3
     misc_feature      51211..60581
                        /note="assembly_fragment:00751"
                        fragment_chain:3
     misc_feature      60682..64492
                        /note="assembly_fragment:00020"
     misc_feature      64593..66337
                        /note="assembly_fragment:00523"
     misc_feature      66738..70822
                        /note="assembly_fragment:00675"
     misc_feature      70923..83280
                        /note="assembly_fragment:00768"
     misc_feature      83381..86703
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ORIGIN
Query Match          97.8%; Score 754.8; DB 2; Length 86703;
Best Local Similarity 99.4%; Pred. No. 4.1e-180;
Matches 767; Conservative 0; Mismatches 41; Indels 1; Gaps 1;
Qy      1 AAAGCGTTCTCGGCGCAGCGCAACACTAGAACGCTGACGACCGGCAACCGCGA 60
Db      22733 AAAGCGTTCTCGGCGCAGCGCAACACTAGAACGCTGACGACCGGCAACCGCGA 22792
Qy      61 CCACACGACGCTACCTCGGCGCAGCGCCCAAGAGAGAAAGCCAGACCTCTAAGAAGA 120

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121	QY	ACGAGGCTCAATGCGCAAGCGTAGCGGAGCGCTCCCGCGCAGACCTCCCAATCGACC	180
22852	Db	ACGACAGCTCCATGCGCAAGCGGTAGCGCAGCGCTCCCGCGAGACCTCCCAATCGACC	22911
181	QY	CCAGCGAGCCCTCTACTGGGAGATGATCCGCTGCGACAACGAATGCCATCGAGTGGT	240
22912	Db	CCAGCGAGCCCTCTACTGGGAGATGATCCGCTGCGACAACGAATGCCATCGAGTGGT	22971
241	QY	TCGCGTCTCGTGCTGAGTCTCAACCATTAACCAAGCGAAGTGGTACTGTTCCAGAT	300
22972	Db	TCGCGTCTCGTGCTGAGTCTCAACCATTAACCAAGCGAAGTGGTACTGTTCCAGAT	23031
301	QY	GCGGGGAAAAGAACGATGGCGAAAGCCCTTGAAAGTCCAGAAAAAAACAGGCTTATA	360
23032	Db	GCGGGGAAAAGAACGATGGCGAAAGCCCTTGAAAGTCCAGAAAAAAACAGGCTTATA	23091
361	QY	ACAGGTAGTTCGGGACATGCGCTCTAATAGTCAGGAGACAAAAAAGCCAGTGTGTA	420
23092	Db	ACAGGTAGTTCGGGACATGCGCTCTAATAGTCAGGAGACAAAAAAGCCAGTGTGTA	23151
421	QY	TTACATTGGCACCTTTGCTGAGGTGCGAAGCTGTAAATGTATATATTTTAAAGAATGTT	480
23152	Db	TTACATTGGCACCTTTGCTGAGGTGCGAAGCTGTAAATGTATATATTTTAAAGAATGTT	23211
481	QY	GTTAGAGGCGGGCGGGTGGCTCAGCGCTGTAAATCCGACGACTTGGGAGCGCGAGCG	540
23212	Db	GTTAGAGGCGGGCGGGTGGCTCAGCGCTGTAAATCCGACGACTTGGGAGCGCGAGCG	23271
541	QY	GTCCGATCAGAGGTACAGAGATCGAGACCATCTGGCTTAAACCGGTGAACCCCGTCTC	600
23272	Db	GTCCGATCAGAGGTACAGAGATCGAGACCATCTGGCTTAAACCGGTGAACCCCGTCTC	23331
601	QY	TACTAAAAATTCAAAAAAAATTTAGCTGGGCGTGTGGCGGGCGCTGTGTAGTCCAGCT	660
23332	Db	TACTAAAAATTCAAAAAAAATTTAGCTGGGCGTGTGGCGGGCGCTGTGTAGTCCAGCT	23391
661	QY	ATTTCGGAGGCTCAGCGCAGAGATGGCGNTGAACCTGGGAGGTGGAGCTTGCAATGAGCC	720
23392	Db	ATTTCGGAGGCTCAGCGCAGAGATGGCGNTGAACCTGGGAGGTGGAGCTTGCAATGAGCC	23451
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23452	Db	AAGGTCCGCGCACTGCACTCCAGCTCCGGCGCAGACGAGCGAGACTCCATCTCT	23503

[illegible]

problem with AL590763 and the overlapping accession BX276092.

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 /organism="Homo sapiens"  
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 /db\_xref="taxon:9606"  
 /chromosome="X"  
 /map="Xq13.1"  
 /clone="PAC RPC1-1 56F19"  
 /clone\_lib="RPC11,3-5 Human PAC library, originating  
 institute: Roswell Park Cancer Institute, Creator: Pieter  
 de Jong, P. Ioannou"  
 /note="region between markers GUB1-DX8559"

ORIGIN

Query Match 97.8%; Score 754.8; DB 9; Length 248968;  
 Best Local Similarity 99.4%; Pred. No. 4.5e-180;  
 Matches 767; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 AAAGGTTCTCGGGCAGCGGCACACTAGAACCGTGTAGAACGGCTCCAGCAACCGCGA 60  
 DB 34025 AAAGGTTCTCGGGCAGCGGCACACTAGAACCGTGTAGAACGGCTCCAGCAACCGCGA 33966

QY 61 CCCACGACGAGCTCACCTCGGGCAGCGCCCAAGGAGAGAAAGCCCAAGACCTCTAAGAAGA 120  
 DB 33965 -CCACGACGAGCTCACCTCGGGCAGCGCCCAAGGAGAGAAAGCCCAAGACCTCTAAGAAGA 33907

QY 121 AGCAGGGTCCATGGCCAAAGCGTAGCGCAGCGCTCCCGCAGACCTCCCCATCGACC 180  
 DB 33906 AGCAGAGTCCATGGCCAAAGCGTAGCGCAGCGCTCCCGCAGACCTCCCCATCGACC 33847

QY 181 CCACGACGCCCTCTTACTGGAGATGATCGCTGGCAACGAATGCCCATCGAGTGGT 240  
 DB 33846 CCACGAGGCCCTCTTACTGGAGATGATCGCTGGCAACGAATGCCCATCGAGTGGT 33787

QY 241 TCGCTTCTCGTGTGTAGTCTCAACCATAAACCAAGCGCAAGTGGTACTGTTCCAGAT 300  
 DB 33786 TCGCTTCTCGTGTGTAGTCTCAACCATAAACCAAGCGCAAGTGGTACTGTTCCAGAT 33727

QY 301 GCGGGGAAAGAACGATCGGCAAGGCCCTTGAGAACTCCAGAAAAAAGACAGGGCTTATA 360  
 DB 33726 GCGGGGAAAGAACGATCGGCAAGGCCCTTGAGAACTCCAGAAAAAAGACAGGGCTTATA 33667

QY 361 ACAGTAGTTGGGACATGCGTCTAATAGTAGGAGAACAAATAAGCCAGTGTCTTGA 420  
 DB 33666 ACAGTAGTTGGGACATGCGTCTAATAGTAGGAGAACAAATAAGCCAGTGTCTTGA 33607

QY 421 TTACATATGCACCTTTGCTGAGGTGCAGGAAGTGTAAATGTATATTTTAAAGAAATGTT 480  
 DB 33606 TTACATATGCACCTTTGCTGAGGTGCAGGAAGTGTAAATGTATATTTTAAAGAAATGTT 33547

QY 481 GTTAGAGCGCGGCGCGTGGCTACGCGCTTAATCCAGACACTTTGGGAGGCGCGGCG 540  
 DB 33546 GTTAGAGCGCGGCGCGTGGCTACGCGCTTAATCCAGACACTTTGGGAGGCGCGGCG 33487

QY 541 GTCCGATACAGAGGTTCAGAGATCGAGACCATCTGGCTAACCGGTGAACCCCGTCTC 600  
 DB 33486 GTCCGATACAGAGGTTCAGAGATCGAGACCATCTGGCTAACCGGTGAACCCCGTCTC 33427

QY 601 TACTAAAAATTCAAAAAAAATTAGCTGGCGCGTGGTGGCGGCGCGCTGTAGTCCACGCT 660  
 DB 33426 TACTAAAAATTCAAAAAAAATTAGCTGGCGCGTGGTGGCGGCGCGCTGTAGTCCACGCT 33367

QY 661 ATTCCGGAGGCTGAGGCAGAGAAATGCGNTGAACCTGGAGGTGGAGCTTGCATGAGCC 720  
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QY 721 AAGGTCCGCCACTGCACTCCAGCGCTGGCGCAGAGCGAGACCTCATCTTA 772  
 DB 33306 AAGGTCCGCCACTGCACTCCAGCGCTGGCGCAGAGCGAGACCTCATCTCA 33255

RESULT 5

AL157820 97465 bp DNA linear PRI 04-JAN-2002  
 LOCUS Human DNA sequence from clone RP11-8D7 on chromosome 13, complete  
 DEFINITION sequence.  
 ACCESSION AL157820  
 VERSION AL157820.27 GI:118072469  
 KEYWORDS HTG.  
 SOURCE Homo sapiens (human).  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 97465)  
 Smith, M.  
 Direct Submission  
 Submitted (04-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,  
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
 humquary@sanger.ac.uk  
 Cloned request: clonerequest@sanger.ac.uk  
 On Jan 6, 2002 this sequence version replaced gi:11754265.  
 During sequence assembly data is compared from overlapping clones.  
 Where differences are found these are annotated as variations  
 together with a note of the overlapping clone name. Note that the  
 variation annotation may not be found in the sequence submission  
 corresponding to the overlapping clone, as we submit sequences with  
 only a small overlap as described above.  
 This sequence was finished as follows unless otherwise noted: all  
 regions were either double-stranded or sequenced with an alternate  
 chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by at least  
 one plasmid subclone or more than one M13 subclone; and the  
 assembly was confirmed by restriction digest. The following  
 abbreviations are used to associate primary accession numbers given  
 in the feature table with their source databases: Em, EMBL; SW,  
 SWISSPROT; Tr, TrEMBL; Wp, WORMPEP; Information on the WORMPEP  
 database can be found at  
 http://www.sanger.ac.uk/Projects/C\_elegans/wormpep  
 This sequence was generated from part of bacterial clone contigs of human  
 chromosome 13, constructed by the Sanger Centre Chromosome 13  
 Mapping Group. Further information can be found at  
 http://www.sanger.ac.uk/HGP/Chr13  
 RP11-8D7 is from the library RPCI-11.1 constructed by the group of  
 Pieter de Jong. For further details see  
 http://www.chori.org/bacpac/home.htm  
 VECTOR: pBAC3.6  
 IMPORTANT: This sequence is not the entire insert of clone RP11-8D7  
 It may be shorter because we sequence overlapping sections only  
 once, except for a short overlap.  
 The true right end of clone RP11-8D7 is at 97465 in this sequence.  
 The true left end of clone RP11-120J20 is at 68161 in this  
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 /note="Single clone region. Assembly confirmed by  
 restriction digest data."  
 misc\_feature 51946..51960  
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 restriction digest data."  
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 Best Local Similarity 81.0%; Pred. NO. 2.2e-59;  
 Matches 423; Conservative 0; Mismatches 59; Indels 40; Gaps 7;  
 QY 2 AACGGTCTCGGGCGGACGACACTAGACCGTGAGAACGGTCCAGCACCGGAC 61  
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Db 57673 AAGCGCTCAGCGGCGGCGGCAACAAACGAGAACCGTGAGAACGCGTCCAGCAACCAAGA- 57731  
 QY 62 CCACGACGACGTCACTCTGGGCGACGCCCAAGAGAGAGAAAGCCCGACCTCTAGAGAA 121  
 |||||  
 Db 57732 CCACGACGACGCGGCGCTCGGGCACACCCAGGAGAGAGAGCCCAAGACCTCCAGAGAA 57791  
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 QY 122 GCAGGGCTCCATGGCCAAAGGGGTAGCGGCGAGGCGCTCCCGCCGACAGACCTCCCATGACCC 181  
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 Db 57792 GAAGCGCTCCAGGCGCAAGGGGAGGAGGCGGTCCCTCCGACCTCCCATGACCC 57851  
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 QY 182 CAGCGAGCC-----CTCTACTGGGAGATGATCGGCTGCGA 57911  
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 Db 57852 CAACGAACCCACGTACTGTGTGTGCAACAGGTCTCTATGGGAGATGATCGGCTGCGA 57911  
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 QY 218 CA---ACGAATCCCCCATCGAGTGTTCGGCTTCCTCGTGTGTGAGTCTCAACCAATAAAC 274  
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 Db 57912 CAACGAGAGTGCCTCATCGAGTGTTCACATTCCTCGTGTGGGGCTCAATCATATAAAC 57971  
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 QY 275 AAAGCGCAAGTGGTACTGTTCAGATGCGGGGAAAGAACG-----ATGGGCAAGC 326  
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 Db 57972 CAAGGCGCAAGTGGTACTGTTCACAGTGCCTGGGGGAGAACGAGAAAGACATGGCAAGC 58031  
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 QY 327 CCTTGAGAGAGTCCAGAAAAAAGAGGGCTTATAACAGTAGTGTGGGAGCATGGCTCTA 386  
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 QY 387 ATAGTGAGGAGAACAAATAAGCAGTGTGTGATTAATCCACCTTCTGAGGTGC 446  
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 Db 58090 GT-GTGAGGAGGACAAATAAAC--GTGTATTATTATCATCTGCTCCTTTGTGAGGTGC 58147  
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 QY 447 AGGAGTGTAAATGTATATTTTAAAGATGTTGTAGAGG 488  
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 Db 58148 AGGAGTGTAAATGTATATTTTAAAGATGTTGTAGAGG 58189  
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 LOCUS Homo sapiens clone RP11-2207, WORKING DRAFT SEQUENCE, 19 unordered  
 DEFINITION pieces.  
 ACCESSION AC013713  
 VERSION AC013713.5 GI:10047774  
 HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 159983)  
 Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
 Homo sapiens, clone RP11-2207  
 Unpublished  
 2 (bases 1 to 159983)  
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,  
 Baldwin, J., Barna, N., Beckerly, R., Boguslavskiy, L., Boukhgalter, B.,  
 Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,  
 Cooke, P., DeArrellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,  
 Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D.,  
 Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,  
 Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,  
 Lecheczy, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,  
 McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J.,  
 Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,  
 Peterson, K., Pollara, V., Riley, K., Roy, A., Santos, R., Severy, P.,  
 Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,  
 Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,  
 Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (13-NOV-1999) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Sep 10, 2000 this sequence version replaced gi:7280307.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence.submissions@genome.wi.mit.edu  
----- Project Information  
Center project name: L4156  
Center clone name: 22 O 7  
----- Summary Statistics  
Sequencing vector: M13; M77815; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.960731  
Consensus quality: 151270 bases at least Q40  
Consensus quality: 155604 bases at least Q30  
Consensus quality: 157124 bases at least Q20  
Insert size: 150000; agarose-fp  
Quality coverage: 4.7 in Q20 bases; agarose-fp  
Quality coverage: 4.7 in Q20 bases; sum-of-contigs

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 19 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 8082: contig of 8082 bp in length  
\* 8083 8182: gap of 100 bp  
\* 8183 11889: contig of 3707 bp in length  
\* 11890 11989: gap of 100 bp  
\* 11990 15437: contig of 3448 bp in length  
\* 15438 15537: gap of 100 bp  
\* 15538 19542: contig of 4005 bp in length  
\* 19543 19642: gap of 100 bp  
\* 19643 24550: contig of 4908 bp in length  
\* 24551 24650: gap of 100 bp  
\* 24651 28406: contig of 3756 bp in length  
\* 28407 28507: gap of 100 bp  
\* 28508 32425: contig of 3819 bp in length  
\* 32426 35721: contig of 3296 bp in length  
\* 35722 35821: gap of 100 bp  
\* 35822 40730: contig of 4909 bp in length  
\* 40731 40830: gap of 100 bp  
\* 40831 46222: contig of 5392 bp in length  
\* 46223 46322: gap of 100 bp  
\* 46323 52597: contig of 6275 bp in length  
\* 52598 52697: gap of 100 bp  
\* 52698 57694: contig of 4937 bp in length  
\* 57695 57794: gap of 100 bp  
\* 57795 65743: contig of 7949 bp in length  
\* 65744 65844: gap of 100 bp  
\* 65844 72187: contig of 6344 bp in length  
\* 72188 72288: gap of 100 bp  
\* 72289 116109: contig of 43822 bp in length  
\* 116110 127751: contig of 11542 bp in length  
\* 127752 127851: gap of 100 bp  
\* 127852 140246: contig of 12395 bp in length  
\* 140247 140347: gap of 100 bp  
\* 140348 152625: contig of 12279 bp in length  
\* 152626 152725: gap of 100 bp  
\* 152726 159983: contig of 7258 bp in length.  
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Best Local Similarity 81.0%; Pred. No. 2.3e-59;  
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Db 149502 AAGCGCTCAOGCGCGCGAGCGCAACAACTAGAACCGTGGAGAACCGTCCAGCAACCGA- 149560  
QY 62 CCACGACGCTCACCTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 121  
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QY 122 GCAGGGCTCCATGCGCGCGAGCGTGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 181  
Db 149621 GAAGCGCTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 149680  
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QY 218 CA---ACGAATGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 274  
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QY 275 AAAGCGCGAGTGGTACTGTTCCAGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 326  
Db 149801 CAGCGCGCGAGTGGTACTGTTCCAGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 149860  
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Db 149919 GT-GTGGAGGAGCAAAATAAACC-GTGTATTTATTACATTCGCTTTGTTGAGGTGC 149976
QY 447 AGGAAGTGAATAATGTATATTTTAAAGAAATGTTGTTAGAGG 488
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RESULT 7
AF149722 AF149722 1074 bp mRNA linear PRI 05-MAR-2000
LOCUS Homo sapiens INGI tumor suppressor, variant B (ING1) mRNA, complete
DEFINITION cds.
ACCESSION AF149722
VERSION AF149722.1 GI:7158366
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1074)
AUTHORS Jager,D., Stockert,E., Scanlan,M.J., Gure,A.O., Jager,E., Knuth,A.,
Old,L.J. and Chen,Y.T.
TITLE Cancer-testis antigens and INGI tumor suppressor gene product are
breast cancer antigens: characterization of a tissue-specific INGI
transcripts and a homologue gene
Cancer Res. 59 (24), 6197-6204 (1999)
JOURNAL
MEDLINE 20090239
PUBMED 10626813
REFERENCE 2 (bases 1 to 1074)
AUTHORS Jager,D.
Direct Submission
TITLE Submitted (11-MAY-1999) Pathology, Cornell University, 1300 York
Avenue, New York, NY 10021, USA
JOURNAL
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Location/Qualifiers
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199..831
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Query Match 35.8%; Score 276; DB 9; Length 1074;
Best Local Similarity 80.8%; Pred. No. 4e-59;
Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;
QY 2 AAGCGTTCTCGCGGAGCGCAACAACTAGAACCGGTGAGAACCGTCCAGCAACCGCGAC 61
Db 433 AAGCGTCTACCGCGGAGCGCAACAACTAGAACCGGTGAGAACCGTCCAGCAACCGCA- 491
QY 62 CCACGACGACGTCACCTCGGGCAGCGCCCAAGGAGAGAAAGCCAGACCTCTAAGAAGAA 121
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218 CA---ACGAATGCCCATCGAGTGGTTCGGCTTCCTGTTGTGTGAGTCTCAACCATTAACC 274
672 CAACGACGAGTGCCTCCATCGAGTGGTTCCTCTTCGTGCGTGGGGCTCAATCATAAACC 731
275 AAAGCGCAAGTGTACTGTTCAGATGCCGGGAAGAACG-----ATGGGCAAAAGC 326
732 CAAGGGCAAGTGTACTGTCCCAAGTGCGGGGGAGAACGAGAGACCATGCAAAAGC 791
327 CTTGAGAGAGTCCAGAAACCAAGGCTTATAACAGGTAGTTTGGGAGCATCGCTCTA 386
792 CTTGAGAGAAATCCA--AAAAGAGAGGGCTTACACAGGTAGTTTGTGACAGGCGCGTG 849
387 ATAGTGGAGAGAACAAATATAGCCAGTGTGTGATTACATTCGCCACCTTTGCTGAGGTGC 446
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908 AAGGAGTGTAAATGTATATTTTAAAGAAATGTTAGAAAAGG 949

RESULT 8
AX367043 AX367043 1143 bp DNA linear PAT 16-FEB-2002
LOCUS Sequence 2 from Patent WO0147959.
DEFINITION AX367043
ACCESSION AX367043
VERSION AX367043.1 GI:18855268
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jager,D., Stockert,E., Scanlan,M., Knuth,A., Old,L., Gure,A. and
Chen,Y.T.
TITLE Isolated nucleic acid molecules encoding cancer associated
antigens, the antigens per se, and uses thereof
Patent: WO 0147959-A 2 05-JUL-2001;
LUDWIG-INSTITUT FÜR KREBLERFORSCHUNG (US); MEMORIAL
SLOAN-KETTERING CANCER CENTER (US); Cornell Research Foundation
(US)
FEATURES
Location/Qualifiers
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ORIGIN
Query Match 35.8%; Score 276; DB 6; Length 1143;
Best Local Similarity 80.8%; Pred. No. 4e-59;
Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;
QY 2 AAGCGTTCTCGCGGAGCGCAACAACTAGAACCGGTGAGAACCGTCCAGCAACCGCGAC 61
Db 502 AAGCGTCTACCGCGGAGCGCAACAACTAGAACCGGTGAGAACCGTCCAGCAACCGCA- 560
QY 62 CCACGACGACGTCACCTCGGGCAGCGCCCAAGGAGAGAAAGCCAGACCTCTAAGAAGAA 121
Db 561 CCACGACGACGCGGCTCGGGCAGCACCCACGAGAGAGAGGACCAAGACCTCCAGAGAA 620
QY 122 GCAGGCGCTCCATGCGCAAGCGGTAGCGGAGCGGTCCCGCGAGACCTCCCATCGACCC 181
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801 CAAGGCAAGTGTGTCTTCCAGATCCCGGGGGAGAACGAGAACCAATGACAAAGC 860  
327 CTTTGAAGTCCAGAAAAAACAAGGGCTTATAACAGGTAGTTTGGGGACATGCGTCTA 386  
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387 ATAGTAGAGCAACAAATAGCCAGTGTGTGATACATTCGCACTTTGCTGAGGTGC 446  
919 GT-GTGAGGAGGACAAATAAAC-GTGTATTTATTACATTCGCTGCTTTGTTGAGGTGC 976  
447 AGGAAGTGTAAATGTATATTTTAAAGATGTTGTAGAGG 488  
977 AAGGAGTGTAAATGTATATTTTAAAGATGTTAGAAAGG 1018

RESULT 9  
AF149723 1189 bp mRNA linear PRI 05-MAR-2000  
LOCUS Homo sapiens INGI tumor suppressor, variant C (ING1) mRNA, complete cds.  
ACCESSION AF149723  
VERSION AF149723.1 GI:7159368  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE  
AUTHORS Jager,D., Stockert,E., Scanlan,M.J., Gure,A.O., Jager,E., Knuth,A., Old,L.J. and Chen,Y.T.  
TITLE Cancer-testis antigens and INGI tumor suppressor gene product are breast cancer antigens: characterization of tissue-specific INGI transcripts and a homologue gene  
JOURNAL Cancer Res. 59 (24), 6197-6204 (1999).  
MEDLINE 20090239  
PUBMED 10826813  
REFERENCE  
AUTHORS Jager,D.  
TITLE Direct Submission  
JOURNAL Submitted (11-MAY-1999) Pathology, Cornell University, 1300 York Avenue, New York, NY 10021, USA

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ORIGIN  
Query Match 35.8%; Score 276; DB 9; Length 1189;  
Best Local Similarity 80.8%; Pred. No. 4e-59;  
Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;

Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;  
QY 2 AAGGTTCTCGCGCGCAGCGCAACAATAAGACCGTGAACCGCTCCAGCAACCGCAG 61  
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QY 122 GCAGGCGCTTCAATGCGCAAGCGGTAGCGCGCAGCGCTCCCGCGCAGACCTCCCATCGACCC 181  
DB 667 GAAGCGCTTCAAGCGCAAGCGGAGCGAGAGCGCTCCCTCGCGACCTCCCATCGACCC 726  
QY 182 CAGCGAGCC-----CTCTACTGGGAGATGATCCGCTGGGA 217  
DB 727 CAACGAACCCACGACTGTCTGTGCAACAGGTCTCTATGGGAGATGATCGGCTGCGA 786  
QY 218 CA---ACGAATGCCCATCGAGTGGTTCCTCGTGTGTGAGTCTCAACATAAAC 274  
DB 787 CACGACGAGTGGCCCATCGAGTGGTTCCTCGTGTGTGAGTCTCAACATAAAC 846  
QY 275 AAAGCGCAAGTGTGTCTTCCAGATCCCGGGGAAGAAGC-----ATGGGCAAGC 326  
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QY 327 CTTTGAAGTCCAGAAAAAACAAGGGCTTATAACAGGTAGTTTGGGGACATCGCTCTA 386  
DB 907 CTTGAGAGAAATCCA--AAAAGAGAGGGCTTACACAGGTAGTTTGGGACAGCGCTG 964  
QY 387 ATAGTAGAGCAACAAATAGCCAGTGTGTGATACATTCGCACTTTGCTGAGGTGC 446  
DB 965 GT-GTGAGGAGGACAAATAAAC-GTGTATTTATTACATTCGCTGCTTTGTTGAGGTGC 1022  
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DB 1023 AAGGAGTGTAAATGTATATTTTAAAGATGTTAGAAAGG 1064

RESULT 10  
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LOCUS Sequence 1 from Patent WO0147959.  
DEFINITION AX367042  
ACCESSION AX367042  
VERSION AX367042.1 GI:18855267  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE  
AUTHORS Jager,D., Stockert,E., Scanlan,M., Knuth,A., Old,L., Gure,A. and Chen,Y.T.  
TITLE Isolated nucleic acid molecules encoding cancer associated antigens, the antigens per se, and uses thereof  
JOURNAL Patent: WO 0147959-A 1 05-JUL-2001.  
LUDWIG INSTITUTE FOR CANCER RESEARCH (US); MEMORIAL SLOAN-KETTERING CANCER CENTER (US); Cornell Research Foundation (US)  
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ORIGIN  
Query Match 35.8%; Score 276; DB 6; Length 1533;  
Best Local Similarity 80.8%; Pred. No. 4.1e-59;  
Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;

QY 2 AAGCGTTCTCGCGCGCAGCGCAACAACGAGAACCGTGAACCGCTCCAGCAACCGCAG 61  
DB 892 AAGCGCTACGCGCGCAGCGCAACAACGAGAACCGTGAACCGCTCCAGCAACCGCA 950

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RESULT 11
AF149721
LOCUS
DEFINITION
Homo sapiens INGI1 tumor suppressor, variant A (ING1) mRNA, complete cds.
AF149721
ACCESSION
AF149721
VERSION
AF149721.1
KEYWORDS
GI:7158364
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1533)
AUTHORS
Jaeger,D., Stockert,E., Scanlan,M.J., Gure,A.O., Jager,E., Knuth,A., Old,L.J. and Chen,Y.T.
TITLE
Cancer-testis antigens and INGI1 tumor suppressor gene product are breast cancer antigens: characterization of tissue-specific INGI1 transcripts and a homologue gene
JOURNAL
Cancer Res. 59 (24), 6197-6204 (1999)
MEDLINE
20090239
PUBMED
10626813
REFERENCE
2 (bases 1 to 1533)
AUTHORS
Jaeger,D.
TITLE
Direct Submission
JOURNAL
Submitted (11-MAY-1999) Pathology, Cornell University, 1300 York Avenue, New York, NY 10021, USA
FEATURES
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gene
CDS

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QY	2	AAGCGTTCTTCGGCGCAGCGCAACAACTAGAACCGTGTGAGAACGCCTCCAGCAACCGCGAC	61		
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QY	62	CACAGCAGCATGTCACTCTGGGCACGCCCAAGAGAGAAAGCCCAGACTCTTAAGAGAAA	121		
Db	951	CCACGACGACGGCGCTCTGGGCACACCACCAAGAGAGAAAGGCCAAGACCTCCAAGAAGAA	1010		
QY	122	CGAGGGCTCCATGGCCAAAGGCGTAGCGGCAGCGCTCCCCCGCAGACCTCCCCCATGCACCC	181		
Db	1011	GAAAGCGCTCCAGGCGCAAGCGCGAGCGGCGTCCCTCGCGACCTCCCATGCACCC	1070		
QY	182	CAGCGAGGC-----CTCTACTGGGAGATGATCCGCTGCGA	217		
Db	1071	CAACGAACCCAGCTACTGTCTGTGCAACCCAGGCTCTCCTATGGGAGATGATCGGCTGCGA	1130		
QY	218	CA---ACGAATCCCATCGAGTGGTTCGGCTTCTCGTGTGAGTCTCAACATAAAACC	274		
Db	1131	CAACGACGAGTGCCTCATCGAGTGGTTCACATTCTCGTGGTGGGCTCAATCATPAAACC	1190		
QY	275	AAAGCGCAAGTGGTACTGTTCCAGATGCCGGGAAAGAACG-----ATGGGCAAAGC	326		
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QY	327	CTTTCAGAAAGTCCAGAAAAAAACAGGGCTTATAACAGGTAGTTTGGGACATGCGTCTA	386		
Db	1251	CCTGAGAAATCCA--AAAAAGAGAGGGCTTACAACAGGTAGTTTGTGACAGGGCGCTG	1308		
QY	387	ATAGTGAGGAGAAACAAATAACCCAGTGTGTGATACATTCACCACCTTGTCTGAGGTGC	446		
Db	1309	GT-GTGAGGAGACAAATAAAC--GTGTATTATTACATTCTGCTTTGTGTGAGGTGC	1366		
QY	447	AGGAAGTGTAAATGTATATTTTTTAAAGAAATGTTGTAGAGG	488		
Db	1367	AAGGAGTGTAAATGTATATTTTTTAAAGAAATGTTGAAAGG	1408		
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LOCUS		1902 bp	DNA	linear	PAT 31-AUG-2000
DEFINITION	Sequence 1 from patent US 5965398.				
ACCESSION	AR079046				
VERSION	AR079046.1	GI:10005792			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 1902)				
AUTHORS	Garkavtsev,I.I. and Riabowol,K.				
TITLE	DNA sequence encoding a tumor suppressor gene				
JOURNAL	Patent: US 5965398-A 1 12-OCT-1999;				
FEATURES	Location/Qualifiers				
source	1..1902				
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ORIGIN					
Query Match	35.8%;	Score 276;	DB 6;	Length 1902;	



Best Local Similarity	80.8%;	Pred. No. 4.2e-59;
Matches 422;	Conservative	0; Mismatches 60; Indels 40; Gaps 7;

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343	AAGCGCTCAGCGCGCAGCGCAACA	ACGAAACCGTTCAGCAACCGCA	401
62	CCACGACGACGTCACCTCGCGCAG	CGCCCAAGAGAGAAAGCCAGACTCT	121
402	CCACGACGACGCGCGCTCGGCGACA	CCCAAGAGAGAAAGCCCAAGACTCT	461
122	GCAGGGCTCATGCGCAAGCGGTAG	CGGCGAGCGGCTCCCGCAGACCTTCC	181
462	GAACGCGTCCAAAGCCAAAGCGAG	CGAGCGCTCCCTGCGCACTCCCATCG	521
182	CAGGCGAGCC-----	CTCCTACTCGGAGATGATCCGCTCGCA	217
522	CAACGAACCCACGCTACTGTC	GTGCAACAGGCTCTCTATCGGGAATG	581
218	CA----AGATGCCCATCAGATGGTT	TCGCTTCGTGTGAGCTCAACCAATAACC	274
582	CAACGACGAGTGCCTCATCGATGGT	TCCACTCTCGTGTGGGGCTCAATCATAAACC	641
275	AAAGCGCAAGTGTACTGTCTCCAGAT	GCAGATGCCGGGGAAGAAACG-----	326
642	CAGGGCAAGTGGTACTGTCTCCAA	GTGTCGGGGGAGACGAGAAGACCAT	701
327	CCTTGAGAGTCCAGAAAAAACAAG	CGGCTTATAACAGGTAGTTTGGGGA	386
702	CCTGGAGAAATCCA--	AAAAAGAGAGCGGCTTACACAGGT	759
387	ATAGTGAGGAGAACAAATAAAG	CCAGTGTGTGATTACATTGCCACCTT	446
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818	AAGAGGTGTAAATGTATATTTTAA	GAAGTGTGTAGAAAGG	859

RESULT 13  
AR087457  
LOCUS AR087457 1902 bp DNA  
DEFINITION Sequence 1 from patent US 5966078.  
ACCESSION AR087457  
VERSION AR087457.1 GI:10014220  
linear PAT 07-SEP-2000

KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES

Unknown.  
Unknown.  
unclassified.  
1 (bases 1 to 1902)  
1 (bases 1 to 1902)  
Garkavtsev, I. and Riabowol, K.  
DNA sequence encoding the tumor suppressor gene INGI  
Patent: US 5986078-A 1 16-NOV-1999;  
Location/Qualifiers  
1..1902  
source

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ORIGIN
Query Match      35.8%; Score 276; DB 6; Length 1902;
Best Local Similarity 80.8%; Pred. No. 4.2e-59;
Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;
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ACCESSION		AR110646.1	GI:12827460
VERSION			
KEYWORDS		Unknown.	
SOURCE		Unknown.	
ORGANISM		Unclassified.	
REFERENCE		1 (bases 1 to 1902)	
AUTHORS		Garkavtsev, I., Riabowol, K. and Gudkov, A.	
TITLE		DNA sequence encoding the tumor suppressor gene INGI	
JOURNAL		Patent: US 6117633-A 1 12-SEP-2000;	
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Best Local Similarity		80.8%; Pred. No. 4.2e-59;	
Matches 422; Conservative		0; Mismatches 60; Indels 40; Gaps 7;	
QY	2	AAGCGTTCTCGGGCAGCGCAACACTAGAACCGTGTAGAACGGCTCAGCAACCGCGAC	61
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QY	62	CCAGCAGACGTCACCTCGGGCAGCGCCCAAGGAGAGAAAGCCAGACCTCTTAAGAGAA	121
Db	402	CCA-CAGCAGCGGGCTCGGGCAGCCACCCAGAGAGAGAAAGCCAGACCTTCAAGAGAA	461
QY	122	GCAGGGTCCATATGCCAAGCGTTCAGCGGAGCGGCTCCCGCGAGACTTCCCATTCGACC	181
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QY 387 ATAGTGAGGAGAACCAAAATTAAGCCAGTGTGTGATTACATTGCCACCTTTGCTGAGGTGC 446  
Db 760 GT-GTGAGGAGGACAAATTAACCC-GTGTATTATTACATTGCTGCCCTTTGTTGAGGTGC 817  
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LOCUS 1902 bp DNA linear PAT 08-AUG-2001

DEFINITION Sequence 1 from patent US 6238918.

ACCESSION AR154563

VERSION AR154563.1 GI:15122616

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1902)

AUTHORS Garkavtsev, I. and Riabowol, K.

TITLE DNA sequence encoding the tumor suppressor gene ING1

JOURNAL Patent: US 6238918-A 1 29-MAY-2001;

FEATURES Location/Qualifiers

source 1..1902

/organism="unknown"

/mol\_type="unassigned DNA"

ORIGIN

Query Match 35.8%; Score 276; DB 6; Length 1902;

Best Local Similarity 80.8%; Pred. No. 4.2e-59;

Matches 422; Conservative 0; Mismatches 60; Indels 40; Gaps 7;

QY 2 AAGCGTTCTCGGCGGAGCGCAACAACCTAGAACCGGTGAGAACCGCTCCAGCAACCGCGAC 61

Db 343 AAGCGCTCACGGCGGAGCGCAACAACGAGAACCGGTGAGAACCGCTCCAGCAACCGCA- 401

QY 62 CCAGGAGCGGTACCTCGGGCAGCGCCAGGAGAGAGAACCCAGACCTCTAAGAGAA 121

Db 402 CCAGGAGCGCGGCTCGGGCAGCGCCAGGAGAGAGAACCCAGACCTCTAAGAGAA 461

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QY 447 AGGAAGTGTAAATGTATATTTTAAAGAAATGTTGTTAGAGG 488

Db 818 AAGGAGTGTAAATGTATATTTTAAAGAAATGTTAGAAAAGG 859

Search completed: May 6, 2004, 10:18:00

Job time : 3364.45 secs

OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 18:25:05 ; Search time 5261 Seconds

(without alignments)  
11522.567 Million cell updates/sec

Title: US-09-451-739H-15

Perfect score: 2030

Sequence: 1 ctctgccttaagatggt.....gaaaaaanaaaaaa 2030

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: em\_estba.\*
- 2: em\_esthum.\*
- 3: em\_estin.\*
- 4: em\_estmu.\*
- 5: em\_estov.\*
- 6: em\_estpl.\*
- 7: em\_estro.\*
- 8: em\_hci.\*
- 9: gb\_estci.\*
- 10: gb\_est2.\*
- 11: gb\_hci.\*
- 12: gb\_est3.\*
- 13: gb\_est4.\*
- 14: gb\_est5.\*
- 15: em\_estfun.\*
- 16: em\_estom.\*
- 17: em\_gss\_hum.\*
- 18: em\_gss\_inv.\*
- 19: em\_gss\_pln.\*
- 20: em\_gss\_vrt.\*
- 21: em\_gss\_fun.\*
- 22: em\_gss\_mam.\*
- 23: em\_gss\_mus.\*
- 24: em\_gss\_pro.\*
- 25: em\_gss\_rod.\*
- 26: em\_gss\_phg.\*
- 27: em\_gss\_vrl.\*
- 28: gb\_gssl.\*
- 29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	514.2	25.3	574	10	BF328582
3	485.8	23.9	3443	11	BC028407
4	478.8	23.6	490	9	AI951118

C	5	471.8	23.2	650	10	BE177744
C	6	399.2	19.7	492	13	BX282243
C	7	381.8	18.8	3794	11	BC036210
C	8	319.4	15.7	886	13	BQ437838
C	9	318	15.7	904	12	BG539426
C	10	314.6	15.5	638	13	BU678550
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C	14	306.8	15.1	862	12	BG431116
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C	19	251	12.4	546	10	BE929777
C	20	250.6	12.3	519	9	AL711745
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C	29	234.8	11.6	1105	13	BQ071543
C	30	229.2	11.3	574	14	CB298280
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ALIGNMENTS

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LOCUS  
DEFINITION  
QV4-BT0534-281299-053-a01 BT0534 Homo sapiens cDNA, mRNA sequence.  
ACCESSION  
AM373574  
VERSION  
AM373574.1  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens

AM373574 565 bp mRNA linear EST 04-FEB-2000  
QV4-BT0534-281299-053-a01 BT0534 Homo sapiens cDNA, mRNA sequence.

REFERENCE  
1 (bases 1 to 565)  
HCGP <http://www.ludwig.org.br/ORESTES>.

AUTHORS  
The FAPESP/LICR Human Cancer Genome Project  
TITLE  
Unpublished (1999)  
JOURNAL  
Contact: Simpson A.J.G.  
COMMENT  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?t1=QV4&t2=QV4-BT0534-281299-053-a01&t3=1999-12-28&t4=1>)

Organism: Homo sapiens  
Taxonomy: Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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High quality sequence stop: 565.  
Location/Qualifiers  
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ORIGIN

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Matches 552; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
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QY 1172 GGAATTCGCCATGCTAAAACCTGGAATAGCCACACTGAAACACCAATACCCAGGAAAAGGA 1231  
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QY 1232 AAATAATACCTTTCAGGACATTAAGATTTTAAAGAAAAGAAAGTCTCAATATAGTGGCAGCTTAA 1291  
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RESULT 2

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DEFINITION BF328582  
ACCESSION BF328582.1 GI:11299317  
VERSION EST.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 574)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
Negai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.,  
Goldman, G.H., Carvalho, A.F., Macukuma, A., Baia, G.S., Simpson, D.H.,  
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,  
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
10737800  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil

JOURNAL

Seq primer: puc 18 forward  
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High quality sequence stop: 525.  
Location/Qualifiers  
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/note="Organ: breast normal; Vector: puc18; Site: 1: Sma1;  
Site 2: Sma1; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the puc 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

FEATURES  
source

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Best Local Similarity 98.3%; Pred. No. 1e-73;  
Matches 530; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  
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QY 493 CCATTGAAATGCAAAAGTCTGTTCCAAATATAAGCCTTGGAAATGAAGATGAACAAACAT 552  
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Query Match 25.3%; Score 514.2; DB 10; Length 574;  
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QY	605	AAATCTCTGGATCTCTGAGAGTCTCCGTCGAGACTGTTTCACAGAGAGTGTGTGTACC	664			
DB	2591	AAATCTCTGGATCTCTGAGAGTCTCCGTCGAGACTGTTTCACAGAGTGTGTGTACC	2650			
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RESULT 4  
AI951118/c  
LOCUS  
DEFINITION wx63905.x1 NCI\_CGAP\_Br18 Homo sapiens cDNA clone IMAGE:2548376 3', mRNA sequence.  
AI951118  
ACCESSION

396 TGAGAGCAGATCAGATGTTCCCTTCAGAAATCAAAACAAAGAGGTTGAAGAAATCTTT 455  
613 GGGATTCGAGAGTCTCCGTCGAGACTGTTTTCACAGAGGATGTTGTGTACCCAGGCTA 672  
456 GTGATTCGAGAGTCTCCGTCGAGACTGTTTTCACAGAGGATGTTGTGTACCCAGGCTA 515  
673 CACATCAAAAGAAATCGATAAATAAGTGGAAATAGAGATTCACACTAGCTATCA 731  
516 CACATCAAAAGATATGATAAATAAGTGGAAATAGAGATTCACACTAGCTATCA 574

RESULT 3	BC028407	3443 bp	mRNA	linear	HTC 25-NOV-2003
LOCUS	Homo sapiens breast cancer antigen NY-BR-1.1, mRNA (cDNA clone IMAGE:4821910), containing frame-shift errors.				
DEFINITION	Homo sapiens (human)				
ACCESSION	BC028407				
VERSION	BC028407.1 GI:22382096				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 3443)				
	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raja, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Kzyvinski, M.I., Skalska, U., Smalish, D.E., Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.				
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)				
MEDLINE	22388257				
PUBMED	12477932				
REFERENCE	2 (bases 1 to 3443)				
AUTHORS	Strausberg, R.				
TITLE	Direct Submission				
JOURNAL	Submitted (23-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				

NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgabps-r@mail.nih.gov](mailto:cgabps-r@mail.nih.gov)  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA sequencing by: Institute for Systems Biology  
<http://www.systemsbio.org>  
contact: [amadnan@systemsbio.org](mailto:amadnan@systemsbio.org)  
Anup Madan, Jessica Fahney, Erin Helton, Mark Kettman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAC Plate: 46 Row: i Column: 20  
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF

VERSION AI951118.1 GI:5743428  
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 REFERENCE 1 (bases 1 to 490)  
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>, National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgaps@mail.nih.gov](mailto:cgaps@mail.nih.gov)  
 Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
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 QY 380 TCTGAAGCTCCCTGCGAGATGAAGTTCTTATCCAACTAAGCCTTAGAATTGGA 439  
 DB 430 TCTGAAGCTCCCTGCGAGATGAAGTTCTTATCCAACTAAGCCTTAGAATTGGA 371  
 QY 440 CATGCAAACTTTCAAAGCAGAGCTCCGAGAGCCATCTGCTTCGAGCTGCCATTGA 499  
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 VERSION BE177744.1 GI:8656896  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 REFERENCE 1 (bases 1 to 650)  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Ngai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.  
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 20202663  
 10737800  
 MEDLINE  
 PUBMED  
 COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?l1=et2=RC1-HT0598-140300-021-b02&l3=2000-03-14&t4=1>)  
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 High quality sequence start: 24  
 High quality sequence stop: 569.  
 Location/Qualifiers  
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 /note="Organ: head neck; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196.716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
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 Query Match 23.2%; Score 471.8; DB 10; Length 650;  
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 QY 1043 ACAACAACCTTGAACAGCGCTCTCAGAAATCAAGATATAGAAATTTAGAGTTAGAAAGTAA 1102  
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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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IMAGE:2659290, mRNA sequence.
BX282243
EST.
BX282243.1 GI:28615040
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,
Radelof, U., Schneider, D. and Korn, B.
Human Unigeneset - RZPD3
Unpublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGE9981196637.
RZPDLIB; I.M.A.G.E. CDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi?response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACAGGAAACAGCTATGAC.
Location/Qualifiers
1. .492
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FEATURES
source

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NCI-GAL-GCBI) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
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Soares and M. Fatima Bonaldo."

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## ORIGIN

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Query Match 19.7%; Score 399.2; DB 13; Length 492;
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Db 418 TTATTTACNATACCATTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 476
QY 2028 AAA 2030
Db 477 ACA 479

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## RESULT 7

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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
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BC036210
Homo sapiens (human)
BC036210.1 GI:23242519
HTC
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3794)
Straussberg,R.

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TITLE  
JOURNAL  
REMARK  
COMMENT  
Direct Submission  
Submitted (31-JUL-2002) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (NEHRI) & Shiraki  
Toshiyuki and Piero Carninci (RIKEN)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Sequencing Group at the Stanford Human Genome  
Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www-shgc.stanford.edu>  
Contact: (Dickson, Mark) [mcdepaxil.stanford.edu](mailto:mcdepaxil.stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,  
R. M.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAC Plate: 63 Row: e Column: 18  
This clone was selected for full length sequencing because it  
passed the following selection criteria: Hexamer frequency ORF  
analysis  
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DB 2505 AGCTTTGTTTTCAGAAATGCAATGGGAAGAGACCTACCCCAACCCAGTGTCAATCCAGGA 2564  
QY 1739 GCTGAACACATGTTCAAAACGAAACAGATNATGTGAACAAACACACTGAGCAGGAG 1798  
DB 2565 ATTCAACAAATGATCAAAATTAACAAATGTA--CTGAAGGAATTCATTGGAAGCAGGAA 2623  
QY 1799 TCTTAGATCAGAAATTTTCAACTACAAAGCAAAATATGCTGCTTCAACAGCAATTA 1858  
DB 2624 TCTGTAGAGCGGAGGCTGTCTCACTGAGAGTGAATATGTTGCTTCCACAGCACTG 2683  
QY 1859 GTTCATGCAATGAAGAAAGCTGACAAACAAAGCAAGATAACAATTTGATTTCA 1912  
DB 2684 GATGATGCTTACAC--AAAGCTGACAACTCAAGAAAGACAAATAATTTACTATCCA 2736

RESULT 8  
BQ437838/c  
LOCUS  
DEFINITION  
BQ437838  
VERSION  
BQ437838.1  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
BQ437838 886 bp mRNA linear EST 24-MAY-2002  
AGENCY: NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE:6157635  
5', mRNA sequence.  
ACCESSION  
BQ437838  
VERSION  
BQ437838.1  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

252	ATAAGTTCCTGTAAGAAGAAGATCTCTCGAAAAAAAGTCATTTGGCTTTAGAAAC-TGTA	194	
1700	CAAAAGAGACCAACGCTGAAGAACACACAGTGTCAAATGAAGGAAGCTGAACATGTNTCAAAC	1759	
193	CATAACACCTTAAGCCAAACACACAGCAGCAAATAAAGGAAATGAAGAGATGTATGAAAAAT	134	
1760	GAAACAAGATNATGTGAACAACAACACACATGANCAGCAGGAGTCTCTAGATCAGAAATATTT	1819	
133	CGAGAAGCTTAAGAGAGATAATTCCTCACTGGAAATGGAGCTGTGTGAAGAGAGAAATATGT	74	
1820	CAACTACAAAGCAAAAAATATATGGCTTCAACAGCAATTAGTTCATGCACATAANGAAAGC	1879	
73	CAACTCCAAATGAAAAATCCGTGCATTGAACAGCACTAGATGATGTTTCATCAAGAAAG	14	
1880	TGACACACAAAG	1891	
13	TATCATAAAGAG	2	
RESULT 9			
RG539426			
LOCUS	602568046F1 NIH_MGC_77 Homo sapiens cdna clone IMAGE:4692635 5',	linear EST 03-APR-2001	
DEFINITION	mRNA sequence.		
ACCESSION	RG539426		
VERSION	RG539426.1 GI:13531659		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgabs-remail.nih.gov">cgabs-remail.nih.gov</a> Tissue Procurement: CLONTECH Laboratories, Inc. cdna Library Preparation: CLONTECH Laboratories, Inc. cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LLCW1513 row: 1 column: 12 High quality sequence stop: 608. Location/Qualifiers		
FEATURES			
Source	1. 904 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:4692635" /lab_host="DH10B (T1 phage-resistant)" /clone_lib="NIH_MGC 77" /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site: 1: SfiI (ggccgcctcgcc); Site 2: SfiI (ggccattatgcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGCCCATATATGCC-3' and 3' adaptor sequence: 5'-ATTCATGAGCGCGGCGGCAGCATG-dt(30)EN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."		
ORIGIN			
Query Match	15.7%; Score 318; DB 12; Length 904;		
Best Local Similarity	68.0%; Pred. No. 5,1e-42;		
Matches 506; Conservative	0; Mismatches 225; Indels 13; Gaps 4;		
QY	767	AGGGGAACCTTCAAAAAGATCACTGTGAACACAGTACAGGAAAAATGGAACAAATCGAAAAA	826
Db	2	ATAAAACCTTAAAGATAACCACTGTGAGCACTTAGACTTAARAATTCCGAACACTGAAAAA	61

Tel: 319 356 4866

Fax: 319 356 7171

Email: paul-mccray@uiowa.edu  
Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com) or from Open Biosystems  
(www.openbiosystems.com).  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES

source

Location/Qualifiers

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/organism="Homo sapiens"  
/mol\_type="mRNA"  
db\_xref="taxon:9606"  
/clone="UI-CF-DUI-aar-o-16-0-UI"  
/tissue\_type="Primary Lung Epithelial Cells"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/clone\_lib="UI-CF-DUI"  
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-CF-DUI is a normalized cDNA library containing the following tissue(s): Primary Lung Epithelial Cells The Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCTGTAGGC.  
TAG TISSUE=Lung Epithelial Cells Tissue nos 359-368  
TAG\_LIB=UI-CF-DUI  
TAG\_SEQ=GGCTGTAGGC"

ORIGIN

Query Match 15.5%; Score 314.6; DB 13; Length 638;  
Best Local Similarity 72.9%; Pred. No. 2e-41;  
Matches 461; Conservative 0; Mismatches 160; Indels 11; Gaps 4;

QY 1117 CTCACACTCATGAATGAATATATCTTACATGAAATTTGCTGTTGAAAAAGGAAA 1176  
Db 638 CTCATAGTCATGAAGAAGAAAAGACCTTCCTCCATAAATAAGCATGTCGAGGAGAAA 579  
QY 1177 TTGCCATGCTAAAACCTGGAATAGCCCACT-GNAACACCAATACCCAGAAAGGAAAAT 1235  
Db 578 TTGCTATGCTAAGACTAGAAATAGACACAATAAAAAAATCAACCCAGGAAAAAGAAAG 519  
QY 1236 AATACCTTTGAGGACATTAAGATTTTAAAGAAAAGAAATGCTGGAACCTTCAGATGCCCTTA 1295  
Db 518 AATGTTTTGAGGACCTTAAAAATTTGAAAGAAAAGAAATGAAGACCTTCAGAGACTATA 459  
QY 1296 AAACCTGAAAAGAGCAATCACTAACTAAAGGGCAATCTCAATATATAGTGGGAGCTTAAAGTT 1355  
Db 458 AAACAGATGAGGAAACATTTAAACAAACAATATCCAGTATAATGGACGGCTTAGTGT 399  
QY 1356 CTGATAGCTGAGAACCAATGCTCCTCTTAATTT---GAAGGAAAACACACAGAGAAA 1412  
Db 398 CTGACAGCTGAGAAATCAATGCTTAAATTTAACTGGAAGTGAAGAAAGCAACAGGAAA 339  
QY 1413 ATACTAGAGCAGAAAATTTGAATCACACCACTCCTAGACTGGCTTCTGCTGTACAAGACCT 1472  
Db 338 AGACTGGAAGCAGAAAGTTGAAATCATACCATCTAGATTGGCTGCTGTATACATGATCGT 279  
QY 1473 GATCAAAATTTGTGATCAAGAAAAGTCAAGAACTGCTTCCAGATTCAGAGAGATG--- 1530  
Db 278 GATCAAAAGTGAGACATCAAAAAGAGAACTAGAACTTGTCTTCCAGAGACGAGAGATGAA 219

QY 827 GAAGTTTGTGTACTGAAAGAAACTGTGAGAGCAAAAGAAATAAATACAGTTAGA 886  
Db 62 TAAGGCTAGTGTACTACAAAGAGAAATATCTGAAAGAAAGAAATAAATCGCAGTTAA 121  
QY 887 GAACCAAAAGTAAATGGGACAGAGCTGCTGAGTGTGAGATTGATTTTAAACCAAGA 946  
Db 122 GCATGAATATCTGAAATGGGAAAGAACTGTGAGTTTGGATTTGCCATACAGCAAGA 181  
QY 947 AGAAGAGAGAGAGAAATGCGGTATATTAATTAATGAAAAAATTAGGGAAGAATTAGAAG 1006  
Db 182 AAAAAAGAAAGAAAGAAATGTTGAAGAGTTGCACCAAAAAAGTTAGGGAAGTTAAGAAT 241  
QY 1007 AATCGAAGAGCAGCATAGGAAGAGTTAGAGTGAACACCAACTTGAACAGCTCTCAG 1066  
Db 242 AACGAGAGAGCAATATAGGATAGAGCTGTGTGACAAACCAATTAACCGGCTCTCAA 301  
QY 1067 AATCAAGATATAGAAATGGAAGCTGTAGAAGTAATTTGAATCAGGTTTCTCACACTCA 1126  
Db 302 ATCAGCAGGTGGAAATTTGAAGACAGGAGGAATAATCAATCAGGTTTCTGAAACTGA 361  
QY 1127 TGAATAAGAAATTTATCTCTTACATGAATTCATGTTGAAAAGGAAATTCGCTGCT 1186  
Db 362 TGAATAAGAGAC---CTGCTGCATGAAACCGCTTGAATGAAGATGAATTCGCAAGCT 418  
QY 1187 AAAACTGGAATAGCCACTGAACACCAATACAGGAAAGGAAATAAATACITTTGA 1246  
Db 419 CAGGCTGGAAAGACACACAATAAATAACCAAACTGGAAAGAAATACITTAAC---A 473  
QY 1247 GGACATTAAGATTTTAAAGAAAGATGCTGAATCTCAGATGACCTTAAACCTGAAGA 1306  
Db 474 AGACTTTGAAATTTGAAAGAAAGACATGAAGACCTTCAAAGGCTCTAAACCGAATGG 533  
QY 1307 GGAATCAATTAATAAAGGCA-TCTCAATATAGTGGCAGCTTAAAGTTCTGATAGCTG 1365  
Db 534 GGAACATTAAGAAAGACATAGCTGCTGTATATGAGCAGCTAGCTGCTGACATG 593  
QY 1366 AGAACACATGCTCACTTCTTAATTAAG---GAAAACAAAGCAAGAAATTAATCTAGAG 1421  
Db 594 ACAACACACGCTCGCTTACAACTGGAGAGACAAAGACGAGCAACGATGGGAA 653  
QY 1422 CGAGAAATTTGAATCACACATCTAGACTGCTTCTGCTGTACAGACCATGATCAAAAT 1481  
Db 654 ACAGAAAGCAATATACATGCTGCTGAGCTGCCAAGGAGCCATGACCAAGG 713  
QY 1482 GTGACATCAAGAAAAGTCAAGAA 1505  
Db 714 CATCCCATCAGAAAGACAAAAA 737

RESULT 10  
BU678550/c  
LOCUS  
DEFINITION  
UI-CF-DUI-aar-o-16-0-UI.s1 UI-CF-DUI Homo sapiens cDNA clone  
UI-CF-DUI-aar-o-16-0-UI 3', mRNA sequence.  
ACCESSION  
BU678550  
VERSION  
BU678550.1 GI:23525612  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 638)  
Bonaldo,M.F., Lennon,G. and Soares,M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)  
JOURNAL  
MEDLINE  
PUBMED  
PUBMED  
COMMENT  
Contact: McCray, PB  
8889548  
University of Iowa  
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA

1531 ----CTTGTTCAGAGAAAATGAATGTTGATGTAGTAGTACCGGATATATACAAATGA 1586  
218 TGTTCGTTTACAGGACAAAATGAATTTTGTGTCTA-ACCTAAAGATACAAATGA 160  
1587 GGTGCTCATCAACCACTTTCAGCTCAAGGATCCANAGGATCCAAATTAATCT 1646  
159 GATTCTTCTCAACAACATATTAAACATGAAGTAACTCAATAGCCTAGAAAATTGAGTT 100  
1647 CAATATATGAGAGATGCTCTAAGAGAGAAAATACATTTGTTTTCAGGAACATGCAACAAGAG 1706  
99 CCATCACACGAGAGATGCCCTCAGAGAAAACATTTGGGTTTAGAACGGGTACAAAAGGA 40  
1707 ACCACGTGAACACACAGTGTCAATGAAGGA 1738  
39 CCTAAGCCCTAAACACAGTGTCAAAAAGAAAAA 8

RESULT 11  
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LOCUS RCI-BT0254-071100-119-a03 BT0254 Homo sapiens cDNA, mRNA sequence.  
DEFINITION BF746270  
ACCESSION BF746270.1 GI:12072946  
VERSION EST.  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 443)  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,  
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
10737800

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=RCI&t2=RCI-BT0254-  
071100-119-a03&t3=2000-11-07&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 9  
High quality sequence stop: 439.  
Location/Qualifiers

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/mol\_type="mRNA"  
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/dev\_stage="Adult"  
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/note="Organ: breast; Vector: puc18; Site 1: SmaI; Site 2:  
SmaI; A mini-library was made by cloning products derived  
from ORSTES PCR (U.S. Letters Patent application No.  
196,716 - Ludwig Institute for Cancer Research) profiles  
into the pUC 18 vector. Reverse transcription of tissue  
mRNA and cDNA amplification were performed under low  
stringency conditions."

ORIGIN  
Query Match 15.2%; Score 309; DB 10; Length 443;  
Best Local Similarity 98.4%; Pred. No. 1.8e-40;

Matches 312; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
93 TTCAAAGCAGAGCCCTCCGAGAGCCATCTGCTCGAGCGCTGCCATTGAATGCARAAG 152  
127 TTACAATCAGAGCCCTCCGAGAGCCATCTGCTCGAGCGCTGCCATTGAATGCARAAG 186  
153 TCTGTTCCTCAATTAAGAGCCCTTGAATTTGAAGATGAACAAACATTCAGAGCAGATGAGATA 212  
187 TCTGTTCCTCAATTAAGAGCCCTTGAATTTGAAGATGAACAAACATTCAGAGCAGATGAGATA 246  
213 CTCCCATCAGAAATCCAAACAAAGGAGCTATGAAGAAAGTTCTTGGGATTCGAGAGTCTC 272  
247 CTCCCATCAGAAATCCAAACAAAGGAGCTATGAAGAAAGTTCTTGGGATTCGAGAGTCTC 306  
273 TGTGAGACTGTTTCACAGAGAGGATGTGTGTTCACCAAGGCTACACATCAAAAAGAAATA 332  
307 TGTGAGACTGTTTCACAGAGAGGATGTGTGTTCACCAAGGCTACACATCAAAAAGAAATA 366  
333 GATAAATAAATGGAAATTAAGAGAGTCTCTGATATGATGGTTTCTGAAGGCTCC 392  
367 GATAAATAAATGGAAATTAAGAGAGTCTCTGATATGATGGTTTCTGAAGGCTCC 426  
393 TGCAGAAATGAAGTTTC 409  
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LOCUS RCI-BT0254-081100-119-a03 BT0254 Homo sapiens cDNA, mRNA sequence.  
DEFINITION BF746340  
ACCESSION BF746340  
VERSION BF746340.1 GI:12073016  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 443)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,  
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
10737800

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=RCI&t2=RCI-BT0254-  
081100-119-a03&t3=2000-11-08&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 9  
High quality sequence stop: 439.  
Location/Qualifiers

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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="BT0254"  
/note="Organ: breast; Vector: puc18; Site 1: SmaI; Site 2:  
SmaI; A mini-library was made by cloning products derived  
from ORSTES PCR (U.S. Letters Patent application No.  
196,716 - Ludwig Institute for Cancer Research) profiles  
into the pUC 18 vector. Reverse transcription of tissue  
mRNA and cDNA amplification were performed under low  
stringency conditions."

Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

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Query Match      15.2%; Score 309; DB 10; Length 443;
Best Local Similarity 98.4%; Pred. No. 1.8e-40;
Matches 312; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 93 TTCAAGCAGAGCTCCGAGAGCCATCTGCTTCAGAGCTGCTGCAATGAAATGCAAAAG 152
Db 127 TTCAATCAGAGCTCCGAGAGCCATCTGCTTCAGAGCTGCTGCAATGAAATGCAAAAG 186
QY 153 TCTGTTCCAAATAAAGCTTCGAATTTGAAGATGAACAAACATTTGAGAGCATGAGATA 212
Db 187 TCTGTTCCAAATAAAGCTTCGAATTTGAAGATGAACAAACATTTGAGAGCATGAGATA 246
QY 213 CTCCATCAGATCCAAACAAAGGACTATCAAGAAAGTTCTTGGGATTTCTGAGGCTC 272
Db 247 CTCCATCAGATCCAAACAAAGGACTATCAAGAAAGTTCTTGGGATTTCTGAGGCTC 306
QY 273 TGTGAGACTGTTTACAGAGAGATGTGTGTTTACCCAGGCTACACATCAAAAAGAAATA 332
Db 307 TGTGAGACTGTTTACAGAGAGATGTGTGTTTACCCAGGCTACACATCAAAAAGAAATA 366
QY 333 GATTAATAAATGGAATTTAGAGAGCTCTCTGATATGATGCTTTCTGAGGCTCCC 392
Db 367 GATTAATAAATGGAATTTAGAGAGCTCTCTGATATGATGCTTTCTGAGGCTCCC 426
QY 393 TGCAGATGAAAGTTTC 409
Db 427 TGCAGATGAAAGTTTC 443
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RESULT 13

CA394381 LOCUS  
DEFINITION cs50h08.y1 Human Retinal pigment epithelium/choroid cDNA  
5', mRNA sequence.

ACCESSION

CA394381  
CA394381.1 GI:24728876  
EST.  
Homo sapiens (human)

KEYWORDS

Homo sapiens  
Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.

ORGANISM

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

Wistow,G., Bernstein,S.L., Wyatt,M.K., Farris,R.N., Behal,A., Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.

Expressed sequence tag analysis of human RPE/choroid for the NEIBank Project: Over 6000 non-redundant transcripts, novel genes and splice variants

TITLE

NEIBank Project: Over 6000 non-redundant transcripts, novel genes and splice variants

JOURNAL

Mol. Vis. 8 (4), 205-220 (2002)

MEDLINE

22103460

PUBMED

12107410

COMMENT

Contact: Wistow G

Section on Molecular Structure and Function

National Eye Institute

6/331, NIH, Bethesda, MD 20892-2740, USA

Tel: 301 402 3452

Fax: 301 496 0078

Email: graeme@helix.nih.gov

Seq primer: MJ3RF1 reverse primer (ABI).

Location/Qualifiers

1..684

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

FEATURES

source

RESULT 14

BG431116

LOCUS

BG431116

862 bp

mRNA

linear

EST 14-MAR-2001

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/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Human Retinal pigment epithelium/choroid cDNA"
(Un-normalized, unamplified): cs
/note="Organ: Eye; Vector: pCMVSPORT6; Two different donor eyes (75-80 years old) yielded approximately 600 mg of dissected RPE/choroid tissue. This in turn yielded 340 ug of total RNA and 7 ug of mRNA. A directionally cloned cDNA library in the pCMVSPORT6 vector was constructed at Life Technologies (Rockville, MD; now part of Invitrogen Corp), essentially following the protocols of the SuperScript plasmid system (Invitrogen Corp).
http://www.invitrogen.com/>). The library code designation was cs. For this library, cDNA inserts were cloned into the NotI/MluI sites of the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."
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ORIGIN

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Query Match      15.2%; Score 308; DB 14; Length 684;
Best Local Similarity 69.0%; Pred. No. 2.3e-40;
Matches 454; Conservative 0; Mismatches 195; Indels 9; Gaps 2;

QY 687 ATGGATAAAATAGTGGAAATTTAGAGATTCACCTACCTATCAAAAATCTTGGATACA 746
Db 36 ATTGATCAACATGAATGAAGTTGTGTTTACCTATTGAAATTTAAAAATACA 95
QY 747 GTTCATTTCTTGAAGAGCAAGGAACTTCAAAAAGATCACTGTGAACAACGTACAGGA 806
Db 96 TTTTGTGTTATGGAAGAAGATTATTAACCTTAAAGATACCACTGTGACCACTTAGAGTA 155
QY 807 AAAATGGAAACAAATGAAAAAGAGTTTGTGTACTGAAAAAGAACTCTGTGAGAGCAAAA 866
Db 156 AAAATTCGAAACTGAAAAATAGGCTAGTGTACTACAAAAGAGAAATCTCTGAAAAAGAA 215
QY 867 GAAATTAATACACTGTAGAGAACCAAAAAGCTTAAATGGGAACAGAGCTCTGCAGTGTG 926
Db 216 GAAATTAATACACTGTAGAGAACCAAAAAGCTTAAATGGGAACAGAGCTCTGCAGTGTG 275
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Db 276 AGATTGACATTTAAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 335
QY 987 ATTAGGAAGATTTAGGAAGATTCGAAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1046
Db 336 GTTAGGGAAGATTTAGGAAGATTCGAAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 395
QY 1047 CAACCTTGAACAGGCTCTCAGAAATACAGATATAGAAATTTGAAGAGTGTAGAAGTAATTG 1106
Db 396 CCNATTAACCGGCTCTCAATCAGCAGAGGTGGAAATTTGAAGACAGAGGAGAAATAATTCA 455
QY 1107 AATCAGGTTTTCACACTCATGAAAATGAAAATTTATCTTACATGAAAATTTGATGTTG 1166
Db 456 AATCAGGTTTTCGAAACTGTATGAAAAGAA---GACCTGTGTCATGAAAACCGCTTGATG 512
QY 1167 AAAAGGAAATTTGCCATGTCTAAAACTGGAAATPAGCCACACTGAAACACCAATACCAGAA 1226
Db 513 CAAGATGAATTTGCCAGGCTCAGGCTGGAAAAGACACAAATAAAAACCAAAACCTGGAA 572
QY 1227 AGGAAAATAAATATCTTTGAGGACATTAAGATTTTAAAGAAAAGAAATGCTGAATTCAG 1286
Db 573 AAG-----AAATACTTTAAAGACTTTGAAATTTGAAAAGAAAGACATGAAGACCTTCAA 626
QY 1287 ATGACCTTAAAACTGAAAGAGGAATCAATTAATAAAAAGGCGCATCTCAATATAGTGGGC 1344
Db 627 AAGGCTCTAAACGGAAATGCGGAACANTTAGCAAAACGATAGCCTGTTATAGTGGAC 684
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DEFINITION 602498742F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4612186 5',
            mRNA sequence.
ACCESSION  BG431116
VERSION    BG431116.1 GI:13337622
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 862)
            NIH-MGC http://mgs.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
AUTHORS    Contact: Robert Strausberg, Ph.D.
TITLE      Tissue Procurement: CLONTECH Laboratories, Inc.
JOURNAL    cDNA Library Preparation: CLONTECH Laboratories, Inc.
COMMENT    cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCMI1360 row: d column: 11
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            /clone="IMAGE:4612186"
            /lab_host="DH10B (T1 phage-resistant)"
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            /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
            SfiI (ggccattatggcc); Site_2: SfiI (ggccattatggcc); 5' and
            3' adaptors were used in cloning as follows: 5' adaptor
            sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
            5'-ATTCTAGAGCGCGGCGGCACATG-dt(30)BN-3' (where B = A,
            C, or G and N = A, C, G, or T). Average insert size 1.65
            kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
            by PCR. This library was enriched for full-length clones
            and was constructed by Clontech Laboratories (Palo Alto,
            CA). Note: this is a NIH_MGC Library."
ORIGIN
Query Match 15.1%; Score 306.8; DB 12; Length 862;
Best Local Similarity 68.3%; Pred No. 3.4e-40;
Matches 516; Conservative 0; Mismatches 224; Indels 16; Gaps 6;
QY 1013 AGAGCAGCATAGGAAGAGTTAGAGTGAACAACTTGAACAGGCTCTCAGAAATACA 1072
DB 76 AGAAGAGATGCCAGATGTTACAGATGGAATCTGACCAATCACCTTTCCAAACAAA 135
QY 1073 AGATATAGATTGAAGAGTGTAGAAGTAATTTGAATCAGTCTTCTCACCTCATGAAA 1132
DB 136 GGAGATTGAATGGCTCAAGAGAAATGAATTT---CTGAGATTCTCATGTATGAGA 192
QY 1133 TGAATAATTATCTTTACATGAAAATTCATGTTGAAAAAGGAAATTCCTATGCTTAAACT 1192
DB 193 AGAAAAAGACCTATCGCATATAAATAGCATGTTGCAGGAAGAAATTCATGCTAAGACT 252
QY 1193 GGAATATGCCACTGAAACCATATACCGAAGAGGAAATATAATATCTTGGAGCAT 1252
DB 253 AGAATATAGACAAATAAATAATCAAAACCGAGGAAAAAGAAAGAAATTTCTGAGGACCT 312
QY 1253 TAAGATTTTAAAGAAAAAGATGCTGAACTTCAGATGACCCCTTAAACTTGAAGAGGATC 1312
DB 313 TAAATTTGTAAGAAAAAGATGAAGACTTCAGAGAACTATAAACAAGATGAGGAAC 372
QY 1313 ATTAATAAGGGGATCTCAATATAGTGGGAGCTTAAAGTTCTGATAGCTGAGAACAC 1372
DB 373 ATTAACACAAACAATATCCAGTATTAATGGACGGCTTAGTTCTTCGACAGCTGAGAATGC 432
QY 1373 AATGCTCACTCTTAAATT---GAAGGAAAAACAAGACAAAGAAATATAGAGGCGAGAAAT 1429

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DB 433 AATGCTAAATTTCTAACTGGAGATGAAAGCAAGCAAGCAAGCAAGCAAGCAAGT 492
QY 1430 TGAATCACACCATCTAGACTGGCTTCTGCTGTACAGACCATGATCAAAATTTGACATC 1489
DB 493 TGAATCATACCATCTAGACTGGCTGCTGTATACATGATCGTGATCAAGATGACATC 552
QY 1490 AAGAAA--AAGTCAAGAAACCTGCTTTCCACATTTGCAGGAGATG-----CTTGTTCGAA 1541
DB 553 AAAAAAGAGAACTAGAACTTCTTTCCAGAGAGCAAGAGATGAATGTTCTCGTTTACAG 612
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DB 613 GACAAAATGAATTTGTGATGTGCTA-ACCTAAAGATACCAATGAGATCTTTCTTCAACA 671
QY 1602 ACTTTCGAGCTCAAGGAAATCCANAAGCCTAAAAATTAATCTCAATATTCAGGAGA 1661
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QY 1662 TGCTCTAAGAGAAATACATTTGGTTTCAGGAACATGCAAGAGACCAACGTTGAAACAC 1721
DB 732 TGGCCTCAGAGAACAGACTTGGGGCTTA-GAACGGGTACCAAGAGGCGCTAGCCAAACAC 790
QY 1722 AGTGTCAATGAAGGAAGCTGAACACATGTTTCAAA 1757
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RESULT 15
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LOCUS     BG622779
DEFINITION 602647567F1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4768912 5',
            mRNA sequence.
ACCESSION  BG622779
VERSION    BG622779.1 GI:13674150
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 821)
            NIH-MGC http://mgs.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
AUTHORS    Contact: Robert Strausberg, Ph.D.
TITLE      Tissue Procurement: CLONTECH Laboratories, Inc.
JOURNAL    cDNA Library Preparation: CLONTECH Laboratories, Inc.
COMMENT    cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCMI633 row: f column: 17
            High quality sequence stop: 818.
FEATURES   Location/Qualifiers
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            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:4768912"
            /lab_host="DH10B (T1 phage-resistant)"
            /clone_lib="NIH_MGC_79"
            /note="Organ: placenta; Vector: pDNR-LIB (Clontech);
            Site_1: SfiI (ggccgcttcggcc); Site_2: SfiI
            (ggccattatggcc); 5' and 3' adaptors were used in cloning
            as follows: 5' adaptor sequence: 5'-CACGCGCATTTATGGCC-3'
            and 3' adaptor sequence:
            5'-ATTCTAGAGCGCGGCGGCACATG-dt(30)BN-3' (where B = A,
            C, or G and N = A, C, G, or T). Average insert size 1.3
            kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
            by PCR. This library was enriched for full-length clones
            and was constructed by Clontech Laboratories (Palo Alto,
            CA). Note: this is a NIH_MGC Library."

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CA). Note: this is a NIH\_MGC Library."

ORIGIN

Query Match		14.3%;	Score 290.4;	DB 12;	Length 821;
Best Local Similarity		68.2%;	Pred. No. 1.5e-37;		
Matches 510;		Conservative	0;	Mismatches 221;	Indels 17; Gaps 7;
Qy	687	ATGGATAAATAAGTGGAAATTAAGAGATTCAACTAGCCTATCAAAAATCTTGGATACA	746		
Db	20	ATTGATCAACATGAAATGAAAGTTGTGTTCACTATTGAAATTAATAAGACA	79		
Qy	747	GTTTCATCTTGTGAAGAGCAAGGAACTTCAMAAAGATCACTGTGAACACGTACAGGA	806		
Db	80	-TTTGTATTATGTAAGAGTTAACAGAACTTAAGATANTCACCTGTGAGCACTTAGGTA	138		
Qy	807	AAATGGAAACAATGAATAAGAAAGTTTGTGTAAGTGAAGAACTGTGAGAGCAAAA	866		
Db	139	AAAATTCGAAACTGAAATAATAGGCTAGTGTACTACAAAAGAGACTATCTGAAAAGAA	198		
Qy	867	GAAATAAATCACAGTTAGAGAACCAAAAAGTTAAATGGGAACAAGAGCTCTGCAGTGTG	926		
Db	199	GAAATAAATCGCAGTTAAGCCTGAACACTTGAATGGGNAAGAACTCTGTAGTTTG	258		
Qy	927	AGATTGACTTTAAACCAAGAAAGAGAGAAAGAAATGCCGATATATTAAATGAAAAA	986		
Db	259	AGATTGGCCATACACAGCAAGAAAAAAGAAAAAGAAATGTTGAAGAGTTGCACCAAAA	318		
Qy	987	ATTAGGGAAGAAATAGGAAGAAATCGAGAGCAGATAGGAAGAGTTAGAGTGAAACAA	1046		
Db	319	GTTAGGGAAAGTTAAGAAATCACAGAGAGCAATATAGGATAGAGCTGTGTGACAAA	378		
Qy	1047	CAACTTGAACAGGCTCTCAGAAATCAAGATATAGAAATGAAGAGTGTAGAAAGTAATTG	1106		
Db	379	CCAAATTAACCCGG-TCTCAATCAGCAGAGGTGGAATTGAAAGACAGGAGGAATAATTCA	437		
Qy	1107	AATCAGGTTTCTCACACTCATGAAATGAATTAATCTCTTACATGAATTTGCATGTTG	1166		
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Qy	1167	AAAAAGGAATGCCATGCTTAAACTGGAATAGCCACACTGAAACACCAATACCAGGAA	1226		
Db	494	CAAGATGAAATTTGCCAGGCTCAGGCTGGAAGAAAGACACAATAAAAAACCAAACTGGAA	553		
Qy	1227	AAGGAAATAAATATCTTTGAGACATTAAAGATTTTAAAGAAAGAAATGCTGAATTCAG	1286		
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Qy	1287	ATGACCCCTAAACTGAAAGAGGAATCATTAACCTAAAGGGCATCTCATATAGTGGG-CA	1345		
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Qy	1346	GCTTAAGTTCTGATAGCTGAGAACACAATGCTCACTTCTAATTG-----AAGGAAAC	1401		
Db	668	AGTTGCTGCTGTCGGGATGAAACACAACTCCCGTTCTAAACGGGGAGAGCAAGAG	727		
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Db	728	AAGGCGGCGAGACTGGAAACAGAAAT	755		

Search completed: May 6, 2004, 22:30:59  
Job time : 5265 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 21:03:19 ; Search time 960 Seconds  
(without alignments)

10692.886 Million cell updates/sec

Title: US-09-451-739H-15

Perfect score: 2030

Sequence: 1 ctgctgcgtaagatggt.....gaaaaaanaaaaaa 2030

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2941586 seqs, 2264995651 residues

Total number of hits satisfying chosen parameters: 5883172

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1940	95.6	4047	14	US-10-007-805-566
2	1940	95.6	4047	15	US-10-076-622-566
3	1940	95.6	4047	15	US-10-124-805-566
4	1940	95.6	4458	13	US-10-058-270A-3
5	1940	95.6	4458	14	US-10-007-805-564
6	1940	95.6	4458	15	US-10-076-622-564
7	1940	95.6	4458	15	US-10-177-293-333
8	1940	95.6	4458	15	US-10-124-805-564
9	1938.4	95.5	3288	14	US-10-007-805-490
10	1938.4	95.5	3288	15	US-10-076-622-490
11	1938.4	95.5	3288	15	US-10-124-805-490
12	1938.4	95.5	3865	9	US-09-604-287A-474
13	1938.4	95.5	3865	10	US-09-551-621-474
14	1938.4	95.5	3865	14	US-10-007-805-474

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Sequence 17, Appl

ALIGNMENTS

RESULT 1

US-10-007-805-566  
; Sequence 566, Application US/10007805  
; Publication No. US20020150581A1  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Durham, Margareta  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER  
; FILE REFERENCE: 210121.470C10  
; CURRENT APPLICATION NUMBER: US/10/007,805  
; CURRENT FILING DATE: 2001-12-07  
; NUMBER OF SEQ ID NOS: 593  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 566  
; LENGTH: 4047  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-007-805-566

Query Match 95.6%; Score 1940; DB 14; Length 4047;  
Best Local Similarity 98.7%; Pred. No. 0;  
Matches 2001; Conservative 0; Mismatches 21; Indels 5; Gaps 5;

QY 5 TGGCGTTAAAGATGGCTTCTCTGAAGCTAATCGCGAATGAAGTTCTATTCCCACTAA 64  
Db 2016 TCCTGTTAAAGATGGCTTCTCTGAAGCTAATCGCGAATGAAGTTCTATTCCCACTAA 2075

65	QY	AGCCTTAGAATTTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCGAGAGCCATCTCG	124
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185	QY	TGAACAAACATTGAGACGAGATGAGATATCCCATCAGAAATCCAAACAAAGACATATGA	244
2196	Db	TGAACAAACATTGAGACGAGATGAGATATCCCATCAGAAATCCAAACAAAGACATATGA	2255
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305	QY	AGCCAAGGCTACACATCAAAAGAAATAGATAAAATTAATGSAATTTAGAGAGTCTCC	364
2316	Db	AGCCAAGGCTACACATCAAAAGAAATAGATAAAATTAATGSAATTTAGAGAGTCTCC	2375
365	QY	TGATATGATGTTTCTTGAAGGCTCCCTGCAGAATGAAAGTTTCTATTCCAACTAAAGC	424
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1145	QY	CTTACATGAAAATTTGCAATGTTTGAAAAAGGAAATTTGCCATGCTTAAAACTGAAAATAGCCAC	1204

## RESULT 2

US-10-076-622-566

; Sequence 566, Application US/10076622

Publication No. US20030023036A1

GENERAL INFORMATION:

APPLICANT: Houghton, Raymond L.

APPLICANT: Sleath, Paul R.

APPLICANT: Persing, David H.

**TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY**

TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER

FILE REFERENCE: 210121.470C11

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CURRENT FILING DATE: 2002-02-13

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; NUMBER OF SEQ ID NOS: 527
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 566
; LENGTH: 4047
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-076-622-566

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Query Match	95.6%;	Score 1940;	DB 15;	Length 4047;
Best Local Similarity	98.7%;	Pred. No. 0;		
Matches 2001; Conservative	0;	Mismatches 21;	Indels 5;	Gaps 5;
QY	5	TGCCGCTTAAAGATGGTCTTCTGAAAGCTTAACCTGCGGAATGAAAGTTTCTTATTCCAACTAA	64	
Db	2016	TCCTGTTAAAGATGGTCTTCTGAAAGCTTAACCTGCGGAATGAAAGTTTCTTATTCCAACTAA	2075	
QY	65	AGCCTTAGAATTGATGGACATGCAAACTTTCAAGCAGAGCCTCCGAGAAAGCCATCTGC	124	
Db	2076	AGCCTTAGAATTGATGGACATGCAAACTTTCAAGCAGAGCCTCCGAGAAAGCCATCTGC	2135	
QY	125	CTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCCTTGGAAATTGAAGAA	184	
Db	2136	CTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCCTTGGAAATTGAAGAA	2195	
QY	185	TGNAACAAACATTGAGACGATGAGTACTCCCATCAGATCCAAACAAAGACATCTGA	244	
Db	2196	TGAACAAACATTGAGACGATGAGTACTCCCATCAGATCCAAACAAAGACATCTGA	2255	
QY	245	AGAAAGTCTCTGGGATTTCTGAGAGTCTCTGTGAGACTGTTTCAAGAGGATGTGTGTTT	304	
Db	2256	AGAAAGTCTCTGGGATTTCTGAGAGTCTCTGTGAGACTGTTTCAAGAGGATGTGTGTTT	2315	
QY	305	ACCCAAGGCTACACATCAAAAGAAATAGATAAAATGGAATGGAATTTAGAAAGTCTCC	364	
Db	2316	ACCCAAGGCTACACATCAAAAGAAATAGATAAAATGGAATTTAGAAAGTCTCC	2375	
QY	365	TGATAATGATGGTGTCTGAAAGCTCCCTGCAGAATGAAAGTTTCTATTCCAACTAAAGC	424	
Db	2376	TGATAATGATGGTGTCTGAAAGCTCCCTGCAGAATGAAAGTTTCTATTCCAACTAAAGC	2435	
QY	425	CTTAGAATTGATGGACATGCAAACTTTCAAGCAGAGCCTCCGAGAAAGCCATCTGCCTT	484	
Db	2436	CTTAGAATTGATGGACATGCAAACTTTCAAGCAGAGCCTCCGAGAAAGCCATCTGCCTT	2495	
QY	485	CGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCCTTGGAAATTGAAGAATGA	544	
Db	2496	CGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCCTTGGAAATTGAAGAATGA	2555	
QY	545	ACAAACATTGAGAGCAGATCAGATGTTCCCTTCAGAAATCAAAACAAAGAGGTTGAAGA	604	
Db	2556	ACAAACATTGAGAGCAGATCAGATGTTCCCTTCAGAAATCAAAACAAAGAGGTTGAAGA	2615	
QY	605	AAATTCTTGGGATTTCTGAGAGTCTCCGTGAGACTGTTTTCAGAAAGGATGTGTGTGTAAC	664	
Db	2616	AAATTCTTGGGATTTCTGAGAGTCTCCGTGAGACTGTTTTCAGAAAGGATGTGTGTGTAAC	2675	
QY	665	CAAGGCTPACATCAAAAGAAATGGATAAAATAAGTGGAAAAATTAGAAGATCAACTAG	724	
Db	2676	CAAGGCTPACATCAAAAGAAATGGATAAAATAAGTGGAAAAATTAGAAGATCAACTAG	2735	
QY	725	CCATACAAAATCTTTGGATACAGTTCAATCTTGTGAAAGACGAGGGAACCTTCAAAAAGA	784	
Db	2736	CCATACAAAATCTTTGGATACAGTTCAATCTTGTGAAAGACGAGGGAACCTTCAAAAAGA	2795	
QY	785	TCACGTGAAACACGTCACGGAAAAATGGAAACAAATGAAAGAAAGTTTGTGTACTGAA	844	
Db	2796	TCACGTGAAACACGTCACGGAAAAATGGAAACAAATGAAAGAAAGTTTGTGTACTGAA	2855	
QY	845	AAAGAACTGTGCAAGCAAAAGAAATAAATAATCAAGTTAGAGAACCAAAAAGTTAAATG	904	
Db	2856	AAAGAACTGTGCAAGCAAAAGAAATAAATAATCAAGTTAGAGAACCAAAAAGTTAAATG	2915	
QY	905	GGACAAAGAGCTCTGCAGTGTGAGATTGACTTTTAAACCAAGAGAAAGAGAGAGAA	964	

Db	3993	TTTAAAAA-CCGTATATATCAATATGAAAAAGAGAAAGCAGAAACA	4038
RESULT 3			
US-10-124-805-566			
; Sequence 566, Application US/10124805			
; Publication No. US20030166022A1			
; GENERAL INFORMATION:			
; APPLICANT: Houghton, Raymond L.			
; APPLICANT: Sleath, Paul R.			
; APPLICANT: Persing, David H.			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY			
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER			
; FILE REFERENCE: 210121.470C12			
; CURRENT APPLICATION NUMBER: US/10/124.805			
; CURRENT FILING DATE: 2002-04-15			
; NUMBER OF SEQ ID NOS: 627			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 565			
; LENGTH: 4047			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-124-805-566			
Query Match 95.6%; Score 1940; DB 15; Length 4047;			
Best Local Similarity 98.7%; Pred. No. 0;			
Matches 2001; Conservative 0; Mismatches 21; Indels 5; Gaps 5;			
QY	5	TGCGGTTAAAGATGCTCTCTGAAGGCTAACTCGGGAATGAAGTTCTTATTCACAACTAA	64
Db	2016	TCCTGTTAAAGATGCTCTCTGAAGGCTAACTCGGGAATGAAGTTCTTATTCACAACTAA	2075
QY	65	AGCCTTAGAATTGATGACATGCAAACTTTCAAGAGCAGAGGCTCCCGAGAGGCTCATCTGC	124
Db	2076	AGCCTTAGAATTGATGACATGCAAACTTTCAAGAGCAGAGGCTCCCGAGAGGCTCATCTGC	2135
QY	135	CTTCGAGGCTGCAATGAAATGCAAAAGCTGTGTTCCAAATTAAGCCTTGGAAATGAAGAA	184
Db	2136	CTTCGAGGCTGCAATGAAATGCAAAAGCTGTGTTCCAAATTAAGCCTTGGAAATGAAGAA	2195
QY	185	TGACCAACATTTAGAGCAGATGATATCTCCATCAGAACTCAAAACAAAGAGGACTATGA	244
Db	2196	TGACCAACATTTAGAGCAGATGATATCTCCATCAGAACTCAAAACAAAGAGGACTATGA	2555
QY	245	AGAAAGTTCTTGGGATCTGAGAGTCTCTGAGAGCTGTTTCAAGAGGATGTTGTTT	304
Db	2256	AGAAAGTTCTTGGGATCTGAGAGTCTCTGAGAGCTGTTTCAAGAGGATGTTGTTT	2315
QY	305	ACCCAGGCTACACATCAAAAGAAATAGATAAATTAATGGAATTAAGAGAGTCTCC	364
Db	2316	ACCCAGGCTACACATCAAAAGAAATAGATAAATTAATGGAATTAAGAGAGTCTCC	2375
QY	365	TGATAATGATGTTTCTGAAGGCTCCCTGAGAGTGAAGTGTCTATTTCCAACTAAAGC	424
Db	2376	TGATAATGATGTTTCTGAAGGCTCCCTGAGAGTGAAGTGTCTATTTCCAACTAAAGC	2435
QY	425	CTTAGAATTGATGACATGCAAACTTTCAAGAGGCTCCCGAGAGGCTCATCTGCCTT	484
Db	2436	CTTAGAATTGATGACATGCAAACTTTCAAGAGGCTCCCGAGAGGCTCATCTGCCTT	2495
QY	485	CGAGGCTGCAATGAAATGCAAAAGCTGTGTTCCAAATTAAGCCTTGGAAATGAAGATGA	544
Db	2496	CGAGGCTGCAATGAAATGCAAAAGCTGTGTTCCAAATTAAGCCTTGGAAATGAAGATGA	2555
QY	545	ACAAACATTTAGAGCAGATGATGTTTCCCTTCAGAACTCAAAACAAAGAGGTTGAAGA	604
Db	2556	ACAAACATTTAGAGCAGATGATGTTTCCCTTCAGAACTCAAAACAAAGAGGTTGAAGA	2615
QY	605	AAATTTCTGGGATTTCTGAGAGTCTCCGTGAGACTGTTTCAAGAGGATGTTGTTGACC	664
Db	2616	AAATTTCTGGGATTTCTGAGAGTCTCCGTGAGACTGTTTCAAGAGGATGTTGTTGACC	2675
QY	665	CAAGGCTACACATCAAAAGAAATGATTAATTAAGTGAAGATTTCAACTAG	724
Db	2676	CAAGGCTACACATCAAAAGAAATGATTAATTAAGTGAAGATTTCAACTAG	2735
QY	725	CCTATCAAAAATCTTGGATACAGTTCTTGTGAAAGAGCAAGGAACTTCAAAAAGA	784
Db	2736	CCTATCAAAAATCTTGGATACAGTTCTTGTGAAAGAGCAAGGAACTTCAAAAAGA	2795
QY	785	TCCTGTGAACAACTGACAGGAAATGGAACAATGGAAGAAGTTTGTGTACTGAA	844
Db	2796	TCCTGTGAACAACTGACAGGAAATGGAACAATGGAAGAAGTTTGTGTACTGAA	2855
QY	845	AAAGAACTGTGACAGAAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	904
Db	2856	AAAGAACTGTGACAGAAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	2915
QY	905	GGACAAAGAGTCTGACAGTGTGAGTTGACTTTTAAACCAAGAGAGAGAGAGAA	964
Db	2916	GGACAAAGAGTCTGACAGTGTGAGTTGACTTTTAAACCAAGAGAGAGAGAGAA	2975
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QY	1025	GAAGAGTTAGAGTGAAGTGAACCAACTTTGAAACAGGCTCTCAGAAATTAAGATTAAGAT	1084
Db	3036	GAAGAGTTAGAGTGAAGTGAACCAACTTTGAAACAGGCTCTCAGAAATTAAGATTAAGAT	3095
QY	1085	GAAGAGTTAGAGTGAAGTGAACCAACTTTGAAACAGGCTCTCAGAAATTAAGATTAAGAT	1144
Db	3096	GAAGAGTTAGAGTGAAGTGAACCAACTTTGAAACAGGCTCTCAGAAATTAAGATTAAGAT	3155
QY	1145	CTTACATGAAATTCATGTTGAAAGAAATTCGCAATGCTTAAACCTGGAATTAAGATTAAGAT	1204
Db	3156	CTTACATGAAATTCATGTTGAAAGAAATTCGCAATGCTTAAACCTGGAATTAAGATTAAGAT	3215
QY	1205	ACTGAAACCAACCACTACAGGAAAGAAATTAATTAATTAATTAATTAATTAATTAATTAAT	1264
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QY	1265	AGAAAGAAATGCTGAACTTCAGATCACTTAAACCTGAAAGAGGAAATTAATTAATTAAG	1324
Db	3276	AGAAAGAAATGCTGAACTTCAGATCACTTAAACCTGAAAGAGGAAATTAATTAATTAAG	3335
QY	1325	GGCATCTCAATATAGTGGGAGCTTAAAGTTCTGATGCTGAGACACAACTGCTCCTTC	1384
Db	3336	GGCATCTCAATATAGTGGGAGCTTAAAGTTCTGATGCTGAGACACAACTGCTCCTTC	3395
QY	1385	TAAATTAAGAGGAAACCAAGACAAAGAAATTAATTAATTAATTAATTAATTAATTAATTAAT	1444
Db	3396	TAAATTAAGAGGAAACCAAGACAAAGAAATTAATTAATTAATTAATTAATTAATTAATTAAT	3455
QY	1445	TAGACTGGCTTCTGCTGTAACAGACCAATGATCAAAATTTGACATCAAGAAAGTCAAGA	1504
Db	3456	TAGACTGGCTTCTGCTGTAACAGACCAATGATCAAAATTTGACATCAAGAAAGTCAAGA	3515
QY	1505	ACCTGCTTTCCACATTCGAGGAGATGCTTGTGTTGAAAGAAAGAAATTAATTAATTAATTAAT	1564
Db	3516	ACCTGCTTTCCACATTCGAGGAGATGCTTGTGTTGAAAGAAAGAAATTAATTAATTAATTAAT	3575
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Db	3576	TAGTACCGATATATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	3634
QY	1625	CCAAAGGCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1684
Db	3635	CCAAAGGCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	3694
QY	1685	TTTCAAGAACTGCAAAAGAGACCAACCTGTAACCACTGCTCAATGAGAGAACTGAA	1744
Db	3695	TTTCA - GAACTGCAAAAGAGACCAACCTGTAACCACTGCTCAATGAGAGAACTGAA	3753
QY	1745	CACATGTTCAAAACCAACCAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1804



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Db 3411 GGCATCTCAATATAGTGGGAGCTTAAAGTTCGTAGCTGAGAACAAATGCTCAGTTC 3470
QY 1385 TAAATTGAAGGAAAAAACAAGACAAAGAAATACTAGAGGAGAGAAATGAATCACACCATCC 1444
Db 3471 TAAATTGAAGGAAAAAACAAGACAAAGAAATACTAGAGGAGAGAAATGAATCACACCATCC 3530
QY 1445 TAGACTGGCTTCCTGCTGTAACAAGACCATGATCAAAATGTCATCAAGAAAGAGTCAAGA 1504
Db 3531 TAGACTGGCTTCCTGCTGTAACAAGACCATGATCAAAATGTCATCAAGAAAGAGTCAAGA 3590
QY 1505 ACTGCTTTCCACATTCGAGGAGATGCTTTGTCAGAAAGAAATGAATGTTGATGAG 1564
Db 3591 ACTGCTTTCCACATTCGAGGAGATGCTTTGTCAGAAAGAAATGAATGTTGATGAG 3650
QY 1565 TAGTACCGATATATAACAATGAGTGTCTCCATCAACCTCTTCTCAAGCTCAAGAGAAAT 1624
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QY 1625 CCNAAAGCCTAAATAATCTCAATATGCGAGGAGTGTCTTAAGAGAAATATACATTGG 1684
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Db 3829 CACATGTCNCAANCAAGCAAGATGATGTAACAAACACATGACAGACAGAGTCTCTA 3888
QY 1805 GATCAGAAATATTTTCAACTACAAAGCAAAATATGTCGCTTCAACAGCAATTAGTTTAT 1864
Db 3889 GATCAGAAATATTTTCAACTACAAAGCAAAATATGTCGCTTCAACAGCAATTAGTTTAT 3948
QY 1865 GCATTAANGAAGCTGCACAAAGCAAGATGATGTAACAAACACATGACAGACAGAGTCTCTA 1924
Db 3949 GCATTAANGAAGCTGCACAAAGCAAGATGATGTAACAAACACATGACAGACAGAGTCTCTA 4007
QY 1925 GAAATATGC-NCATCATCTTCTTAAAGAGAGAAATGAGGAGATATTTNATACNATAACCA 1983
Db 4008 GAAATATGCATCATCTCTTAAAGAGAGAAATGAGGAGATATTTNATACNATAACCA 4067
QY 1984 TTTAAAGACCGTATATTTTCAATGATGTAACAAAGCAAAATATGTCGCTTCAACAGCAATTAGTTTAT 2030
Db 4068 TTTAAAGACCGTATATTTTCAATGATGTAACAAAGCAAAATATGTCGCTTCAACAGCAATTAGTTTAT 4113

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RESULT 5
US-10-007-805-564
; Sequence 564, Application US/10007805
; Publication No. US20020150581A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Durham, Margerita
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.470C10
; CURRENT APPLICATION NUMBER: US/10/007,805
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 593
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 564
; LENGTH: 4458

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; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-007-805-564
Query Match 95.6%; Score 1940; DB 14; Length 4458;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 2001; Conservative 0; Mismatches 21; Indels 5; Gaps 5;
QY 5 TCCGCTTAAAGATGCTCTTCTGAAGGCTAACTCGGGAATGAAAGTTTCTATTCCAACTAA 64
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QY 65 ACCCTTAGAATGTGAGACATGCAAACTTTCAAAGCAGAGCTCCCGAGAGCCATCTGC 124
Db 2151 ACCCTTAGAATGTGAGACATGCAAACTTTCAAAGCAGAGCTCCCGAGAGCCATCTGC 2210
QY 125 CTTGAGGCTGCCATTGAATGCAAAAGTCTGTTCAAATAAAGCCCTTGAATGAAGAA 184
Db 2211 CTTGAGGCTGCCATTGAATGCAAAAGTCTGTTCAAATAAAGCCCTTGAATGAAGAA 2270
QY 185 TGAACAAACATTTGAGAGCAGATGAGATACCTCCATCAGAAATCCAAACAAAGAGCTATGA 244
Db 2271 TGAACAAACATTTGAGAGCAGATGAGATACCTCCATCAGAAATCCAAACAAAGAGCTATGA 2330
QY 245 AGAAAGTTCTTGGGATTTCTGAGAGTCTCTGTGAGACTGTTTTCACAGAGATGTGTGTT 304
Db 2331 AGAAAGTTCTTGGGATTTCTGAGAGTCTCTGTGAGACTGTTTTCACAGAGATGTGTGTT 2390
QY 305 ACCCAAGGCTACACATCAAAAGAAATAGATAAAATAAATGGAATAAATAGAGAGCTCC 364
Db 2391 ACCCAAGGCTACACATCAAAAGAAATAGATAAAATAAATGGAATAAATAGAGAGCTCC 2450
QY 365 TGATAATGATGTTTCTGAGAGCTCCCTGCAGAGTGAAGTTTCTATTCCAACTAAAGC 424
Db 2451 TGATAATGATGTTTCTGAGAGCTCCCTGCAGAGTGAAGTTTCTATTCCAACTAAAGC 2510
QY 425 CTTAGAAATGATGAGACATGCAAACTTTCAAAGCAGAGCTCCCGAGAGCCATCTGCCTT 484
Db 2511 CTTAGAAATGATGAGACATGCAAACTTTCAAAGCAGAGCTCCCGAGAGCCATCTGCCTT 2570
QY 485 CGAGCTCCCATTTGAATGCAAAAGTCTGTTCCAAATAAAGCCCTTGAATGAGATGA 544
Db 2571 CGAGCTCCCATTTGAATGCAAAAGTCTGTTCCAAATAAAGCCCTTGAATGAGATGA 2630
QY 545 ACACAAATTTGAGAGCAGATCAGATGTTCCCTTCAGAAATCAAAACAAAGAGGTTGAAGA 604
Db 2631 ACACAAATTTGAGAGCAGATCAGATGTTCCCTTCAGAAATCAAAACAAAGAGGTTGAAGA 2690
QY 605 AATTTCTTGGGATTTCTGAGAGTCTCCGTGAGACTGTTTCACAGAGATGTGTGTATC 664
Db 2691 AATTTCTTGGGATTTCTGAGAGTCTCCGTGAGACTGTTTCACAGAGATGTGTGTATC 2750
QY 665 CAAGCTACACATCAAAAGAAATGGAATAAAATGGAATAAAATGGAATAAAATGGAATAA 724
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QY 725 CCTATCAAAATCTTGATACAGTTCTGTTGAGAGCAAGAGGAGCTTCAAAAGCA 784
Db 2811 CCTATCAAAATCTTGATACAGTTCTGTTGAGAGCAAGAGGAGCTTCAAAAGCA 2870
QY 785 TCACTGTGAACACAGTACAGGAAATGGAACAAATGGAACAAATGGAACAAATGGAACAAAT 844
Db 2871 TCACTGTGAACACAGTACAGGAAATGGAACAAATGGAACAAATGGAACAAATGGAACAAAT 2930
QY 845 AAGGAACTGTGAGAGCAAGGAAATGGAACAAATGGAACAAATGGAACAAATGGAACAAAT 904
Db 2931 AAGGAACTGTGAGAGCAAGGAAATGGAACAAATGGAACAAATGGAACAAATGGAACAAAT 2990
QY 905 GGAACAGAGCTCTGAGTGTGAGATGACTTTAAACCAAGAGAGAGAGAGAGAGAGAGAGAG 964
Db 2991 GGAACAGAGCTCTGAGTGTGAGATGACTTTAAACCAAGAGAGAGAGAGAGAGAGAGAGAG 3050
QY 965 TGCCGATATATTAATGAAABAAATAGGGAAGAAATAGGGAAGAAATAGGGAAGAGAGAGAG 1024

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Db 3051 TCCGATATATAAATGAAAAATTTAGGAAAGAAATTTAGGAAGATCGAAGAGCGCATAG 3110  
Qy 1025 GAAAGAGTTAGAGTGAACCAACAACTTGAAACGGCTCTCAGATACAAAGATATAGAAAT 1084  
Db 3111 GAAAGAGTTAGAGTGAACCAACAACTTGAAACGGCTCTCAGATACAAAGATATAGAAAT 3170  
Qy 1085 GAAGAGTGTAGAAATTTGAATCAAGTTCTCAGATCATCAATCAATCAATCAATCAATCAAT 1144  
Db 3171 GAAGAGTGTAGAAATTTGAATCAAGTTCTCAGATCATCAATCAATCAATCAATCAATCAAT 3230  
Qy 1145 CTTACATGAAATTTGATTTGAAAGAAAGAAATTTGCCATGCTAAATTTGGAATAGCCAC 1204  
Db 3231 CTTACATGAAATTTGATTTGAAAGAAAGAAATTTGCCATGCTAAATTTGGAATAGCCAC 3290  
Qy 1205 ACTGAAACCAATATACAGGAAAGAAAGAAATTTGAGGACATTAAGATTTTAAA 1264  
Db 3291 ACTGAAACCAATATACAGGAAAGAAAGAAATTTGAGGACATTAAGATTTTAAA 3350  
Qy 1265 AGAAAGAAATGCTGAACCTTCAGATGACCTTAAATTTGAAAGGAAATCAATTAATAAAG 1324  
Db 3351 AGAAAGAAATGCTGAACCTTCAGATGACCTTAAATTTGAAAGGAAATCAATTAATAAAG 3410  
Qy 1325 GGCATCTCAATATAGTGGGAGCTTAAAGTTCTGATAGCTGAGAACCAATGCTCACTTC 1384  
Db 3411 GGCATCTCAATATAGTGGGAGCTTAAAGTTCTGATAGCTGAGAACCAATGCTCACTTC 3470  
Qy 1385 TAAATTTGAAGGAAAGAAAGAAAGAAATTTAGAGGAGGAGAAATTTGAATCACACCATCC 1444  
Db 3471 TAAATTTGAAGGAAAGAAAGAAAGAAATTTAGAGGAGGAGAAATTTGAATCACACCATCC 3530  
Qy 1445 TAGACTGGCTTCTGCTGTACAGACCATGATCAATTTGTGACATCAAGAAAGATCAAGA 1504  
Db 3531 TAGACTGGCTTCTGCTGTACAGACCATGATCAATTTGTGACATCAAGAAAGATCAAGA 3590  
Qy 1505 ACTGCTTTCCATTTGACAGGAGATGCTTTGTTGCAAGAAAGAAATTTGATTTGATGGAG 1564  
Db 3591 ACTGCTTTCCATTTGACAGGAGATGCTTTGTTGCAAGAAAGAAATTTGATTTGATGGAG 3650  
Qy 1565 TAGTACCGATATATAACATAGGTTGCTCCATCAACACTTTCTGAGCTCAAGGAAAT 1624  
Db 3651 TAGTA-CGATATATAACATAGGTTGCTCCATCAACACTTTCTGAGCTCAAGGAAAT 3709  
Qy 1625 CCNAAAGCTTAAATTTAATCTCAATTTATGAGGAGATGCTTAAAGGAAATACATTTGG 1684  
Db 3710 CCNAAAGCTTAAATTTAATCTCAATTTATGAGGAGATGCTTAAAGGAAATACATTTGG 3769  
Qy 1685 TTTTCAGGAACATGCAACAAAGAGACCAACGTGAAACACACAGTGTCAATGAAGGAGCTGAA 1744  
Db 3770 TTTTCA-GAATGCAACAAAGAGACCAACGTGAAACACACAGTGTCAATGAAGGAGCTGAA 3828  
Qy 1745 CACATGTTTCAANGGACAGATATGTTGACAAACACACACTGANCAGCAGGATCTCTA 1804  
Db 3829 CACATGTTTCAANGGACAGATATGTTGACAAACACACACTGANCAGCAGGATCTCTA 3888  
Qy 1805 GATCAGAAATTTTCAACTACAAAGCAAAATATSTGGCTTCAACACCAATTTAGTTTCAT 1864  
Db 3889 GATCAGAAATTTTCAACTACAAAGCAAAATATSTGGCTTCAACACCAATTTAGTTTCAT 3948  
Qy 1865 GCACATANGAAGCTGACAAACAAAGGACAGATATGATTTGATTTTCTTTGAGAG 1924  
Db 3949 GCACATANGAAGCTGACAAACAAAGGACAGATATGATTTGATTTTCTTTGAGAG 4007  
Qy 1925 GAAATGTC-NCATCATCTTTCTTAAAGAGAAATAGGAGATATTTTAAATTAACATTAACCA 1983  
Db 4008 GAAATGTCACATCATCTCTTAAAGAGAAATAGGAGATATTTTAAATTAACATTAACCA 4067  
Qy 1984 TTTTAAAAAACCCTATATTTTCAATATGGAATTTTAAAAAATAAAAAA 2030  
Db 4068 TTTTAAAAA-CCGTATATATCAATATGGAATTTTAAAAAAGAGAAACCA 4113

RESULT 6

US-10-076-622-564  
; Sequence 564, Application US/10076622  
; Publication No. US20030023036A1  
; GENERAL INFORMATION:  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Sleath, Paul R.  
; APPLICANT: Persing, David H.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.470C11  
; CURRENT APPLICATION NUMBER: US/10/076,622  
; NUMBER OF SEQ ID NOS: 627  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 564  
; LENGTH: 4458  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-076-622-564

Query Match 95.6%; Score 1940; DB 15; Length 4458;  
Best Local Similarity 98.7%; Pred. No. 0;  
Matches 2001; Conservative 0; Mismatches 21; Indels 5; Gaps 5;  
Qy 5 TGGCGTTAAGATGCTCTCTGAAGCTAACTGCGGAATGAAAGTTTCTATTCCAACTAA 64  
Db 2091 TCTGTATAAGATGGTCTTCTGAAGCTAACTGCGGAATGAAAGTTTCTATTCCACTAA 2150  
Qy 65 AGCTTTAGAAATTTGATGGACATGCAAACTTTCAAAGCAGAGCTCCCGAAGAGCCATCTGC 124  
Db 2151 AGCTTTAGAAATTTGATGGACATGCAAACTTTCAAAGCAGAGCTCCCGAAGAGCCATCTGC 2210  
Qy 125 CTTGAGCCCTGCCATTTGAATGCAAAAGCTGTTTCCAAATGAAAGCTTTGGATTCAAGAA 184  
Db 2211 CTTGAGCCCTGCCATTTGAATGCAAAAGCTGTTTCCAAATGAAAGCTTTGGATTCAAGAA 2270  
Qy 185 TGAACAAACATTTGAGAGCAGATGAGATCTCCCATCAGAAATCCAAACAAAGAGACTATGA 244  
Db 2271 TGAACAAACATTTGAGAGCAGATGAGATCTCCCATCAGAAATCCAAACAAAGAGACTATGA 2330  
Qy 245 AGAAATCTTTGGGATTTGAGAGTCTCTGTGAGACTGTTTCCAGAGAGGATGTGTGTT 304  
Db 2331 AGAAATCTTTGGGATTTGAGAGTCTCTGTGAGACTGTTTCCAGAGAGGATGTGTGTT 2390  
Qy 305 ACCCAAGGCTTACATCAACAAAGAAATAGATAAAATTAATGAAATTTAGAAAGACTCTCC 364  
Db 2391 ACCCAAGGCTTACATCAACAAAGAAATAGATAAAATTAATGAAATTTAGAAAGACTCTCC 2450  
Qy 365 TGATAATGATGTTTCTGAGGCTCCCTGCGAGATGAAAGTTTCTATTCCAACTAAAGC 424  
Db 2451 TGATAATGATGTTTCTGAGGCTCCCTGCGAGATGAAAGTTTCTATTCCAACTAAAGC 2510  
Qy 425 CTTAGAAATTTGAGCAGATGCAAACTTTCAAAGCAGAGCTCCCGAAGAGCCATCTGCTTC 484  
Db 2511 CTTAGAAATTTGAGCAGATGCAAACTTTCAAAGCAGAGCTCCCGAAGAGCCATCTGCTTC 2570  
Qy 485 CGAGCCTGCCATTTGAAATGCAAAAGTCTGTTCCAAATAAAGCTTTGGAATTTGAAGATGA 544  
Db 2571 CGAGCCTGCCATTTGAAATGCAAAAGTCTGTTCCAAATAAAGCTTTGGAATTTGAAGATGA 2630  
Qy 545 ACAACATTTGAGCAGATGAGATGTTCCCTTCAGAAATCAAAACAAAGAGGTTGAAGA 604  
Db 2631 ACAACATTTGAGCAGATGAGATGTTCCCTTCAGAAATCAAAACAAAGAGGTTGAAGA 2690  
Qy 605 AAATTTCTTGGGATTTCTGAGAGTCTCCGTGAGACTGTTTCCAGAGAGGATGTGTGTATCC 664  
Db 2691 AAATTTCTTGGGATTTCTGAGAGTCTCCGTGAGACTGTTTCCAGAGAGGATGTGTGTATCC 2750  
Qy 665 CAAGGCTTACATCAACAAAGAAATGATTAATTAAGTGGAAATTTAGAGATTTCACTAG 724  
Db 2751 CAAGGCTTACATCAACAAAGAAATGATTAATTAAGTGGAAATTTAGAGATTTCACTAG 2810  
Qy 725 CCTATCAAAATCTTGGATACAGTTCATTTCTTGTGAAGAGCAGAGGAACTTCAAAAGA 784



[illegible]

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Db      3889  GATCAGAAATTTATTTCAACTACAAGCAAAAATATGTGCTTCAACAGCAATTAGTTCAT 3944
Qy      1865  GCACATAANGAAAGCTGACACAAACAAAGCAAGATAACAATGTATNTTCATNTTCTTGAGAG 1924
Db      3949  GCACATAA--GAAAGCTGACACAAACAAAGCAAGATAACAATGTATTTTCTTGAGAG 4007
Qy      1925  GAAATGCG-NCATCATCTTCTTAAAGAGAGAAAATGAGGAGATATTTTATTCNATAACCA 1983
Db      4008  GAAATGCAACATCATCTCTTAAGAGAGAAAATGAGGAGATATTTTATTCATAACCA 4067
Qy      1984  TTTAAAAAACCCGTATATTTTCAATATGTGAAAAAAAANAAAAA 2030
Db      4068  TTTAAAAA--CCGTATATATCAATATGAAAAAGAGAAACAGAAACA 4113

RESULT 7
US-10-177-293-333
; Sequence 333, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavarpu, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Pusztai, Lajos
; APPLICANT: Mexic, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSES-
; TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MEI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: BlastSeq for Windows Version 4.0
; SEQ ID NO 333
; LENGTH: 4456
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-177-293-333

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		95.6%	Score 1940;	DB 15;	Length 4458;
		Best Local Similarity 98.7%;	Pred. No. 0;		
		Matches 2001;	Conservative 0;	Mismatches 21;	Indels 5; Gaps 5;
Qy	5	TGCGGTAAAGATGCTTCTGAAAGCTAACTGCGGAATGAAAGTTCTATTCCAACTAA	64		
Db	2091	TCTGTTTAAGATGCTTCTGAAAGCTAACTGCGGAATGAAAGTTCTATTCCAACTAA	2150		
Qy	65	AGCCTTAGAATTGATGGACATGCAAACTTTTCAAGACAGACGCTCCGAGGAAGCGCATCTGC	124		

Db 2151 AGCCTTAGAATTGATGGACATCAAACTTTCAAAGCAGAGCCTCCCGAAGACCACTGTC 2210  
Qy 125 CTTGAGCCTGCAATGTAATCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATGAAGAA 184  
Db 2211 CTTGAGCCTGCAATGTAATCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATGAAGAA 2270  
Qy 185 TGAACAAACATTTGAGAGCAGATGAGATCTCCATCAGATCCAAACAAAGGACTATGA 244  
Db 2271 TGAACAAACATTTGAGAGCAGATGAGATCTCCATCAGATCCAAACAAAGGACTATGA 2330  
Qy 245 AGAAGTCTTCGGATTTCTGAGACTCTCTGTGAGACTGTTTCAACAAGGATGTGTGTT 304  
Db 2331 AGAAGTCTTCGGATTTCTGAGACTCTCTGTGAGACTGTTTCAACAAGGATGTGTGTT 2390  
Qy 305 ACCAAGGCTACACATCAAAAAGAAATAGATAAAATAAATGAAATTAAGAGAGTCTCC 364  
Db 2391 ACCAAGGCTACACATCAAAAAGAAATAGATAAAATAAATGAAATTAAGAGAGTCTCC 2450  
Qy 365 TGATAATGATGTTTTCTGAAGGCTCCCTGAGAAATGAAGTTTCTATTCCAACTAAAGC 424  
Db 2451 TGATAATGATGTTTTCTGAAGGCTCCCTGAGAAATGAAGTTTCTATTCCAACTAAAGC 2510  
Qy 425 CTTAGAAATGATGGACATCAAACTTTCAAAGCAGGCTCCCGAAGACCACTGCTT 484  
Db 2511 CTTAGAAATGATGGACATCAAACTTTCAAAGCAGGCTCCCGAAGACCACTGCTT 2570  
Qy 485 CGAGCCTGCCATTGAAATGAAAAGTCTGTTCCAAATAAAGCCTTGGAAATGAAGATGA 544  
Db 2571 CGAGCCTGCCATTGAAATGAAAAGTCTGTTCCAAATAAAGCCTTGGAAATGAAGATGA 2630  
Qy 545 ACAACATTTGAGAGCAGATCAGATGTTCCCTTCAGATCAAAACAAAGAGGTTGAAGA 604  
Db 2631 ACAACATTTGAGAGCAGATCAGATGTTCCCTTCAGATCAAAACAAAGAGGTTGAAGA 2690  
Qy 605 AAATCTTGGGATTTCTGAGACTCCGTGAGACTGTTTCAACAAGGATGTGTGTACC 664  
Db 2691 AAATCTTGGGATTTCTGAGACTCCGTGAGACTGTTTCAACAAGGATGTGTGTACC 2750  
Qy 665 CAAAGCTACACATCAAAAAGAAATGGAATAAATAGTGGAATTAAGAGATTCAACTAG 724  
Db 2751 CAAAGCTACACATCAAAAAGAAATGGAATAAATAGTGGAATTAAGAGATTCAACTAG 2810  
Qy 725 CTTATCAAAAATCTTGATACAGTTTCACTTCTGAAAGAGCAAGGAACTTCAAAAAGA 784  
Db 2811 CTTATCAAAAATCTTGATACAGTTTCACTTCTGAAAGAGCAAGGAACTTCAAAAAGA 2870  
Qy 785 TCACTGTGAACCACTGACAGGAAATGGAACAAATGAAAGAAAGTTTGTGTACTGAA 844  
Db 2871 TCACTGTGAACCACTGACAGGAAATGGAACAAATGAAAGAAAGTTTGTGTACTGAA 2930  
Qy 845 AAAGAACTGTGAGAGCAAGAAATGAAATCAAGTTGAGACCAAGAAAGTTAAATG 904  
Db 2931 AAAGAACTGTGAGAGCAAGAAATGAAATCAAGTTGAGACCAAGAAAGTTAAATG 2990  
Qy 905 GGAACAAGAGCTCTGCAAGTGTGAGATTTGACTTTAAACCAAGAGAGAGAGAGAGAA 964  
Db 2991 GGAACAAGAGCTCTGCAAGTGTGAGATTTGACTTTAAACCAAGAGAGAGAGAGAA 3050  
Qy 965 TCCGATATATTAATGAAATTAAGGAAATTAAGGAAATTAAGGAAATTAAGGAAATTAAG 1024  
Db 3051 TCCGATATATTAATGAAATTAAGGAAATTAAGGAAATTAAGGAAATTAAGGAAATTAAG 3110  
Qy 1025 GAAAGAGTTAGAAGTGAACCAACCTTGAACAGGCTCTCAGAAATCAAGATATAGAAT 1084  
Db 3111 GAAAGAGTTAGAAGTGAACCAACCTTGAACAGGCTCTCAGAAATCAAGATATAGAAT 3170  
Qy 1085 GAAGAGTTAGAAGTGAATTTGAATCAGGTTTCTACACTCATGAAATGAATTAATCT 1144  
Db 3171 GAAGAGTTAGAAGTGAATTTGAATCAGGTTTCTACACTCATGAAATGAATTAATCT 3230  
Qy 1145 CTTACATGAATTTGATGTTGAAAAGGAAATGCAATGCTTAAACCTGGAATAGCCAC 1204  
Db 3231 CTTACATGAATTTGATGTTGAAAAGGAAATGCAATGCTTAAACCTGGAATAGCCAC 3290

Qy 1205 ACTGAAACACCATAACACGAAAGGAAATAAATACTTTGAGGACATTAAGATTTTAA 1264  
Db 3291 ACTGAAACACCATAACACGAAAGGAAATAAATACTTTGAGGACATTAAGATTTTAA 3350  
Qy 1265 AGAAAGAAATGCTGAACTTCAGATGACCTTGAAGAGGAAATCAATTAACATAAAG 1324  
Db 3351 AGAAAGAAATGCTGAACTTCAGATGACCTTGAAGAGGAAATCAATTAACATAAAG 3410  
Qy 1325 GGATCTCAATATAGTGGGAGCTTAAAGTTCTGATAGCTGAGAACACAAATGCTCACTTC 1384  
Db 3411 GGATCTCAATATAGTGGGAGCTTAAAGTTCTGATAGCTGAGAACACAAATGCTCACTTC 3470  
Qy 1385 TAAATGAAGGAAACAAAGACAAAGAAATCTTAGAGGAGAAATTAATCAACCATCC 1444  
Db 3471 TAAATGAAGGAAACAAAGACAAAGAAATCTTAGAGGAGAAATTAATCAACCATCC 3530  
Qy 1445 TAGACTGGCTTCTGCTTCAAGACCAATGATCAAAATTTGACATCAAGAAAAGTCAAGA 1504  
Db 3531 TAGACTGGCTTCTGCTTCAAGACCAATGATCAAAATTTGACATCAAGAAAAGTCAAGA 3590  
Qy 1505 ACCTGCTTTCACATTCAGGAGATGCTTGTGAAAGAAAATAAATGATGTGTGAG 1564  
Db 3591 ACCTGCTTTCACATTCAGGAGATGCTTGTGAAAGAAAATAAATGATGTGTGAG 3650  
Qy 1565 TAGTACCGATATATAAATGAGGCTCCATCAACCACTTTCTGAGCTCAAGGAAAT 1624  
Db 3651 TAGTACCGATATATAAATGAGGCTCCATCAACCACTTTCTGAGCTCAAGGAAAT 3709  
Qy 1625 CCNAGGCTTAAATAATTAATCTCAATATGCGAGGATGCTCTAAGAGAAAATAACATCG 1684  
Db 3710 CCNAGGCTTAAATAATTAATCTCAATATGCGAGGATGCTCTAAGAGAAAATAACATCG 3769  
Qy 1685 TTTTCAAGCAATGACCAAGAGAGACCAAGCTGAAACACAGCTGCAAGGAAAGCTGAA 1744  
Db 3770 TTTTCAAGCAATGACCAAGAGAGACCAAGCTGAAACACAGCTGCAAGGAAAGCTGAA 3828  
Qy 1745 CACATGTCNCAANCAAGCAAGATNATGTAACAAACACACTGANCAGCAGGAGTCTCTA 1804  
Db 3829 CACATGTCNCAANCAAGCAAGATNATGTAACAAACACACTGANCAGCAGGAGTCTCTA 3888  
Qy 1805 GATCAGAAATTTTCAACTTCAAGGAAATATGCTGGCTTCAACAGCAATTAGTTCTAT 1864  
Db 3889 GATCAGAAATTTTCAACTTCAAGGAAATATGCTGGCTTCAACAGCAATTAGTTCTAT 3948  
Qy 1865 GCACATNCAAGAGCTGACAAACAAAGAGATACAAATGATNTTCAATNTCTTGAGAG 1924  
Db 3949 GCACATNCAAGAGCTGACAAACAAAGAGATACAAATGATNTTCAATNTCTTGAGAG 4007  
Qy 1925 GAAATGTCNCAATGATTTTCAATATGAGGAAATTAAGGAGATTTTAAATCAATAACCA 1983  
Db 4008 GAAATGTCNCAATGATTTTCAATATGAGGAAATTAAGGAGATTTTAAATCAATAACCA 4067  
Qy 1984 TTTAAAAAACCCGTATATTTCAATATGAGGAAATTAAGGAGATTTTAAATCAATAACCA 2030  
Db 4068 TTTAAAAAACCCGTATATTTCAATATGAGGAAATTAAGGAGATTTTAAATCAATAACCA 4113

RESULT 8

US-10-124-805-564  
; Sequence 564, Application US/10124805  
; Publication No. US2003016602A1  
; GENERAL INFORMATION:  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Sleath, Paul R.  
; APPLICANT: Persing, David H.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER  
; FILE REFERENCE: 210121.470C12  
; CURRENT FILING DATE: 2002-04-15  
; NUMBER OF SEQ ID NOS: 627  
; SOFTWARE: Fast-Seq for Windows Version 4.0

; SEQ ID NO 564  
; LENGTH: 4458  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-124-805-564

Query Match 95.6%; Score 1940; DB 15; Length 4458;  
Best Local Similarity 98.7%; Pred. No. 0;  
Matches 2001; Conservative 0; Mismatches 21; Indels 5; Gaps 5;

QY	5	TGCCGTTAAAGATGGTCTTCTGAAGGCTAACTGCGGAATGAAGTTTCTATTCCAACTAA	64
DB	2091	TCCTGTTAAAGATGGTCTTCTGAAGGCTAACTGCGGAATGAAGTTTCTATTCCAACTAA	2150
QY	65	AGCCTTAGAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAGCCATCTGC	124
DB	2151	AGCCTTAGAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAGCCATCTGC	2210
QY	125	CTTGAGGCTGCCATTGAAATGCAAAAGTCTGTCCAAATTAAGCCTTGAATTTAGAA	184
DB	2211	CTTGAGGCTGCCATTGAAATGCAAAAGTCTGTCCAAATTAAGCCTTGAATTTAGAA	2270
QY	185	TGAACAAACATTGAGAGCAGATGAGATACTCCCATCAGAAATCCAAACAAAGGACTATGA	244
DB	2271	TGAACAAACATTGAGAGCAGATGAGATACTCCCATCAGAAATCCAAACAAAGGACTATGA	2330
QY	245	AGAAAGTCTTGGGATTCGTGAGTCTCTGTGAGACTGTTCACAGAGGATGTGTTTT	304
DB	2331	AGAAAGTCTTGGGATTCGTGAGTCTCTGTGAGACTGTTCACAGAGGATGTGTTTT	2390
QY	305	ACCCAAAGCTACACATCAAAAGAAATAGATAAAATTAATGGAAATTTAGAAAGTCTCC	364
DB	2391	ACCCAAAGCTACACATCAAAAGAAATAGATAAAATTAATGGAAATTTAGAAAGTCTCC	2450
QY	365	TGATAATGATGTTTTCTGAGGCTCCCTGAGAGATGAAGTTTCTATTCCAACTAAAGC	424
DB	2451	TGATAATGATGTTTTCTGAGGCTCCCTGAGAGATGAAGTTTCTATTCCAACTAAAGC	2510
QY	425	CTTAGAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCGAGAGCCATCTGCCTT	484
DB	2511	CTTAGAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCGAGAGCCATCTGCCTT	2570
QY	485	CGAGCCTGCAATTGAAATGCAAAAGTCTGTTCCAAATTAAGCCTTGGAAATTTGAAGATGA	544
DB	2571	CGAGCCTGCAATTGAAATGCAAAAGTCTGTTCCAAATTAAGCCTTGGAAATTTGAAGATGA	2630
QY	545	ACAAACATTGAGAGCAGATCAGATGTCCTTCAGAAATCAAAACAAAGAGGTTGAGA	604
DB	2631	ACAAACATTGAGAGCAGATCAGATGTCCTTCAGAAATCAAAACAAAGAGGTTGAGA	2690
QY	605	AAATTCCTTGGGATTCGTGAGAGTCTCCGTGAGACTGTTCACAGAGGATGTGTGTACC	664
DB	2691	AAATTCCTTGGGATTCGTGAGAGTCTCCGTGAGACTGTTCACAGAGGATGTGTGTACC	2750
QY	665	CAAGGCTACACATCAAAAGAAATGGATAAAATTAAGTGAATTTAGAAATTTCAACTAG	724
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QY	725	CCTATCAAAATCTTGGATACAGTTCAATCTTGTGAAGAGCAAGGAACTTCAAAAAGA	784
DB	2811	CCTATCAAAATCTTGGATACAGTTCAATCTTGTGAAGAGCAAGGAACTTCAAAAAGA	2870
QY	785	TCCTGTGAACACGCTACAGGAAATTTGGAACAAATTAAGTGAATTTGTGTACTGAA	844
DB	2871	TCCTGTGAACACGCTACAGGAAATTTGGAACAAATTAAGTGAATTTGTGTACTGAA	2930
QY	845	AAAGAACTGTCAAGAGCAAAAGAAATTAATCAAGTTAGAGAACCAAAAAGTTAAATG	904
DB	2931	AAAGAACTGTCAAGAGCAAAAGAAATTAATCAAGTTAGAGAACCAAAAAGTTAAATG	2990
QY	905	GGAAACAGAGCTCTGCAGTGTGAGATTGATTTTAAACCAAGAGAGAGAGAGAGAAA	964
DB	2991	GGAAACAGAGCTCTGCAGTGTGAGATTGATTTTAAACCAAGAGAGAGAGAGAGAAA	3050

QY	965	TGCCGATATATTAAATGAAAAAATTAGGGAAGAAATTAGGAAGAAATCGAAGAGCAGCATAG	1024
DB	3051	TGCCGATATATTAAATGAAAAAATTAGGGAAGAAATTAGGAAGAAATCGAAGAGCAGCATAG	3110
QY	1025	GAAAGAGTTAGAGTGAAGCAACAACTTGAACAGGCTCTCAGATAACAAGATATAGAAAT	1084
DB	3111	GAAAGAGTTAGAGTGAAGCAACAACTTGAACAGGCTCTCAGATAACAAGATATAGAAAT	3170
QY	1085	GAAAGAGTTAGAGTGAAGTAAATTTGAATCAGGTTTCTCACATCATGAAATGAAATTTATCT	1144
DB	3171	GAAAGAGTTAGAGTGAAGTAAATTTGAATCAGGTTTCTCACATCATGAAATGAAATTTATCT	3230
QY	1145	CTTACATGAAATTCGATGTTGAAAAAGGAAATTTGCCATGCTAAACCTGGAATATAGCCAC	1204
DB	3231	CTTACATGAAATTCGATGTTGAAAAAGGAAATTTGCCATGCTAAACCTGGAATATAGCCAC	3290
QY	1205	ACTGAAACACCAATACACAGGAAAGGAAATTAATTAATCTTTGAGGACATTAAGATTTTAA	1264
DB	3291	ACTGAAACACCAATACACAGGAAAGGAAATTAATTAATCTTTGAGGACATTAAGATTTTAA	3350
QY	1265	AGAAAGAAATGCTGAACTTCAAGATGACCTTAAACTGAAAGGAAATCATTAACCTAAAG	1324
DB	3351	AGAAAGAAATGCTGAACTTCAAGATGACCTTAAACTGAAAGGAAATCATTAACCTAAAG	3410
QY	1325	GGCATCTCAATATAGTGGGACGCTTAAAGTTCTGATAGCTGAGAACACAATGCTCCTTC	1384
DB	3411	GGCATCTCAATATAGTGGGACGCTTAAAGTTCTGATAGCTGAGAACACAATGCTCCTTC	3470
QY	1385	TAAATGAAAGGAAACAAAGCAAAAGAAATTAAGTGAAGGAGAAATTAATCACCCTTCC	1444
DB	3471	TAAATGAAAGGAAACAAAGCAAAAGAAATTAAGTGAAGGAGAAATTAATCACCCTTCC	3530
QY	1445	TAGACTGGCTTCTGCTGTCAAGACCATGATCAAAATTTGACATCAAGAAAAAGTCAAGA	1504
DB	3531	TAGACTGGCTTCTGCTGTCAAGACCATGATCAAAATTTGACATCAAGAAAAAGTCAAGA	3590
QY	1505	ACCTGCTTCCCATTTGCAAGGAGATGCTTTGTTGCAAGAAAAATTAATGTTGATGTGAG	1564
DB	3591	ACCTGCTTCCCATTTGCAAGGAGATGCTTTGTTGCAAGAAAAATTAATGTTGATGTGAG	3650
QY	1565	TAGTCCGATATATACAAATGAGGCTGCTCCTCAACCACTTTCTGAAGCTCAAGGAAAT	1624
DB	3651	TAGTCCGATATATACAAATGAGGCTGCTCCTCAACCACTTTCTGAAGCTCAAGGAAAT	3709
QY	1625	CCAAAGCCTTAAATTAATCTCAATTTATGAGGAGATGCTCTAAGAGAAATATCATTTGG	1684
DB	3710	CCAAAGCCTTAAATTAATCTCAATTTATGAGGAGATGCTCTAAGAGAAATATCATTTGG	3769
QY	1685	TTTCAGGAACTGCAAAAGAGACCAACGCTGAACACACAGTGTCAAAATGAAGAACTGAA	1744
DB	3770	TTTCA - GAACATGCAAAAGAGACCAACGCTGAACACACAGTGTCAAAATGAAGAACTGAA	3828
QY	1745	CACATGTTTCAAANCGAACAAAGATNAATGTGAACAAAACACACTGAACAGAGGCTCTA	1804
DB	3829	CACATGTTTCAAANCGAACAAAGATNAATGTGAACAAAACACACTGAACAGAGGCTCTA	3888
QY	1805	GATCAGAAATTTTCACTCAAGAGCAAAATATGTTGGCTTCAACAGCAATTTAGTTTCA	1864
DB	3889	GATCAGAAATTTTCACTCAAGAGCAAAATATGTTGGCTTCAACAGCAATTTAGTTTCA	3948
QY	1865	GCATTAAGGAAAGCTGACAAACAAAGCAAGATTAACAATTTGATTTTCAATTTCTTGAGAG	1924
DB	3949	GCATTAAGGAAAGCTGACAAACAAAGCAAGATTAACAATTTGATTTTCAATTTCTTGAGAG	4007
QY	1925	GAAATGCT - NCATCATCTTCTTAAGAGAAATTAAGGAGATTTTATTTACNATTAACCA	1983
DB	4008	GAAATGCT - NCATCATCTTCTTAAGAGAAATTAAGGAGATTTTATTTACNATTAACCA	4067
QY	1984	TTTAAAAAACCCGTATATTTTCAATATGAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2030
DB	4068	TTTAAAAAACCCGTATATATCAATATGAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG	4113

QY	605	AAATCTTTGGGATTTCTGAGAGTCTCCGTTGAGACTGTTTTCACAGAAAGATGTGTGTGTAAC	664
DB	1854	AAATCTTTGGGATTTCTGAGAGTCTCCGTTGAGACTGTTTTCACAGAAAGATGTGTGTGTAAC	1913
QY	665	CAAGCTACACATCAAAAGAAATGGATTAATTAAGTGGAAATTAAGAAATTCACATAG	724
DB	1914	CAAGCTACACATCAAAAGAAATGGATTAATTAAGTGGAAATTAAGAAATTCACATAG	1973
QY	725	CCTATCAAAATCTTTGGATACAGATTCATTCTTTGTAAGACCAAGGAACTTCAAAAGA	784
DB	1974	CCTATCAAAATCTTTGGATACAGATTCATTCTTTGTAAGACCAAGGAACTTCAAAAGA	2033
QY	785	TCATCTGTAACCAACGTACAGGAAATGGAAATTAAGTGGAAATTAAGAAATTCACATAG	844
DB	2034	TCATCTGTAACCAACGTACAGGAAATGGAAATTAAGTGGAAATTAAGAAATTCACATAG	2093
QY	845	AAAGAAATCTTCAGAAACCAAAAGAAATTAATTAAGTGGAAATTAAGAAATTCACATAG	904
DB	2094	AAAGAAATCTTCAGAAACCAAAAGAAATTAATTAAGTGGAAATTAAGAAATTCACATAG	2153
QY	905	GGAAACAAGAGCTCTGAGTGTGAGATTCATCTTTAAACCAAGAAAGAAAGAAAGAA	964
DB	2154	GGAAACAAGAGCTCTGAGTGTGAGATTCATCTTTAAACCAAGAAAGAAAGAAAGAA	2213
QY	965	TGCCGATATTAATTAAGAAATTAAGTGGAAATTAAGTGGAAATTAAGTGGAAATTAAGTGG	1024
DB	2214	TGCCGATATTAATTAAGAAATTAAGTGGAAATTAAGTGGAAATTAAGTGGAAATTAAGTGG	2273
QY	1025	GAAAGGTTTGAAGTGAACCAACACTTGAACAGAGCTCTCAGAAATTAAGTGGAAATTAAGTGG	1084
DB	2274	GAAAGGTTTGAAGTGAACCAACACTTGAACAGAGCTCTCAGAAATTAAGTGGAAATTAAGTGG	2333
QY	1085	GAAAGGTTTGAAGTGAACCAACACTTGAACAGAGCTCTCAGAAATTAAGTGGAAATTAAGTGG	1144
DB	2334	GAAAGGTTTGAAGTGAACCAACACTTGAACAGAGCTCTCAGAAATTAAGTGGAAATTAAGTGG	2393
QY	1145	CTTACATGAAATTTGATCTTTGAAAGAAAGAAATTCATCTTTAAACCAAGAAAGAAAGAA	1204
DB	2394	CTTACATGAAATTTGATCTTTGAAAGAAAGAAATTCATCTTTAAACCAAGAAAGAAAGAA	2453
QY	1205	ACTGAAACCAATTAAGTGGAAATTAAGTGGAAATTAAGTGGAAATTAAGTGGAAATTAAGTGG	1264
DB	2454	ACTGAAACCAATTAAGTGGAAATTAAGTGGAAATTAAGTGGAAATTAAGTGGAAATTAAGTGG	2513
QY	1265	AGAAAGAAATTTGATCTTTGAAAGAAAGAAATTCATCTTTAAACCAAGAAAGAAAGAA	1324
DB	2514	AGAAAGAAATTTGATCTTTGAAAGAAAGAAATTCATCTTTAAACCAAGAAAGAAAGAA	2573
QY	1325	GGCATCTCAATATAGTGGGAGCTTAAAGTCTGTGATGATGAGACATCAATCTCCTCCTTC	1384
DB	2574	GGCATCTCAATATAGTGGGAGCTTAAAGTCTGTGATGATGAGACATCAATCTCCTCCTTC	2633
QY	1385	TAAATTTGAAGGAAACCAAGACCAAGAAATTAAGTGGAAATTAAGTGGAAATTAAGTGGAA	1444
DB	2634	TAAATTTGAAGGAAACCAAGACCAAGAAATTAAGTGGAAATTAAGTGGAAATTAAGTGGAA	2693
QY	1445	TAGACTGGCTTCTGCTGTACAGACCATGATCAAAATTTGATGATGAGACATCAAGAAAGTCAAG	1504
DB	2694	TAGACTGGCTTCTGCTGTACAGACCATGATCAAAATTTGATGATGAGACATCAAGAAAGTCAAG	2753
QY	1505	ACCTGCTTTCCATTTGAGGAGATCTGTTTTCAGAAAGAAATTAAGTGGAAATTAAGTGGAA	1564
DB	2754	ACCTGCTTTCCATTTGAGGAGATCTGTTTTCAGAAAGAAATTAAGTGGAAATTAAGTGGAA	2813
QY	1565	TAGTACCGATATATAAATTAAGTGGTCTCAATCAACCTCTTCTGAGCTCAAGAAATTAAGTGG	1624
DB	2814	TAGTACCGATATATAAATTAAGTGGTCTCAATCAACCTCTTCTGAGCTCAAGAAATTAAGTGG	2872
QY	1625	CCAAAGCTTAAATTAATCTCAATTAAGTGGAGATCTCTTAAGGAAATTAAGTGGAGAAATTAAGTGG	1684
DB	2873	CCAAAGCTTAAATTAATCTCAATTAAGTGGAGATCTCTTAAGGAAATTAAGTGGAGAAATTAAGTGG	2932

QY	5	TGCCGTTAAAGATGGTCTTCTGAGGCTAACTGCGGAATGAAGTTTCTATTCACAACTAA	64
DB	1254	TCCGTTAAAGATGGTCTTCTGAGGCTAACTGCGGAATGAAGTTTCTATTCACAACTAA	1313
QY	65	AGCCTTAGAATTTGAGGATGCAAACTTTCAAGCAGAGCTCCCGAGAGCCATCTGC	124
DB	1314	AGCCTTAGAATTTGAGGATGCAAACTTTCAAGCAGAGCTCCCGAGAGCCATCTGC	1373
QY	125	CTTCAGAGCTGCAATTTGAATGCAAAAGTCTGTTCCAAATTAAGCTTTGGAATTTGAAGAA	184
DB	1374	CTTCAGAGCTGCAATTTGAATGCAAAAGTCTGTTCCAAATTAAGCTTTGGAATTTGAAGAA	1433
QY	185	TGAACAAACATTTGAGAGCAGATGATATCTCCATCAGAAATCCAAACCAAGGACTATGA	244
DB	1434	TGAACAAACATTTGAGAGCAGATGATATCTCCATCAGAAATCCAAACCAAGGACTATGA	1493
QY	245	AGAAAGTTCTTGGGATTTCTGAGAGTCTCTGTGAGACTGTTTCAAGAAAGGATGTGTGTT	304
DB	1494	AGAAAGTTCTTGGGATTTCTGAGAGTCTCTGTGAGACTGTTTCAAGAAAGGATGTGTGTT	1553
QY	305	ACCCAGGCTACATCAAAAGAAATAGATATAAATTAAGTGGAAATTAAGTGGAAATTAAGTGG	364
DB	1554	ACCCAGGCTACATCAAAAGAAATAGATATAAATTAAGTGGAAATTAAGTGGAAATTAAGTGG	1613
QY	365	TGATATGATGTTTCTGAGGCTCCCTGAGAGTGAAGTTTCTATTCACAACTTAAAGC	424
DB	1614	TGATATGATGTTTCTGAGGCTCCCTGAGAGTGAAGTTTCTATTCACAACTTAAAGC	1673
QY	425	CTTAGAATTTGATGAGATCAAACTTTCAAGCAGAGCTCCCGAGAGCCATCTGCCTT	484
DB	1674	CTTAGAATTTGATGAGATCAAACTTTCAAGCAGAGCTCCCGAGAGCCATCTGCCTT	1733
QY	485	CGAGCTGCTGATTAAGTCAAAAGTCTGTTCCAAATTAAGCTTTGGAATTTGAAGATGA	544
DB	1734	CGAGCTGCTGATTAAGTCAAAAGTCTGTTCCAAATTAAGCTTTGGAATTTGAAGATGA	1793
QY	545	ACAAACATTTGAGAGCAGATCAGATGTTTCCCTTTCAAGATCAAAACCAAGAGGTTGAAGA	604
DB	1794	ACAAACATTTGAGAGCAGATCAGATGTTTCCCTTTCAAGATCAAAACCAAGAGGTTGAAGA	1853

RESULT 9  
US-10-007-805-490  
; Sequence 490, Application US/10007805  
; Publication No. US20020150581A1  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Dillon, Devin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedick, Thomas S.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Durham, Margareta  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER  
; FILE REFERENCE: 210121.470C10  
; CURRENT APPLICATION NUMBER: US/10/007.805  
; CURRENT FILING DATE: 2001-12-07  
; NUMBER OF SEQ ID NOS: 593  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 490  
; LENGTH: 3288  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-007-805-490

Query Match 95.5%; Score 1938.4; DB 14; Length 3288;  
Best Local Similarity 98.5%; Pred. No. 0;  
Matches 1997; Conservative 4; Mismatches 21; Indels 5; Gaps 5;  
QY 5 TGCCGTTAAAGATGGTCTTCTGAGGCTAACTGCGGAATGAAGTTTCTATTCACAACTAA 64  
DB 1254 TCCGTTAAAGATGGTCTTCTGAGGCTAACTGCGGAATGAAGTTTCTATTCACAACTAA 1313  
QY 65 AGCCTTAGAATTTGAGGATGCAAACTTTCAAGCAGAGCTCCCGAGAGCCATCTGC 124  
DB 1314 AGCCTTAGAATTTGAGGATGCAAACTTTCAAGCAGAGCTCCCGAGAGCCATCTGC 1373  
QY 125 CTTCAGAGCTGCAATTTGAATGCAAAAGTCTGTTCCAAATTAAGCTTTGGAATTTGAAGAA 184  
DB 1374 CTTCAGAGCTGCAATTTGAATGCAAAAGTCTGTTCCAAATTAAGCTTTGGAATTTGAAGAA 1433  
QY 185 TGAACAAACATTTGAGAGCAGATGATATCTCCATCAGAAATCCAAACCAAGGACTATGA 244  
DB 1434 TGAACAAACATTTGAGAGCAGATGATATCTCCATCAGAAATCCAAACCAAGGACTATGA 1493  
QY 245 AGAAAGTTCTTGGGATTTCTGAGAGTCTCTGTGAGACTGTTTCAAGAAAGGATGTGTGTT 304  
DB 1494 AGAAAGTTCTTGGGATTTCTGAGAGTCTCTGTGAGACTGTTTCAAGAAAGGATGTGTGTT 1553  
QY 305 ACCCAGGCTACATCAAAAGAAATAGATATAAATTAAGTGGAAATTAAGTGGAAATTAAGTGG 364  
DB 1554 ACCCAGGCTACATCAAAAGAAATAGATATAAATTAAGTGGAAATTAAGTGGAAATTAAGTGG 1613  
QY 365 TGATATGATGTTTCTGAGGCTCCCTGAGAGTGAAGTTTCTATTCACAACTTAAAGC 424  
DB 1614 TGATATGATGTTTCTGAGGCTCCCTGAGAGTGAAGTTTCTATTCACAACTTAAAGC 1673  
QY 425 CTTAGAATTTGATGAGATCAAACTTTCAAGCAGAGCTCCCGAGAGCCATCTGCCTT 484  
DB 1674 CTTAGAATTTGATGAGATCAAACTTTCAAGCAGAGCTCCCGAGAGCCATCTGCCTT 1733  
QY 485 CGAGCTGCTGATTAAGTCAAAAGTCTGTTCCAAATTAAGCTTTGGAATTTGAAGATGA 544  
DB 1734 CGAGCTGCTGATTAAGTCAAAAGTCTGTTCCAAATTAAGCTTTGGAATTTGAAGATGA 1793  
QY 545 ACAAACATTTGAGAGCAGATCAGATGTTTCCCTTTCAAGATCAAAACCAAGAGGTTGAAGA 604  
DB 1794 ACAAACATTTGAGAGCAGATCAGATGTTTCCCTTTCAAGATCAAAACCAAGAGGTTGAAGA 1853

QY	365	TGATAATGATGGTTTTCTGAAGGCTCCCTGCAGAAATGAAGTTTCTATTCCAACCTAAAGC	424
Db	1614	TGATAATGATGGTTTTCTGAAGGCTCCCTGCAGAAATGAAGTTTCTATTCCAACCTAAAGC	1673
QY	425	CTTPAGAATTGATGGACATGCCTAAACCTTTCAAACAGAGCGCTCCGAGAGGCCATCTGCCTT	484
Db	1674	CTTPAGAATTGATGGACATGCCTAAACCTTTCAAACAGAGCGCTCCGAGAGGCCATCTGCCTT	1733
QY	485	CGAGCGCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATTGAAGAATGA	544
Db	1734	CGAGCGCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATTGAAGAATGA	1793
QY	545	ACAAACATTGAGAGCAGATCAGATGTTTCCCTTCAGAAATCAAAACAAAGAGAGGTTGAAGA	604
Db	1794	ACAAACATTGAGAGCAGATCAGATGTTTCCCTTCAGAAATCAAAACAAAGAGAGGTTGAAGA	1853
QY	605	AAATTCTTGGGATTCCTGAGAGTCCCGTGAGACTGTTTTCACAGAAGGATGTGTGTACCC	664
Db	1854	AAATTCTTGGGATTCCTGAGAGTCCCGTGAGACTGTTTTCACAGAAGGATGTGTGTACCC	1913
QY	665	CAAGGCTACACATCAAAAGAAATGATAAATAAGTGGAAATATAGAGATTCAACTAG	724

QY	725	CCTATCAAAATCTTGGATACAGTTCATTCTTGGAAGAGCAAGGGAATCTTCAAAAAGA	784
D5	1974	CCTATCAAAATCTTGGATACAGTTCATTCTTGGAAGAGCAAGGGAATCTTCAAAAAGA	2033
QY	785	TCACTGTGAACAGTACAGGAAAAATGGACAATAAAGAAAGACTTTTGTGTACTGAA	844
D5	2034	TCATCTGTGAACAGTACAGGAAAAATGGACAATAAAGAAAGACTTTTGTGTACTGAA	2093
QY	845	AAGAAACTGTGAGAGCAAAGAAATAAAATCACAGTTTAGAACCAAAAAGTTAAATG	904
D5	2094	AAGAAACTGTGAGAGCAAAGAAATAAAATCACAGTTTAGAACCAAAAAGTTAAATG	2153
QY	905	GGAACAAGAGCTCTCGAGTGTGAGATTGAATTTAAACCAGAAAGAGAGAGAAAGAAA	964
D5	2154	GGAACAAGAGCTCTCGAGTGTGAGATTGAATTTAAACCAGAAAGAGAGAGAAAGAAA	2213
QY	965	TGCCGATATTAAATGAAAAATTAGGAGAGAAATTAGGAAGAAATCGAAGAGCAGCATAG	1024
D5	2214	TGCCGATATTAAATGAAAAATTAGGAGAGAAATTAGGAAGAAATCGAAGAGCAGCATAG	2273
D5			1084

2274	GAAGAGTTAGAGTGAAACACACCTTGACAGGCTCTCAGAAATCAAGATATAGAATT	2333
1085	GAAGAGTGTAGAAAGTAAATTGTAATCAGGTTTCTCACCTCATCGAAATGAAAATATATCT	1144
2334	GAAGAGTGTAGAAAGTAAATTGTAATCAGGTTTCTCACCTCATCGAAATGAAAATATATCT	2393
1145	CTTACATGAAATTCGATGTTGAAAAAGGAAATTCCTCATGCTAAAACCTGGAAATAGCCAC	1204
2394	CTTACATGAAATTCGATGTTGAAAAAGGAAATTCCTCATGCTAAAACCTGGAAATAGCCAC	2453
1205	ACTGAAACACCAATACACAGGAAAAAGGAAATAAATACTTTGAGGACATTAAGATTTTTAAA	1264
2454	ACTGAAACACCAATACACAGGAAAAAGGAAATAAATACTTTGAGGACATTAAGATTTTTAAA	2513
1265	AGAAAAGAATCGTGAATTCAGATGAGCCTAAAACTGAAAGAGGAATCATTTAACTAAAG	1324
2514	AGAAAAGAATCGTGAATTCAGATGAGCCTAAAACTGAAAGAGGAATCATTTAACTAAAG	2573
1325	GGCATCTCAATATAGTGGCGAGCTTAAAGTTCTGATAGCTGAGAAACAATGCTCACTTC	1384
2574	GGCATCTCAATATAGTGGCGAGCTTAAAGTTCTGATAGCTGAGAAACAATGCTCACTTC	2633
1385	TAAATTGAAGGAAAAACAAGACAAGAAATACTAGAGCGAAAATTGGAATCACACCATCC	1444
2634	TAAATTGAAGGAAAAACAAGACAAGAAATACTAGAGCGAAAATTGGAATCACACCATCC	2693

Qy	1445	TAGACTGGCTTCTGCTGTACAAAGACCATGATCAAAATGTGTGACATCAAGAAAAAGTCAAGA	1504
Db	2694	TAGACTGGCTTCTGCTGTACAAAGACCATGATCAAAATGTGTGACATCAAGAAAAAGTCAAGA	2753
Qy	1505	ACCTGCTTTCCACATTCGACGAGATGCTTGTTGCGAAGAAAATGAATGCTTCATCTGAG	1564
Db	2754	ACCTGCTTTCCACATTCGACGAGATGCTTGTTGCGAAGAAAATGAATGCTTCATCTGAG	2813
Qy	1565	TAGTACCGATATATAACAATGAGGTGCTCCATCAACCAACCTTCTGAAGCTCAAAGAAAT	1624
Db	2814	TAGTA-CGATATATAACAATGAGGTGCTCCATCAACCAACCTTCTGAAGCTCAAAGAAAT	2872
Qy	1625	CCANAAGCCTAAAAATTAATCTCAATTATCGACGAGATGCTCTAAGAGAAAATACATTGG	1684
Db	2873	CCANAAGCCTAAAAATTAATCTCAATTATCGMGAGATGCTCTAAGAGAAAATACATTGG	2932
Qy	1685	TTTCAGGAACATGCACAAAGACGACCAACGCTGAAACACAGTGTCAAATGAAGGAAGCTGAA	1744
Db	2933	TTTCA-GAACATGCACAAAGACGACCAACGCTGAAACACAGTGTCAAATGAAGGAAGCTGAA	2991
Qy	1745	CACATGNTCAAANGCAACAAAGATNATGTGAAACAAACACACTGANCAGCAGGAGTCTCTA	1804
Db	2992	CACATGNTCAAANGCAACAAAGATNATGTGAAACAAACACACTGANCAGCAGGAGTCTCTA	3051
Qy	1805	GATCAGAAATTTATTTCAACTPACAAAGCAAAATATGTGGCTTCAAACAGCAATTTAGTTTCA	1864
Db	3052	GATCAGAAATTTATTTCAACTPACAAAGCAAAATATGTGGCTTCAAACAGCAATTTAGTTTCA	3111
Qy	1865	GCACATNAGAAAGCTGACCAACAAAGCAAGATAACAATTCATNTTCTTGAGAG	1924
Db	3112	GCACATAA-GAAAGCTGACCAACAAAGCAAGATAACAATTCATNTTCTTGAGAG	3170
Qy	1925	GAAAAATGC-NCATCATCTTCTTAAAGAGAAAATGAGGAGATATTNATTAACNATAACCA	1983
Db	3171	GAAAAATGCACATCATCTTCTTAAAGAGAAAATGAGGAGATATTNATTAACNATAACCA	3230
Qy	1984	TTTAAAAAACCCGTATATTTCAATATATGAAAAAANAANAANAANAANAANAANAANAANA	2030
Db	3231	TTTAAAAAA-CCGTATATATCAATATGAAAAAAGAAAAGCAGAAAAACA	3276

RESULT 11

US-10-124-805-490

; Sequence 490, Application US/10124805

; Publication No. US20030166022A1

; GENERAL INFORMATION:

; APPLICANT: Houghton, Raymond L.

; APPLICANT: Sleath, Paul R.

; APPLICANT: Persing, David H.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER

; FILE REFERENCE: 210121.470C12

; CURRENT APPLICATION NUMBER: US/10/124,805

; CURRENT FILING DATE: 2002-04-15

; NUMBER OF SEQ ID NOS: 627

; SOFTWARE: Fast-Seq for Windows Version 4.0

; SEQ ID NO 490

; LENGTH: 3288

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-124-805-490

Query Match 95.5%; Score 1938.4; DB 15; Length 3288;

Best Local Similarity 98.5%; Pred. No. 0;

Matches 1997; Conservative 4; Mismatches 21; Indels 5; Gaps 5;

Qy	5	TGCGTTAAAGATGGCTTCTTGAGGCGTAACTGCGGAATGAAGTTTCTATTCCAACTAA	64
Db	1254	TCCTGTTAAGATGGCTTCTTGAGGCGTAACTGCGGAATGAAGTTTCTATTCCAACTAA	1313
Qy	65	AGCCTTAGAATGTATGACATGCAAACTTTCAAAGCAGAGCGCTCCCGAAGCCATCTGC	124
Db	1314	AGCCTTAGAATGTATGACATGCAAACTTTCAAAGCAGAGCGCTCCCGAAGCCATCTGC	1373







Db 2366 AAGAAAGCTGTGAGAGCAAGAAAGAAATATAATTCAGTTAGAGAACCAAAAGTTAAATG 2425  
Qy 905 GGAACAAGAGCTCTGAGTGTGAGATTTGACTTTTAAACCAAGAGAGAGAGAGAGAA 964  
Db 2426 GGAACAAGAGCTCTGAGTGTGAGATTTGACTTTTAAACCAAGAGAGAGAGAGAGAA 2485  
Qy 965 TGCCGATATATTAAATGAAATATTAGGAAGAAATAGGAAGAAATCGAAGAGCAGCATAG 1024  
Db 2486 TGCCGATATATTAAATGAAATATTAGGAAGAAATATTAGGAAGAAATCGAAGAGCAGCATAG 2545  
Qy 1025 GAAAGAGTTAGAGTGAACCAACACTTGAACAGGCTCTCAGATATACAGATATAGAAAT 1084  
Db 2546 GAAAGAGTTAGAGTGAACCAACACTTGAACAGGCTCTCAGATATACAGATATAGAAAT 2605  
Qy 1085 GAAGAGTGTAGAGTGAATTTGAAATGAGTGTCTCAGCTCATGATGAATGAATTTACT 1144  
Db 2606 GAAGAGTGTAGAGTGAATTTGAAATGAGTGTCTCAGCTCATGATGAATGAATTTACT 2665  
Qy 1145 CTTACATGAAATTTGATGTTGAAAGAGAAATTTGCCATGCTTAAACCTGGAATAGCCAC 1204  
Db 2666 CTTACATGAAATTTGATGTTGAAAGAGAAATTTGCCATGCTTAAACCTGGAATAGCCAC 2725  
Qy 1205 ACTGAAACCAATACAGGAAAGAAATTAATTAATTTGAGGACATTAAGATTTTAA 1264  
Db 2726 ACTGAAACCAATACAGGAAAGAAATTAATTAATTTGAGGACATTAAGATTTTAA 2785  
Qy 1265 AGAAAGAGTGTGAACTTCAGATGACCTTAAACTGAAAGAGGAAATCAATTAATAAG 1324  
Db 2786 AGAAAGAGTGTGAACTTCAGATGACCTTAAACTGAAAGAGGAAATCAATTAATAAG 2845  
Qy 1325 GGATCTCAATATAGTGGGAGCTTAAAGTTCTGATAGCTGAGAACACAAATGCTCACTTC 1384  
Db 2846 GGATCTCAATATAGTGGGAGCTTAAAGTTCTGATAGCTGAGAACACAAATGCTCACTTC 2905  
Qy 1385 TAAATTTGAAGGAAACCAAGACAAAGAAATTAATTAAGGAGGAAATTTGAATCAACATCC 1444  
Db 2906 TAAATTTGAAGGAAACCAAGACAAAGAAATTAATTAAGGAGGAAATTTGAATCAACATCC 2965  
Qy 1445 TAGACTGGCTTCTGCTGTACAAGACCATGATCAAAATTTGATCAAGAAAAAGTCAAGA 1504  
Db 2966 TAGACTGGCTTCTGCTGTACAAGACCATGATCAAAATTTGATCAAGAAAAAGTCAAGA 3025  
Qy 1505 ACCTGCTTTCCATTCAGGAGATGCTTGTGTCGAAGAAATTAATTTGATGTGAG 1564  
Db 3026 ACCTGCTTTCCATTCAGGAGATGCTTGTGTCGAAGAAATTAATTTGATGTGAG 3085  
Qy 1565 TAGTACCGATATATAAATGAGGTGCTCCATCAACCATCTTTCTGAAGCTCAAGGAAAT 1624  
Db 3086 TAGTA -CGATATATAAATGAGGTGCTCCATCAACCATCTTTCTGAAGCTCAAGGAAAT 3144  
Qy 1625 CCNAAAGCTTAAATTAATCTCAATATGAGGAGATGCTCTAAGAGAAATACATTTGG 1684  
Db 3145 CCAAAAGCTTAAATTAATCTCAATATGCMGGAGATGCTCTAAGAGAAATACATTTGG 3204  
Qy 1685 TTTTCAGGAAATGCAACAAAGAGACCAAGCTGAAACACAGTGTCAATGAAGGAGCTGAA 1744  
Db 3205 TTTTCA -GAAATGCAACAAAGAGACCAAGCTGAAACACAGTGTCAATGAAGGAGCTGAA 3263  
Qy 1745 CACATGNTCAAANGCAAGATTAATGTAACAAACACATGANCAGGAGGTCTCTA 1804  
Db 3264 CACATGNTCAAANGCAAGATTAATGTAACAAACACATGANCAGGAGGTCTCTA 3323  
Qy 1805 GATCAGAAATTTTCAACTTACAAAGCAAAATATGTGGCTTCAACAGCAATTAGTTTCAT 1864  
Db 3324 GATCAGAAATTTTCAACTTACAAAGCAAAATATGTGGCTTCAACAGCAATTAGTTTCAT 3383  
Qy 1865 GCATTAANGAAGCTGACAAACAAAGCAAGATTAATGATNTTCATNTCTTGAGAG 1924  
Db 3384 GCATTAANGAAGCTGACAAACAAAGCAAGATTAATGATNTTCATNTCTTGAGAG 3442  
Qy 1925 GAAATGCT -NCATCATCTTCTTAAAGGAGAAATAGGAGATATTTTATTCATNATTAACCA 1983

Db 3443 GAAATGCAACATCATCTCTTAAAGAGAGAAATAGAGAGATATTATTAATTAACATAACCA 3502  
Qy 1984 TTTTAAACCCGCTATATTTCATATGGAAGAAATTAATTAATTAACATAACCA 2030  
Db 3503 TTTTAAACCCGCTATATTTCATATGGAAGAAATTAATTAATTAACATAACCA 3548  
RESULT 13  
US-09-551-621-474  
; Sequence 474, Application US/09551621  
; Publication No. US20030104366A1  
; GENERAL INFORMATION:  
; APPLICANT: Yuqiu, Jiang  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND  
; FILE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE  
; FILE REFERENCE: 210121.470C5  
; CURRENT APPLICATION NUMBER: US/09/551,621  
; CURRENT FILING DATE: 2000-04-17  
; NUMBER OF SEQ ID NOS: 479  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 474  
; LENGTH: 3865  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (2448)...(2631)  
; OTHER INFORMATION: 184 bp insert of B726P splice form  
US-09-551-621-474  
Query Match 95.5%; Score 1938.4; DB 10; Length 3865;  
Best Local Similarity 98.5%; Pred. No. 0;  
Matches 1997; Conservative  
Qy 5 TGCCGTTAAAGATGCTTCTTGAAGGCTAACTCGGAATGGAAGTTTCTATTCCAACTAA 64  
Db 1526 TCCTGTAAAGATGCTTCTTGAAGGCTAACTCGGAATGGAAGTTTCTATTCCAACTAA 1585  
Qy 65 AGCCTTAGAATTTGATGACATGCAAACTTTCAAAGCAGAGCCCTCCGAGAGCCATCTGC 124  
Db 1586 AGCCTTAGAATTTGATGACATGCAAACTTTCAAAGCAGAGCCCTCCGAGAGCCATCTGC 1645  
Qy 125 CTTGAGGCTGCCATTGAAATGCAAAAGTCTGTTCGAAATAGAGCTTTCGAATTAAGAA 184  
Db 1646 CTTGAGGCTGCCATTGAAATGCAAAAGTCTGTTCGAAATAGAGCTTTCGAATTAAGAA 1705  
Qy 185 TGAACAAACATTGAGAGCAGATGAGATACCTCCATCAGAAATCCAAACAAAGAGGACTATGA 244  
Db 1706 TGAACAAACATTGAGAGCAGATGAGATACCTCCATCAGAAATCCAAACAAAGAGGACTATGA 1765  
Qy 245 AGAAAGTTCTTGGATTCCTGAGAGTCTCTGTGAGACTGTTCACAGAGGATGTGTGTT 304  
Db 1766 AGAAAGTTCTTGGATTCCTGAGAGTCTCTGTGAGACTGTTCACAGAGGATGTGTGTT 1825  
Qy 305 ACCCAAGCTACACATCAAAAGAGAAATAGATATAATTAATGGAATAATAGAGAGTCTCC 364  
Db 1826 ACCCAAGCTACACATCAAAAGAGAAATAGATATAATTAATGGAATAATAGAGAGTCTCC 1885  
Qy 365 TGATAATGATGTTTCTGAGAGGCTCCCTGAGAGTGAAGTTTCTTCTTCAACTAAGC 424  
Db 1886 TGATAATGATGTTTCTGAGAGGCTCCCTGAGAGTGAAGTTTCTTCTTCAACTAAGC 1945  
Qy 425 CTTAGAAATGATGACATGCAAACTTTCAAAGCAGAGCCCTCCGAGAGGCTCTCTGCTT 484  
Db 1946 CTTAGAAATGATGACATGCAAACTTTCAAAGCAGAGCCCTCCGAGAGGCTCTCTGCTT 2005  
Qy 485 CGAGCTGCCATTGAAATGCAAAAGTCTGTTCGAAATTAAGCCCTTGAATTAAGAGATGA 544  
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QY 545 ACAAACATTGAGAGAGATCAGATGTTCCCTTCAGAAATCAAAACAAAAGAGGTTGAGA 604  
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QY 605 AAATTCITGGGATTCAGAGTCTCCGTGAGACTGTTTTCAGAGAGGATGTTGTGTACC 664  
Db 2126 AAATTCITGGGATTCAGAGTCTCCGTGAGACTGTTTTCAGAGAGGATGTTGTGTACC 2185  
QY 665 CAAGGCTACACATCAAAAGAAATGGATTAATTAAGTGGAAATTAAGATTCNACTAG 724  
Db 2186 CAAGGCTACACATCAAAAGAAATGGATTAATTAAGTGGAAATTAAGATTCNACTAG 2245  
QY 725 CCTATCAAAATTCITGGATACAGTTCATTCITGTTGAAAGAGCAAGGGAATTCAAAAGA 784  
Db 2246 CCTATCAAAATTCITGGATACAGTTCATTCITGTTGAAAGAGCAAGGGAATTCAAAAGA 2305  
QY 785 TCACGTGGAACAACTGACAGAAATGGATTAATTAAGTGGAAATTAAGATTCNACTAG 844  
Db 2306 TCACGTGGAACAACTGACAGAAATGGATTAATTAAGTGGAAATTAAGATTCNACTAG 2365  
QY 845 AAAGAAATCTGCAGAGCAAAAGAAATAAATCAAGTTCAGAGCAAAAGGTTAAATG 904  
Db 2366 AAAGAAATCTGCAGAGCAAAAGAAATAAATCAAGTTCAGAGCAAAAGGTTAAATG 2425  
QY 905 GGAACAAGAGCTTCAGTGTGAGTTCAGTTCATTAACCAAGAGAGAGAGAGAA 964  
Db 2426 GGAACAAGAGCTTCAGTGTGAGTTCAGTTCATTAACCAAGAGAGAGAGAGAA 2485  
QY 965 TCCCATATATTAAATGAAATATAGGAAAGAAATAGGAAATCGAAGAGCAGCATAG 1024  
Db 2486 TCCCATATATTAAATGAAATATAGGAAAGAAATAGGAAATCGAAGAGCAGCATAG 2545  
QY 1025 GAAAGATTAGAGTGAACAACTTGAACAGGCTCTCAGATACAAAGATATAGAAAT 1084  
Db 2546 GAAAGATTAGAGTGAACAACTTGAACAGGCTCTCAGATACAAAGATATAGAAAT 2605  
QY 1085 GAAGAGTGTAGAGTGAATTTGAATCAGGTTCTCAGACTCATGAATGAAATTTACT 1144  
Db 2606 GAAGAGTGTAGAGTGAATTTGAATCAGGTTCTCAGACTCATGAATGAAATTTACT 2665  
QY 1145 CTTACATGAAATTCATGTTGAAAGGAAATTCCTATGCTTAAACTGGAATAGCCAC 1204  
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QY 1205 ACTGAACACCAATCCAGGAAAGAAATTAATTAATCTGAGGACATTAAGATTTAA 1264  
Db 2726 ACTGAACACCAATCCAGGAAAGAAATTAATTAATCTGAGGACATTAAGATTTAA 2785  
QY 1265 AGAAGAAATGCTGAACCTTTCAGATGACCCCTTAAACTGAAAGGGAATCATTAACCTAAAG 1324  
Db 2786 AGAAGAAATGCTGAACCTTTCAGATGACCCCTTAAACTGAAAGGGAATCATTAACCTAAAG 2845  
QY 1325 GGCATCTCAATATAGTGGCAGCTTAAAGTTCGTAGTGTGAGACCAATGCTCACTTC 1384  
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QY 1385 TAAATTAAGGAGAAACAAAGAAATTAATTAATCTAGAGGAGAAATGAAATCAACCATCC 1444  
Db 2906 TAAATTAAGGAGAAACAAAGAAATTAATTAATCTAGAGGAGAAATGAAATCAACCATCC 2965  
QY 1445 TAGACTGGCTTCGTGTTCAAGACCAATGATCAATTAATGATCAAGAAAGTCAAGA 1504  
Db 2966 TAGACTGGCTTCGTGTTCAAGACCAATGATCAATTAATGATCAAGAAAGTCAAGA 3025  
QY 1505 ACCTGCTTTCCATTCAGAGGAGATGCTTGTGTTTGAAGAAATTAATGATGTTGAG 1564  
Db 3026 ACCTGCTTTCCATTCAGAGGAGATGCTTGTGTTTGAAGAAATTAATGATGTTGAG 3085  
QY 1565 TAGTACGATATATACATGAGGCTCTCAGTCAACCATCTTCTGAGCTCAAGGAAAT 1624  
Db 3086 TAGTACGATATATACATGAGGCTCTCAGTCAACCATCTTCTGAGCTCAAGGAAAT 3144

QY 1625 CCANAAGCCTAAATTAATCTCAATTTATGAGAGATGCTCTAAGAGAAAATACATTGG 1684  
Db 3145 CCANAAGCCTAAATTAATCTCAATTTATGAGAGATGCTCTAAGAGAAAATACATTGG 3204  
QY 1685 TTTTCAAGACATGCAAGAGAGCAAGCTGCAAGTGTCAATTAAGAGAGGAGCTGAA 1744  
Db 3205 TTTTCA-GAACATGCAAGAGAGCAAGCTGCAAGTGTCAATTAAGAGAGGAGCTGAA 3263  
QY 1745 CACATGTTTCAAAAGCAAGATGATGTAACAAACACACTGACAGCAGGAGTCTCTA 1804  
Db 3264 CACATGTTTCAAAAGCAAGATGATGTAACAAACACACTGACAGCAGGAGTCTCTA 3323  
QY 1805 GATCAGAAATTTATTTCAACTCAAGCAAAATATGTTGGCTTCAACAGCAATTTAGTTCA 1864  
Db 3324 GATCAGAAATTTATTTCAACTCAAGCAAAATATGTTGGCTTCAACAGCAATTTAGTTCA 3383  
QY 1865 GCACATTAAGAAAGCTGCAACAAAGCAAGATTAATGTAACAAACACTGATTTCTTGAGAG 1924  
Db 3384 GCACATTAAGAAAGCTGCAACAAAGCAAGATTAATGTAACAAACACTGATTTCTTGAGAG 3442  
QY 1925 GAAATGTC-NCATCTCTTTTAAAGAGAAAATGAGGAGATATTTTATTAACNATAACCA 1983  
Db 3443 GAAATGTCACATCATCTCTTAAAGAGAAAATGAGGAGATATTTTATTAACNATAACCA 3502  
QY 1984 TTTAAAAACCCCTATATTTCAATATGAAAAAANAAAAA 2030  
Db 3503 TTTAAAAA-CCGTATATCAATATGAAAAAGAGAGAGAGAAACA 3548

## RESULT 14

US-10-007-805-474  
; Sequence 474, Application US/10007805  
; Publication No. US20020150581A1  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yuqiu  
; APPLICANT: Dillon, Devin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Durham, Margarita  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER  
; FILE REFERENCE: 210121.470C10  
; CURRENT FILING DATE: 2001-12-07  
; NUMBER OF SEQ ID NOS: 593  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 474  
; LENGTH: 3865  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-007-805-474

Query Match 95.5%; Score 1938.4; DB 14; Length 3865;  
Best Local Similarity 98.5%; Pred. No. 0;  
Matches 1997; Conservative 4; Mismatches 21; Indels 5; Gaps 5;

QY 5 TGCGGTAAAGATGCTTCTGAGGCTAACTGCGAATGAAAGTTTCTATTCCAACTAA 64  
Db 1526 TCCTGTTAAAGATGGTCTTCTGAGGCTAACTGCGAATGAAAGTTTCTATTCCAACTAA 1585  
QY 65 AGCCTTAGAATTGATGACATGCAAACTTTCAAAGCAGAGCCTCCGAGAGAGCCATCTGC 124  
Db 1586 AGCCTTAGAATTGATGACATGCAAACTTTCAAAGCAGAGCCTCCGAGAGAGCCATCTGC 1645  
QY 125 CTTGAGCCTGCCATTGAATGCAAGTCTGTTCCAAATGAAGCCTTCGAATTTGAAGAA 184  
Db 1646 CTTGAGCCTGCCATTGAATGCAAGTCTGTTCCAAATGAAGCCTTCGAATTTGAAGAA 1705



Query Match									
Best Local Similarity 95.5%; Score 1938.4; DB 15; Length 3865;									
Matches 1997; Conservative 4; Mismatches 21; Indels 5; Gaps 5;									
QY	5	TCGCGTTAAAGATGGTCTTCTCAAGGCTAACTGGGAATGAAGTTTCTATTCCAACTAA	64						
DB	1526	TCCTGTAAAGATGGTCTTCTGAAGGCTAACTGGGAATGAAGTTTCTATTCCAACTAA	1585						
QY	65	AGCCTTACAAATGATGGACATGCAAACTTTCAAGAGAGAGGCTCCGAGAGCCATCTGC	124						
DB	1586	AGCCTTACAAATGATGGACATGCAAACTTTCAAGAGAGAGGCTCCGAGAGCCATCTGC	1645						
QY	125	CTTCGAGCCTGCCATTTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATGAAGAA	184						
DB	1646	CTTCGAGCCTGCCATTTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATGAAGAA	1705						
QY	185	TGAACAAACATTTGAGAGCAGATGATATCTCCATCAGAAATCCAAACAAAGAGCTATGA	244						
DB	1706	TGAACAAACATTTGAGAGCAGATGATATCTCCATCAGAAATCCAAACAAAGAGCTATGA	1765						
QY	245	AGAAAGTTCTGGGATTTCTGAGAGTCTCTGTGAGACTGTTTCAAGAGAGATGTGTGTTT	304						
DB	1766	AGAAAGTTCTGGGATTTCTGAGAGTCTCTGTGAGACTGTTTCAAGAGAGATGTGTGTTT	1825						
QY	305	ACCCAGGCTACACATCAAAAGAAATAGATATAATGGAATTAATGGAAGAGTCTCC	364						
DB	1826	ACCCAGGCTACACATCAAAAGAAATAGATATAATGGAATTAATGGAAGAGTCTCC	1885						
QY	365	TGATAATGATGGTTTCTGAAGGCTCCCTCGAGAGTGAAGTTTCTATTCCAACTAAAGC	424						
DB	1886	TGATAATGATGGTTTCTGAAGGCTCCCTCGAGAGTGAAGTTTCTATTCCAACTAAAGC	1945						
QY	425	CTTAGAATGATGGACATGCAAACTTTCAAGAGAGGCTCCGAGAGCCATCTGCCTT	484						
DB	1946	CTTAGAATGATGGACATGCAAACTTTCAAGAGAGGCTCCGAGAGCCATCTGCCTT	2005						
QY	485	CGAGCCTGCCATTTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGAAGTGAAGATGA	544						
DB	2006	CGAGCCTGCCATTTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGAAGTGAAGATGA	2065						
QY	545	ACAAACATTTGAGAGCAGATCAGATGTTCCCTTCAGAAATCAAAACAAAGAGGTTGAAGA	604						
DB	2066	ACAAACATTTGAGAGCAGATCAGATGTTCCCTTCAGAAATCAAAACAAAGAGGTTGAAGA	2125						
QY	605	AAATTTCTGGGATTTCTGAGAGTCTCCGTGAGACTGTTTCAAGAGAGGATGTGTGTACC	664						
DB	2126	AAATTTCTGGGATTTCTGAGAGTCTCCGTGAGACTGTTTCAAGAGAGGATGTGTGTACC	2185						
QY	665	CAAGGCTACACATCAAAAGAAATGGATAAATAGTGGAATAATAGGAATTCAACTAG	724						
DB	2186	CAAGGCTACACATCAAAAGAAATGGATAAATAGTGGAATAATAGGAATTCAACTAG	2245						
QY	725	CCTATCAAAATCTTTGGATACAGTTTCATTCTTGTGAAAGAGCAAGGGAACCTCAAAAGA	784						
DB	2246	CCTATCAAAATCTTTGGATACAGTTTCATTCTTGTGAAAGAGCAAGGGAACCTCAAAAGA	2305						
QY	785	TCATGTGAAACAACTGACAGGAAATGGACAAATGAAAGAAAGTTTGTGTACTGAA	844						
DB	2306	TCATGTGAAACAACTGACAGGAAATGGACAAATGAAAGAAAGTTTGTGTACTGAA	2365						
QY	845	AAAGAAACTGTCAGAGCAAAAGAAATGAATTCAGTTAGGACCAAAAGTTTAAATG	904						
DB	2366	AAAGAAACTGTCAGAGCAAAAGAAATGAATTCAGTTAGGACCAAAAGTTTAAATG	2425						
QY	905	GGAAACAAAGAGCTCTGAGGTGTGAGATGATCTTTAAACCAAGAGAGAGAGAGAGAA	964						
DB	2426	GGAAACAAAGAGCTCTGAGGTGTGAGATGATCTTTAAACCAAGAGAGAGAGAGAGAA	2485						
QY	965	TGCCGATATATTAATGAAATTAATGAGGAGAAATAGGAAGATTCGAGAGCGCATAG	1024						
DB	2486	TGCCGATATATTAATGAAATTAATGAGGAGAAATAGGAAGATTCGAGAGCGCATAG	2545						

QY	1025	GAAGAGTTAGAAAGTGAAACCAACATTTGAACAGGCTCTCAGAAATCAAGATATAGAAAT	1084						
DB	2546	GAAGAGTTAGAAAGTGAAACCAACATTTGAACAGGCTCTCAGAAATCAAGATATAGAAAT	2605						
QY	1085	GAAGAGTTAGAAAGTTAAATTTGAATCAGTTTCTCAGACTCATGAAATGAAATTTATCT	1144						
DB	2606	GAAGAGTTAGAAAGTTAAATTTGAATCAGTTTCTCAGACTCATGAAATGAAATTTATCT	2665						
QY	1145	CTTACATGAAATTTGCATGTTTGAAGAGGAAATTTGCCATGTCTAAACCTGGAATAGCCAC	1204						
DB	2666	CTTACATGAAATTTGCATGTTTGAAGAGGAAATTTGCCATGTCTAAACCTGGAATAGCCAC	2725						
QY	1205	ACTGAAACACCAATACACAGGAAAGGAAATTAATTTCTTGGAGCATTAAGATTTTAA	1264						
DB	2726	ACTGAAACACCAATACACAGGAAAGGAAATTAATTTCTTGGAGCATTAAGATTTTAA	2785						
QY	1265	AGAAAGAAATGCTGAACCTTCAAGATCAACCTTAAACCTGAAAGAGGAAATCATTAACCTAAAG	1324						
DB	2786	AGAAAGAAATGCTGAACCTTCAAGATCAACCTTAAACCTGAAAGAGGAAATCATTAACCTAAAG	2845						
QY	1325	GGCATCTCAATATAGTGGCAGCTTAAAGTTCTGATAGTGTGAGAACACAAATGCTCCTTC	1384						
DB	2846	GGCATCTCAATATAGTGGCAGCTTAAAGTTCTGATAGTGTGAGAACACAAATGCTCCTTC	2905						
QY	1385	TAAATTTGAAGGAAATCAAGACAAAGAAATCTAGAGGACAGAAATTTGAATCACCATCTCC	1444						
DB	2906	TAAATTTGAAGGAAATCAAGACAAAGAAATCTAGAGGACAGAAATTTGAATCACCATCTCC	2965						
QY	1445	TGAGCTGGCTCTGCTGTCAAGACCATGATCAAAATTTGTGACATCAAGAAAGTCAAGA	1504						
DB	2966	TGAGCTGGCTCTGCTGTCAAGACCATGATCAAAATTTGTGACATCAAGAAAGTCAAGA	3025						
QY	1505	ACCTGCTTTCCACATTTGAGAGGATGCTTTGTTGCAAGAAATTTGAATTTGATGTGAG	1564						
DB	3026	ACCTGCTTTCCACATTTGAGAGGATGCTTTGTTGCAAGAAATTTGAATTTGATGTGAG	3085						
QY	1565	TAGTACCGATATATAACAAATGAGTGTCCATCAACCACTTTCTGAAGCTCAAGGAAAT	1624						
DB	3086	TAGTACCGATATATAACAAATGAGTGTCCATCAACCACTTTCTGAAGCTCAAGGAAAT	3144						
QY	1625	CCAAAGCCTTAAATTTAATCTCAATTTGAGGAGATGCTCTTAAGAGAAATACATTGG	1684						
DB	3145	CCAAAGCCTTAAATTTAATCTCAATTTGAGGAGATGCTCTTAAGAGAAATACATTGG	3204						
QY	1685	TTTCAGGACATGCAACAAAGAGACCAACGTGAAACACAGTGTCAATGAAGGAGCTGAA	1744						
DB	3205	TTTCA-GAACATGCAACAAAGAGACCAACGTGAAACACAGTGTCAATGAAGGAGCTGAA	3263						
QY	1745	CACATGTTCAAAACGAAAGATGATGTAACCAACACACTGANCACAGGAGTCTCTA	1804						
DB	3264	CACATGTTCAAAACGAAAGATGATGTAACCAACACACTGANCACAGGAGTCTCTA	3323						
QY	1805	GATCAGAAATTTTCAACTACAAAGCAAAATATGTGGCTTCAACAGCAATTTAGTTTCA	1864						
DB	3324	GATCAGAAATTTTCAACTACAAAGCAAAATATGTGGCTTCAACAGCAATTTAGTTTCA	3383						
QY	1865	GCACATTAAGAAAGCTGACAAACAAAGAGAAATTAATTTGATTTTCTTCTTGGAG	1924						
DB	3384	GCACATTAAGAAAGCTGACAAACAAAGAGAAATTAATTTGATTTTCTTCTTGGAG	3442						
QY	1925	GAAATATGC-NCATCATCTTTCTAAAGAGAAATGAGGAGATATTNNATTACNATAACCA	1983						
DB	3443	GAAATATGC-NCATCATCTTTCTAAAGAGAAATGAGGAGATATTNNATTACNATAACCA	3502						
QY	1984	TTTTAAAAACCCGTATATTTCATATATGGAAGAAATTAATTTGAGGAGATATTNNATTACNATAACCA	2030						
DB	3503	TTTTAAAAACCCGTATATTTCATATATGGAAGAAATTAATTTGAGGAGATATTNNATTACNATAACCA	3548						

Search completed: May 7, 2004, 00:44:40  
Job time : 863 secs

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RESULT 1
; US-09-620-405B-490
; Sequence 490, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 490
; LENGTH: 3288
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-620-405B-490

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Query Match	95.5%;	Score 1938.4;	DB 4;	Length 3288;
Best Local Similarity	98.5%;	Pred. No. 0;		
Matches 1997;	Conservative	4;	Mismatches 21;	Indels 5; Gaps 5;
Qy	5	TGCGTTTAAAGATGGCTTCTCTCAAGGCTAACTGCGGAATGAAAGTTTCTATTCTCAACTAA	64	
Db	1254	TCCTGTTTAAAGATGGCTTCTCTGAGGCTAACTGCGGAATGAAAGTTTCTATTCTCAACTAA	1313	
Qy	65	AGCCTTAGAATTGATGGACATCAAACTTTTCAAGCAGAGCCTCCGAGAAGCCATCTGC	124	
Db	1314	AGCCTTAGAATTGATGGACATCAAACTTTCAAGCAGAGCCTCCGAGAAGCCATCTGC	1373	
Qy	125	CTTCGAGCCTGCCATTGGAATCAAAAGTCTGTTCCCAATTAAGAGCCTTGGAATTTGAAGAA	184	
Db	1374	CTTCGAGCCTGCCATTGGAATCAAAAGTCTGTTCCCAATTAAGAGCCTTGGAATTTGAAGAA	1433	
Qy	185	TGAACAAACATTGAGAGCAGATGAGATCTCCATCAGAATCCAAACAAAGAGCATGTA	244	
Db	1434	TGAACAAACATTGAGAGCAGATGAGATCTCCATCAGAATCCAAACAAAGAGCATGTA	1493	
Qy	245	AGAAAGTCTTGGATCTTGAGAGTCTGTGAGACTGTTTTCACAGAGAGGATGTGTGTTT	304	
Db	1494	AGAAAGTCTTGGATCTTGAGAGTCTGTGAGACTGTTTTCACAGAGAGGATGTGTGTTT	1553	
Qy	305	ACCCAAGGCTACATCAAAAAAGAAATAGATAAAATAAATTGAAATTTAGAAGAGTCTCC	364	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	1938.4	95.5	3288	4	US-09-620-405B-490	Sequence 490, App	
2	1938.4	95.5	3288	4	US-09-834-759-430	Sequence 490, App	
3	1938.4	95.5	3865	4	US-09-620-405B-474	Sequence 474, App	
4	1938.4	95.5	3865	4	US-09-604-287A-474	Sequence 474, App	
5	1938.4	95.5	3865	4	US-09-834-759-474	Sequence 474, App	
6	1560.4	76.9	3681	4	US-09-620-405B-463	Sequence 463, App	
7	1560.4	76.9	3681	4	US-09-433-836B-463	Sequence 463, App	
8	1560.4	76.9	3681	4	US-09-604-287A-463	Sequence 463, App	
9	1560.4	76.9	3681	4	US-09-834-759-463	Sequence 463, App	
10	1558.8	76.8	2307	4	US-09-620-405B-468	Sequence 468, App	
11	1558.8	76.8	2307	4	US-09-433-836B-468	Sequence 468, App	
12	1558.8	76.8	2307	4	US-09-604-287A-468	Sequence 468, App	
13	1558.8	76.8	2307	4	US-09-834-759-468	Sequence 468, App	
14	1282.6	63.2	1337	4	US-09-620-405B-467	Sequence 467, App	
15	1282.6	63.2	1337	4	US-09-433-836B-467	Sequence 467, App	
16	1282.6	63.2	1337	4	US-09-604-287A-467	Sequence 467, App	
17	1282.6	63.2	1337	4	US-09-834-759-467	Sequence 467, App	
18	1197.6	59.0	1681	4	US-09-389-681-180	Sequence 180, App	
19	1197.6	59.0	1681	4	US-09-620-405B-180	Sequence 180, App	
20	1197.6	59.0	1681	4	US-09-339-338-180	Sequence 180, App	
21	1197.6	59.0	1681	4	US-09-433-826B-180	Sequence 180, App	
22	1197.6	59.0	1681	4	US-09-604-287A-180	Sequence 180, App	
23	1197.6	59.0	1681	4	US-09-285-480-180	Sequence 180, App	
24	1197.6	59.0	1681	4	US-09-834-759-180	Sequence 180, App	
25	1116.2	55.0	1665	4	US-09-389-681-178	Sequence 178, App	
26	1116.2	55.0	1665	4	US-09-620-405B-178	Sequence 178, App	
27	1116.2	55.0	1665	4	US-09-339-338-178	Sequence 178, App	

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1614	DB	TG	ATAATG	TGTTTCT	GAAGGCTCCCT	CGAGAAATGAAAGTTCT	TATTCAAACTAAAGC	1673
425	QY	CTT	AGAAATG	ATG	GCATCCAACTT	CAAGACAGAGCTCC	CGAGAGAGCCATCTGCCTT	484
1674	DB	CTT	AGAAATG	ATG	GCATCCAACTT	CAAGACAGAGCTCC	CGAGAGAGCCATCTGCCTT	1733
485	QY	CG	AGCTG	CCAT	TGAAATG	CAAAAGTCTGTTCC	AAATAAGCCTTGGAAATGGAAGATGA	544
1734	DB	CG	AGCTG	CCAT	TGAAATG	CAAAAGTCTGTTCC	AAATAAGCCTTGGAAATGGAAGATGA	1793
545	QY	AC	AAACAT	TGAGAGCAGAT	CAGATGTTCCCTT	CAGAATCAAAA	CAAAAAGAGAGTTGAAGA	604
1794	DB	AC	AAACAT	TGAGAGCAGAT	CAGATGTTCCCTT	CAGAATCAAAA	CAAAAAGAGAGTTGAAGA	1853
605	QY	AAA	TTCTTGGGAT	CTG	AGAGTCTCCG	TGAGACTGTTT	CACAGAGGATGCTGTGTGTACC	664
1854	DB	AAA	TTCTTGGGAT	CTG	AGAGTCTCCG	TGAGACTGTTT	CACAGAGGATGCTGTGTGTACC	1913
665	QY	CA	AGGCTACACAT	CAAAAAGAAATG	GATATAAATAAGT	GGAATAATAG	AAAGATTTCAACTAG	724
1914	DB	CA	AGGCTACACAT	CAAAAAGAAATG	GATATAAATAAGT	GGAATAATAG	AAAGATTTCAACTAG	1973
725	QY	CT	TATCAAAAAT	CTTGGATAC	AGTTCA	TCTTGTGAAAGAC	AGGGAATTTCAAAAGA	784
1974	DB	CT	TATCAAAAAT	CTTGGATAC	AGTTCA	TCTTGTGAAAGAC	AGGGAATTTCAAAAGA	2033
785	QY	TC	ACTGTGAACAC	AGTACAG	GAATAATG	GAACAAATG	AAAAAGAAAGTTTGTGTACTGAA	844
2034	DB	TC	ACTGTGAACAC	AGTACAG	GAATAATG	GAACAAATG	AAAAAGAAAGTTTGTGTACTGAA	2093
845	QY	AA	AGAACTGTCAG	AGCAAAAGAAAT	TAATAATC	ACAGTTAGAGAAC	CAAAAAGTTTAAATG	904
2094	DB	AA	AGAACTGTCAG	AGCAAAAGAAAT	TAATAATC	ACAGTTAGAGAAC	CAAAAAGTTTAAATG	2153
905	QY	GG	ACAGAGCTCTG	CAGTCTGAG	ATGACTTT	TAACCAAGAGAGAGAGAGAGAGAA	964	
2154	DB	GG	ACAGAGCTCTG	CAGTCTGAG	ATGACTTT	TAACCAAGAGAGAGAGAGAGAGAA	2213	
965	QY	TG	CGGATATATTAAT	TGAAAAAT	TAGGGAAGAAAT	TAGNAGAAATCG	AGAGCAGCATAG	1024
2214	DB	TG	CGGATATATTAAT	TGAAAAAT	TAGGGAAGAAAT	TAGNAGAAATCG	AGAGCAGCATAG	2273
1025	QY	GAA	AGGTTAGAAAGT	GAAACAA	CAACTTGAA	CAGGCTCTCAGAAAT	CAAGATATGAATTT	1084
2274	DB	GAA	AGGTTAGAAAGT	GAAACAA	CAACTTGAA	CAGGCTCTCAGAAAT	CAAGATATGAATTT	2333
1085	QY	GA	AGGTTAGAAAGT	ATTTGAAAT	CTAGGTTTCT	CACACTCA	GAAAAAGAAATTTATCT	1144
2334	DB	GA	AGGTTAGAAAGT	ATTTGAAAT	CTAGGTTTCT	CACACTCA	GAAAAAGAAATTTATCT	2393
1145	QY	CTT	ACATG	AAAAAT	TGCTGTTG	AAAAAGGAAAT	TGCCATGCTAAAACTGCAATAGCCAC	1204
2394	DB	CTT	ACATG	AAAAAT	TGCTGTTG	AAAAAGGAAAT	TGCCATGCTAAAACTGCAATAGCCAC	2453
1205	QY	ACT	GAAACACCAAT	TAC	CAGGAAAGGAAAT	TAATATCTTT	GAGACATTAAGATTTTAA	1264
2454	DB	ACT	GAAACACCAAT	TAC	CAGGAAAGGAAAT	TAATATCTTT	GAGACATTAAGATTTTAA	2513
1265	QY	AG	AAAAAGAAAT	GCTGAACT	CTCAGATG	ACCTAAAA	CTGAAAAGAGAAATCATTAATCAAAAG	1324
2514	DB	AG	AAAAAGAAAT	GCTGAACT	CTCAGATG	ACCTAAAA	CTGAAAAGAGAAATCATTAATCAAAAG	2573
1325	QY	GG	CATCTCAATAT	TAGTGGCAGCTT	TAAGTCTG	ATAGCTGAG	AAACAACAATGCTCACTTC	1384
2574	DB	GG	CATCTCAATAT	TAGTGGCAGCTT	TAAGTCTG	ATAGCTGAG	AAACAACAATGCTCACTTC	2633
1385	QY	TAA	ATTGAAGGAAAA	CAAGCAAAAGAAAT	ACTAG	GGCGGAAAT	TGAAATCACACCATCC	1444
2634	DB	TAA	ATTGAAGGAAAA	CAAGCAAAAGAAAT	ACTAG	GGCGGAAAT	TGAAATCACACCATCC	2693

## RESULT 2

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US-09-834-759-490
; Sequence 490, Application US/09834759
; Patent No. 5680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Micham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Repler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; TITLE OF INVENTION: DIAGNOSIS OF BREAST
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 490
; LENGTH: 3288
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-834-759-490

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Query Match	95.5%;	Score 1938.4;	DB 4;	Length 3288;
Best Local Similarity	98.5%;	Pred. No. 0;		
Matches 1997; Conservative	4;	Mismatches 21;	Indels 5;	Caps 5;

5 TGCCGTTAAAGATGGTCTTCTGAAGGCTAACTGCGGAATGAAAGTTTCTATTCCAACTAA 64



1254	DB	TCCTGTTAAAGATGGTCTCTCTGGAAGCTAACTGCGGAATGAAAGTTTCTATTTCCAACTAA	1313
65	QY	AGCCTTAGAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCGAGAAGCCATCTGC	124
1314	DB	AGCCTTAGAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCGAGAAGCCATCTGC	1373
125	QY	CTTGGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAGCCTTGGAAATTGAAGAA	184
1374	DB	CTTGGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAGCCTTGGAAATTGAAGAA	1433
185	QY	TGAACAAAACATTGAGAGCAGATCAGATACTCCCATCAGAATCCAAACAAAAGGACTATGA	244
1434	DB	TGAACAAAACATTGAGAGCAGATCAGATACTCCCATCAGAATCCAAACAAAAGGACTATGA	1493
245	QY	AGAAAGTTCTTGGATTCTGAGAGTCTCTGTGAGACTGTTTACAGAAAGGATGTGTGTTT	304
1494	DB	AGAAAGTTCTTGGATTCTGAGAGTCTCTGTGAGACTGTTTACAGAAAGGATGTGTGTTT	1553
305	QY	ACCCAAAGGCTACACATCAAAAAGAAATAGATAAAATAAATGGAATAATAGAAAGAGTCTCC	364
1554	DB	ACCCAAAGGCTACACATCAAAAAGAAATAGATAAAATAAATGGAATAATAGAAAGAGTCTCC	1613
365	QY	TGATAATGATGGTTTTCTGAAGGCTCCCTGCAGAAATGAAAGTTTCTATTCCAACTAAAGC	424
1614	DB	TGATAATGATGGTTTTCTGAAGGCTCCCTGCAGAAATGAAAGTTTCTATTCCAACTAAAGC	1673
425	QY	CTTAGAATTTCATGGACATGCAAACTTTCAAAGCAGAGCCTCCGAGAAGCCATCTGCCTT	484
1674	DB	CTTAGAATTTCATGGACATGCAAACTTTCAAAGCAGAGCCTCCGAGAAGCCATCTGCCTT	1733
485	QY	CGAGCCTGCCAATTGAAATGCAAAAAGTCTGTTCCAAATAAAGCCTTGGAAATGAAGAAATGA	544
1734	DB	CGAGCCTGCCAATTGAAATGCAAAAAGTCTGTTCCAAATAAAGCCTTGGAAATGAAGAAATGA	1793
545	QY	ACAAACATTGAGAGCAGATCAGATGTTCCCTTCAGATCAAAACAAAAGAGTTTCAAGA	604
1794	DB	ACAAACATTGAGAGCAGATCAGATGTTCCCTTCAGATCAAAACAAAAGAGAGTTTCAAGA	1853
605	QY	AAATTCTTGGATTCTCAGAGTCTCCGTGAGACTGTTTTCACAGAAGGATGTGTGTGTACC	664
1854	DB	AAATTCTTGGATTCTCAGAGTCTCCGTGAGACTGTTTTCACAGAAGGATGTGTGTGTACC	1913
665	QY	CAAGGCTACATCAAAAAGAAATGGATAAAATAAGTGGAAAAATTAGAGATTCAACTAG	724
1914	DB	CAAGGCTACATCAAAAAGAAATGGATAAAATAAGTGGAAAAATTAGAGATTCAACTAG	1973
725	QY	CCTATCAAAATCTTGGATACAGTTCATTCTTGTGAAAGCAAGGGAACCTTCAAAAAGA	784
1974	DB	CCTATCAAAATCTTGGATACAGTTCATTCTTGTGAAAGCAAGGGAACCTTCAAAAAGA	2033
785	QY	TCACTGTGAACACGTCACAGAAAAAATGGACAAATGAAAAGAGTTTGTGTACTGAA	844
2034	DB	TCACTGTGAACACGTCACAGAAAAAATGGACAAATGAAAAGAGTTTGTGTACTGAA	2093
845	QY	AAAGAACTGTGAGAACCAAGAAATATAATACAGTTAGAGAACCAAAAAGTTTAAATG	904
2094	DB	AAAGAACTGTGAGAACCAAGAAATATAATACAGTTAGAGAACCAAAAAGTTTAAATG	2153
905	QY	GGAAACAAGAGCTCTGCAGTGTGAGATTGACTTTTAAACCAAGAAAGAGAGAGAGAA	964
2154	DB	GGAAACAAGAGCTCTGCAGTGTGAGATTGACTTTTAAACCAAGAAAGAGAGAGAGAA	2213
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2214	DB	TGCCGATATATAATGAAAAAATTAGGAAGAAATTAGGAAGATCCAGAGCAGCATAG	2273
1025	QY	GAAGAGGTTTGAAGTGMAACCAACACTTGAACAGGCTCTCAGAATACAAAGATATAGAATT	1084
2274	DB	GAAGAGGTTTGAAGTGMAACCAACACTTGAACAGGCTCTCAGAATACAAAGATATAGAATT	2333
1085	QY	GAAGAGTGTAGAAAGTAATTGTAATCAGGTTTCTCACACTCATGAAAAATGAAATTATCT	1144
2334	DB	GAAGAGTGTAGAAAGTAATTGTAATCAGGTTTCTCACACTCATGAAAAATGAAATTATCT	2393

Qy	1145	CTTACATGAAATTTGATGTTTGAAAAAGGAATTCGCATGCTTAAACCTCGGAATAGCCAC	1204
Db	2394	CTTACATGAAATTTGATGTTTGAAAAAGGAATTCGCATGCTTAAACCTCGGAATAGCCAC	2453
Qy	1205	ACTGAAACACCAATACACGAGAAAAGAAAATAAATCTTTGAGGACATTAAGATTTAAA	1264
Db	2454	ACTGAAACACCAATACACGAGAAAAGAAAATAAATCTTTGAGGACATTAAGATTTAAA	2513
Qy	1265	AGAAAAGATGCTGAACTTCAGATGAGCCCTAAACCTGAAAGAGGAATCATTAACATAAAG	1324
Db	2514	AGAAAAGATGCTGAACTTCAGATGAGCCCTAAACCTGAAAGAGGAATCATTAACATAAAG	2573
Qy	1325	GGCATCTCAATATPAGTGGGACGCTTAAAGTCTGTATGCTGAGAAACAAATGCTCACTTC	1384
Db	2574	GGCATCTCAATATPAGTGGGACGCTTAAAGTCTGTATGCTGAGAAACAAATGCTCACTTC	2633
Qy	1385	TAAATTTGAAGGAAAAACAGACAAAAGAAATCTAGAGGCGAGAAAATTGAATCAACCATCC	1444
Db	2634	TAAATTTGAAGGAAAAACAGACAAAAGAAATCTAGAGGCGAGAAAATTGAATCAACCATCC	2693
Qy	1445	TAGACTGGCTTCTGCTGTACAGACCATGATCAAATTTGTGACATCAAGAAAAAGTCAAGA	1504
Db	2694	TAGACTGGCTTCTGCTGTACAGACCATGATCAAATTTGTGACATCAAGAAAAAGTCAAGA	2753
Qy	1505	ACCTGCTTTCCACATTTGCAGGAGATGCTTTTTCGCAAGAAAAAATGAATTTGATGTGAG	1564
Db	2754	ACCTGCTTTCCACATTTGCAGGAGATGCTTTTTCGCAAGAAAAAATGAATTTGATGTGAG	2813
Qy	1565	TAGTACCGATATATACAAATGAGGTGCTCCATCAACCACTTTCTGAGCTCAAGAGGAAT	1624
Db	2814	TAGTACCGATATATACAAATGAGGTGCTCCATCAACCACTTTCTGAGCTCAAGAGGAAT	2873
Qy	1625	CCAAAGCCCTAAAAATTAATCTCAATTTATGCGAGAGATGCTTCAAGAGAAAAATACATGG	1684
Db	2873	CCAAAGCCCTAAAAATTAATCTCAATTTATGCGAGAGATGCTTCAAGAGAAAAATACATGG	2932
Qy	1685	TTTCAGGAACATGCAACAAAGAGACCAACGTGAAACACACAGTGTCAAATGAAGGAAGTGA	1744
Db	2933	TTTCA - GAAATGCAACAAAGAGACCAACGTGAAACACACAGTGTCAAATGAAGGAAGTGA	2991
Qy	1745	CACATGNTCAAANCAGAACCAAGATNATGTGAAACAAACACACTGANCAGCAGGAGTCTCTA	1804
Db	2992	CACATGATCAAAACGAAACCAAGATNATGTGAAACAAACACACTGAAACAGCAGGAGTCTCTA	3051
Qy	1805	GATCAGAAATATTTCAACTTACAAAGCAAAAATATGTGGCTTCAACAGCAATTTAGTTTCAT	1864
Db	3052	GATCAGAAATATTTCAACTTACAAAGCAAAAATATGTGGCTTCAACAGCAATTTAGTTTCAT	3111
Qy	1865	GCACATGAAGAAAGCTGACAAACAAAAGCAAGATAACAATTTGATNTTCTTGAGAG	1924
Db	3112	GCACATAA - GAAAGCTGACAAACAAAAGCAAGATAACAATTTGATNTTCTTGAGAG	3170
Qy	1925	GAAATGCG - NCATCATCTTTCAAGGAAAAATGAGGAGATATTTNATTTACNATTAACCA	1983
Db	3171	GAAATGCGACATCATCTCTTAAAGGAAAAATGAGGAGATATTTNATTTCAATTAACCA	3230
Qy	1984	TTTAAAAAACCCGTATATTTCAATATCGAAAAAANAANAANAANAANAANAANAANAANA	2030
Db	3231	TTTAAAAAA - CCGTATATATCAATATGAAAAAGGAAAAAGCAGAAACA	3276

RESIT.T 3

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RES001 3
US-09-620-405B-474
; Sequence 474, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.

```



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; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470CB
; CURRENT APPLICATION NUMBER: US/09/620.405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 474
; LENGTH: 3665
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2448)..(2631)
; OTHER INFORMATION: 184 bp insert of B726P splice form
US-09-620-405B-474

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Query Match	95.5%;	Score 1938.4;	DB 4;	Length 3865;
Best Local Similarity	98.5%;	Pred. No. 0;		
Matches 1997;	Conservative	4;	Mismatches 21;	Indels 5; Gaps 5;
QY	5	TGCGGTTAAAGATGGCTCTCTCGAAGGCTAACTGCGGAATGAAAGTTTCTATTCCAACTAA	64	
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QY	65	AGCCTTAGAATTGATGGACATGCAAACTTTCAAGCAGAGCCCTCCGAGGAAGCATCTGC	124	
Db	1586	AGCCTTAGAATTGATGGACATGCAAACTTTCAAGCAGAGCCCTCCGAGGAAGCATCTGC	1645	
QY	125	CTTCGAGCCTGCCATTGAATGCAAAAGTCTGTTCAAATAAAGCCTTGGAATTGAAGAA	184	
Db	1646	CTTCGAGCCTGCCATTGAATGCAAAAGTCTGTTCAAATAAAGCCTTGGAATTGAAGAA	1705	
QY	185	TGAACAAACATTGAGACGAGATGAGATPACCCCATCAGAATCCAAACAAAGGACATGA	244	
Db	1706	TGACAAACATTGAGACGAGATGAGATPACCCCATCAGAATCCAAACAAAGGACATGA	1765	
QY	245	AGAAAGTCTTGGGATTCAGAGTCTCTGTGAGACTGTGTTTCACAGAAGGATGTGTGTTT	304	
Db	1766	AGAAAGTCTTGGGATTCAGAGTCTCTGTGAGACTGTGTTTCACAGAAGGATGTGTGTTT	1825	
QY	305	ACCCAGGCTACACATCAAAAGAGAAATAGATATAAATAAATGGAAAAATTGAGAGGCTCC	364	
Db	1826	ACCCAGGCTACACATCAAAAGAGAAATAGATATAAATAAATGGAAAAATTGAGAGGCTCC	1885	
QY	365	TGATAATGATGGTCTCTCGAAGGCTCCCTGAGAGCTGTTTTCACAACTAAAGC	424	
Db	1886	TGATAATGATGGTCTCTCGAAGGCTCCCTGAGAGCTGTTTTCACAACTAAAGC	1945	
QY	425	CTTAGAATTTGATGGACATGCAAACTTTCAAGCAGAGCCCTCCGAGGAAGCATCTGCCTT	484	
Db	1946	CTTAGAATTTGATGGACATGCAAACTTTCAAGCAGAGCCCTCCGAGGAAGCATCTGCCTT	2005	
QY	485	CGAGCCTGCCATTGAATGCAAAAGTCTGTTCAAATAAAGCCTTGGAATTGAAGATGA	544	
Db	2006	CGAGCCTGCCATTGAATGCAAAAGTCTGTTCAAATAAAGCCTTGGAATTGAAGATGA	2065	
QY	545	ACAAACATTGAGACGAGATCAGATGTTCCCTTCAGAAATCAAAACAAAGAGGTTGAAGA	604	
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QY	605	AAATTCCTGGGATTCAGAGTCTCCGCTGAGACTGTTTTCACAGAAGCATGTGTGTACC	664	
Db	2126	AAATTCCTGGGATTCAGAGTCTCCGCTGAGACTGTTTTCACAGAAGCATGTGTGTACC	2185	
QY	665	CAAGGCTACACATCAAAAGAGAAATGGATATAAATAAGTGGAAAAATTAGAAGATTCACATG	724	
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QY	725	CCTATCAAAATCTTGGATCAGTTTCATCTTGTGGAAGAGCAAGGAACTTCAAAAAGA	784	
Db	2246	CCTATCAAAATCTTGGATCAGTTTCATCTTGTGGAAGAGCAAGGAACTTCAAAAAGA	2305	

QY	785	TCAC	TGTG	GAAC	CAAC	TGTA	CAGG	HA	AAAT	TGGA	CAAA	TGAA	AAAG	AAAT	TTTGTG	TACT	GAA	844
DB	2306	TCACT	GTG	AAC	CAAC	TGTA	CAGG	HA	AAAT	TGGA	CAAA	TGAA	AAAG	AAAT	TTTGTG	TACT	GAA	2365
QY	845	AAAG	AAACT	TGTC	GAAG	CAAA	AGAA	AT	TA	AAAT	TCAC	AGTT	TAG	AGA	ACC	AAAA	AST	904
DB	2366	AAAG	AAACT	TGTC	GAAG	CAAA	AGAA	AT	TA	AAAT	TCAC	AGTT	TAG	AGA	ACC	AAAA	AGTT	2425
QY	905	GGAA	CAAG	AGCT	CTCG	AGTG	TGAG	ATTG	AC	TTTAA	CCCA	AGN	AGN	AGN	AGN	AGN	AGAA	964
DB	2426	GGAA	CAAG	AGCT	CTCG	AGTG	TGAG	ATTG	AC	TTTAA	CCCA	AGN	AGN	AGN	AGN	AGN	AGAA	2485
QY	965	TCCG	CAT	ATAT	TAT	TAAAT	TG	AAAA	AT	TAGG	GA	GAAT	TAGG	GA	GAAT	TG	CA	1024
DB	2486	TCCG	CAT	ATAT	TAT	TAAAT	TG	AAAA	AT	TAGG	GA	GAAT	TAGG	GA	GAAT	TG	CA	2545
QY	1025	GAAG	AGTT	TAG	AGT	GA	AGT	GA	CA	ACTTTG	AA	CAGG	CTCT	CAGA	AT	CA	AGAT	1084
DB	2546	GAAG	AGTT	TAG	AGT	GA	AGT	GA	CA	ACTTTG	AA	CAGG	CTCT	CAGA	AT	CA	AGAT	2605
QY	1085	GAAG	AGTT	TAG	AAAGT	TAAT	TTG	GAAT	CA	GGTTTCT	CA	CA	CTCAT	GA	AAAA	TTAT	CT	1144
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QY	1145	CTT	ACAT	GAAA	AT	TG	CAT	GTTC	CA	AAAA	GG	AAAT	TGCC	ATGCT	TAAA	CT	GGA	1204
DB	2666	CTT	ACAT	GAAA	AT	TG	CAT	GTTC	CA	AAAA	GG	AAAT	TGCC	ATGCT	TAAA	CT	GGA	2725
QY	1205	ACT	GAA	CA	CC	AAAT	CC	AG	AAAA	GG	AAAA	TAA	AT	TAA	CTTT	GAG	CA	1264
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QY	1265	AGAA	AA	GAAT	TGCT	GAA	CTT	CAG	AT	GAC	CCCT	TAAA	CT	TGAA	AG	AGG	AA	1324
DB	2786	AGAA	AA	GAAT	TGCT	GAA	CTT	CAG	AT	GAC	CCCT	TAAA	CT	TGAA	AG	AGG	AA	2845
QY	1325	GG	AT	CT	CA	AT	TAG	TGG	CG	CG	CTTAA	AGTT	CT	GAT	G	AG	CA	1384
DB	2846	GG	AT	CT	CA	AT	TAG	TGG	CG	CG	CTTAA	AGTT	CT	GAT	G	AG	CA	2905
QY	1385	TAA	TT	TG	AGG	AAAA	CA	AG	CA	AA	AAAT	TA	CT	TAG	AGG	CAG	AAAA	1444
DB	2906	TAA	TT	TG	AGG	AAAA	CA	AG	CA	AA	AAAT	TA	CT	TAG	AGG	CAG	AAAA	2965
QY	1445	TAG	ACT	GG	CTTCT	G	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	1504
DB	2966	TAG	ACT	GG	CTTCT	G	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	3025
QY	1505	AC	CT	GCTTTT	CC	CA	AT	TG	CAGG	AG	ATGCT	TTG	TTT	GC	AAAA	AAAA	TG	1564
DB	3026	AC	CT	GCTTTT	CC	CA	AT	TG	CAGG	AG	ATGCT	TTG	TTT	GC	AAAA	AAAA	TG	3085
QY	1565	TAG	TAC	CG	AT	TAT	TA	CA	AT	TAG	GTG	CT	CA	CA	CC	ACTTTT	TG	1624
DB	3086	TAG	TAC	CG	AT	TAT	TA	CA	AT	TAG	GTG	CT	CA	CA	CC	ACTTTT	TG	3144
QY	1625	CC	AAAA	GCCT	TAAA	AT	TAA	CT	CA	ATTAT	TG	CAGG	AG	ATGCT	CT	T	AG	1684
DB	3145	CC	AAAA	GCCT	TAAA	AT	TAA	CT	CA	ATTAT	TG	CAGG	AG	ATGCT	CT	T	AG	3204
QY	1685	TTT	CAG	AA	CA	TG	CA	AA	AG	CA	CA	AGT	GA	AA	CAC	AGT	CT	1744
DB	3205	TTT	CA	-														

3384 GCACATAA-GAAAGCTGCAACAAAGCAAGATACAAATTGATATTCATTTCTTGAGAG 3442
1925 GAAATGTC-NCATCATCTCTTAAAGAGAGAAAATGAGGAGATATTNATTACNATAACCA 1983
3443 GAAATGCAACATCATCTCTTAAGAGAGAAAATGAGGAGATATTNATTACATACCA 3502
1984 TTTAAAAACCCGTATTTTCAATATGGAANAAAAAANAAAAA 2030
3503 TTTAAAAA-CCGTATATATCATATGAAAAAGAGAAAGCAAAACA 3548
RESULT 4
US-09-604-287A-474
; Sequence 474, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 474
; LENGTH: 3865
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2448)...(2631)
; OTHER INFORMATION: 184 bp insert of B726P splice form
US-09-604-287A-474
Query Match 95.5%; Score 1938.4; DB 4; Length 3865;
Best Local Similarity 98.5%; Pred No. 0;
Matches 1997; Conservative 4; Mismatches 21; Indels 5; Gaps 5;
5 TCCCGTTAAAGATGGTCTCTGAGGCTAACTGCGGAATGAAAGTTCTATTCOAACCTAA 64
1526 TCCGTGTTAAAGATGGTCTCTGAGGCTAACTGCGGAATGAAAGTTCTATTCOAACCTAA 1585
65 AGCCTTAGAATTGATGGACATGCAACTTTCAAGCAGAGCTCCCGAGAGCCATCTGC 124
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245 AGAAAGTTCTGGGATCTGAGAGTCTGTTGAGAGTCTGTTGAGAGTCTGTTGAGAGTCTGTT 304
1766 AGAAAGTTCTGGGATCTGAGAGTCTGTTGAGAGTCTGTTGAGAGTCTGTTGAGAGTCTGTT 1825
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425 CTTAGAAATTGATGGACATGCAAACTTTCAAGCAGAGCTCCCGAGAGCCATCTGCCTT 484

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2126 AAATTCCTGGGATCTGAGAGTCTCGTGAGAGTCTTTTCAAGAGAGTGTGTGTGATCC 2185
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2186 CAAGGCTACACATCAAAAGAAATGGAATAAGTGGAAATTAAGAGATTCAACTAG 2245
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RESULT 6

US-09-620-405B-463  
; Sequence 463. Application US/09620405B  
; Patent No. 6528054  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Hepler, William T.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER  
; FILE REFERENCE: 210121.470C8

; CURRENT APPLICATION NUMBER: US/09/620,405B  
; CURRENT FILING DATE: 2000-07-20  
; NUMBER OF SEQ ID NOS: 495  
; SOFTWARE: FastSeq For Windows Version 3.0  
; SEQ ID NO 463  
; LENGTH: 3681  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-09-620-405B-463  
  
Query Match 76.9%; Score 1560.4; DB 4; Length 3681;  
Best Local Similarity 89.4%; Pred. No. 0;  
Matches 1813; Conservative 4; Mismatches 21; Indels 189; Gaps 6;  
  
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RESULT 7  
US-09-433-826B-463  
; Sequence 463, Application US/09433826B  
; Patent No. 6579973  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yuqi  
; APPLICANT: Dillon, Devin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND  
; FILE REFERENCE: 210121.470C4  
; CURRENT APPLICATION NUMBER: US/09/433.826B  
; CURRENT FILING DATE: 1999-11-03  
; NUMBER OF SEQ ID NOS: 474  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 463  
; LENGTH: 3681  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-433-826B-463  
Query Match 76.9%; Score 1560.4; DB 4; Length 3681;  
Best Local Similarity 89.4%; Pred. No. 0;  
Matches 1813; Conservative 4; Mismatches 21; Indels 189; Gaps 6;  
QY 5 TGCCTTAAAGATGTCTCTGAGGCTAACTGCGGAATGAAAGTTTCTATTCCTAACTAA 64  
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RESULT 8  
US-09-604-287A-463  
; Sequence 463, Application US/09604287A  
; Patent No. 6586572  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Dillon, Devin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Hepler, William T.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER  
; FILE REFERENCE: 210121.470C7  
; CURRENT APPLICATION NUMBER: US/09/604,287A  
; NUMBER OF SEQ ID NOS: 489  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 463  
; LENGTH: 3681  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-604-287A-463  
Query Match 76.9%; Score 1560.4; DB 4; Length 3681;  
Best Local Similarity 89.4%; Pred. No. 0;  
Matches 1813; Conservative 4; Mismatches 21; Indels 189; Gaps 6;  
Qy 5 TCCCGTTAAAGATGGTCTTCTGAAAGCTTAACCTGCGGAATGAAAGTTTCTATTCCAACTAA 64  
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Qy 905 GGAACAAGAGCTCTGAGTGTGAGATTGACTTTTAAACCAAGAGAGAGAGAGAA 964  
Db 2426 GGAACAAGAGCTCTGAGTGTG----- 2447  
Qy 965 TGCCGATATATAATGAAAAATTAGGAGAAATTAGGAGAAATCGAAGAGCAGCATAG 1024  
Db 2448 ----- 2447  
Qy 1025 GAAAGAGTTAGAAGTGAAACAACTTTGAACAGGCTCTCAGATACAGATATAGAATT 1084  
Db 2448 ----- 2447  
Qy 1085 GAAGAGTGAAGAAATTTGAATCAGTTTCTCAGCTCAGTCACTGAAATGAAATTTATCT 1144  
Db 2448 -----AGGTTTCTCAGCTCAGTCACTGAAATGAAATTTATCT 2481  
Qy 1145 CTTACATGAAATTTGCAATTTGAAAAAGAAATGCGATGCTAAACTGGAATAGCCAC 1204  
Db 2482 CTTACATGAAATTTGCAATTTGAAAAAGAAATTTGCGATGCTAAACTGGAATAGCCAC 2541  
Qy 1205 ACTGAAACCAATATCAGAGAAAGAAATTAATATCTTTGAGGACATTAAGATTTAAA 1264  
Db 2542 ACTGAAACCAATATCAGAGAAAGAAATTAATATCTTTGAGGACATTAAGATTTAAA 2601  
Qy 1265 AGAAAGAAATGCTGAATTTGAGTGAACCTTAAACTGAAAGAGGAATCATTAATAAAG 1324  
Db 2602 AGAAAGAAATGCTGAATTTGAGTGAACCTTAAACTGAAAGAGGAATCATTAATAAAG 2661  
Qy 1325 GGCATCTCAATATAGTGGGAGCTTTAAAGTTCTGATAGCTGAGAAACAATGCTCACTTC 1384  
Db 2662 GGCATCTCAATATAGTGGGAGCTTTAAAGTTCTGATAGCTGAGAAACAATGCTCACTTC 2721  
Qy 1385 TAAATTGAGGAAACCAAGCAAGAAATTAATAGAGGAGAAATTTGAATCAACACCATCC 1444  
Db 2722 TAAATTGAGGAAACCAAGCAAGAAATTAATAGAGGAGAAATTTGAATCAACACCATCC 2781

Qy 1445 TAGACTGGCTTCTCTGTACAGACCAGATGATCAAAATTTGTGACATCAAGAAAAAGTCAAGA 1504  
Db 2782 TAGACTGGCTTCTCTGTACAGACCAGATGATCAAAATTTGTGACATCAAGAAAAAGTCAAGA 2841  
Qy 1505 ACCTGCTTTCCACATTTGAGGAGATGCTGTTTGCAGAGAAATTAATGATGTTGATGTGAG 1564  
Db 2842 ACCTGCTTTCCACATTTGAGGAGATGCTGTTTGCAGAGAAATTAATGATGTTGATGTGAG 2901  
Qy 1565 TAGTACCGATATATAAACAATGAGTGTCCATCAACCACTTTCTGAAAGCTCAAGGAAAT 1624  
Db 2902 TAGTA-CGATATATAAACAATGAGTGTCCATCAACCACTTTCTGAAAGCTCAAGGAAAT 2960  
Qy 1625 CCANAGCCTAAAAATTAATCTCAATTTATGAGGAGATGCTTCAAGAGAAAAATACATTGG 1684  
Db 2961 CCANAGCCTAAAAATTAATCTCAATTTATGAGGAGATGCTTCAAGAGAAAAATACATTGG 3020  
Qy 1685 TTTCAAGAACATGACAAAGAGACCAACGTTGAACACACAGTGTCAATTAAGAGGAGCTGAA 1744  
Db 3021 TTTCA-GAACATGACAAAGAGACCAACGTTGAACACACAGTGTCAATTAAGAGGAGCTGAA 3079  
Qy 1745 CACATGTTTCAANCGACAGATTAATGTGAACAAACACACTGANCAGAGGAGTCTCTA 1804  
Db 3080 CACATGTTTCAANCGACAGATTAATGTGAACAAACACACTGANCAGAGGAGTCTCTA 3139  
Qy 1805 GATCAGAAATTTATTTCAACTACAAAGCAAAATATGTTGGCTTCAACAGCAATTTAGTTTCA 1864  
Db 3140 GATCAGAAATTTATTTCAACTACAAAGCAAAATATGTTGGCTTCAACAGCAATTTAGTTTCA 3199  
Qy 1865 GCACATTAAGAAAGCTGACACAAAGCAAGATTAACAAATTTGATNTTCTTTGAGAG 1924  
Db 3200 GCACATTA-GAAAGCTGACACAAAGCAAGATTAACAAATTTGATNTTCTTTGAGAG 3258  
Qy 1925 GAAATATGC-NCATCATCTTTCTAAAGAGAAAAATGAGGAGATATTTTACNATAACCA 1983  
Db 3259 GAAATATGCACATCATCTCTTAAAGAGAAAAATGAGGAGATATTTTACNATAACCA 3318  
Qy 1984 TTTAAAAAACCCGTTATTTTCAATATGAAAAAANAANAANAANAANAANAANAANAANA 2030  
Db 3319 TTTAAAAAAA-CGGTATATCAATATGAAAAAAGAGAAAGCAGAAAAA 3364

RESULT 9  
US-09-834-759-463  
; Sequence 463, Application US/09834759  
; Patent No. 6680197  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Heppler, William T.  
; APPLICANT: Henderson, Robert A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE OF INVENTION: DIAGNOSIS OF BREAST CANCER  
; FILE REFERENCE: 210121.470C9  
; CURRENT APPLICATION NUMBER: US/09/834,759  
; CURRENT FILING DATE: 2001-04-13  
; NUMBER OF SEQ ID NOS: 547  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 463  
; LENGTH: 3681  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-834-759-463

Query Match 76.9%; Score 1560.4; DB 4; Length 3681;  
Best Local Similarity 89.4%; Pred. No. 0;  
Matches 1813; Conservative 4; Mismatches 21; Indels 189; Gaps 6;

Qy 5 TGCCGTTAAAGATGCTTCTGAGGCTAACTGCGGAATGAAGTTTCTATTCCAACTAA 64



1526 TCCTGTTAAAGATGGTCTTCTGAAGGCTAACTGGGATGAAGATTTCTATTCCAACTAA 1585  
65 AGCCTTAGAATTGATGGACATGCCAAACTTTCAAGCAGAGAGCTCCCGAAGAGCCATCTGC 124  
1586 AGCCTTAGAATTGATGGACATGCCAAACTTTCAAGCAGAGAGCTCCCGAAGAGCCATCTGC 1645  
125 CTTGGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATGAAGAA 184  
1646 CTTGGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATGAAGAA 1705  
185 TGAACAAACATTTAGAGAGAGATGATACTCCCATCAGAATCCAAACAAAGAGGACTATGA 244  
1706 TGAACAAACATTTAGAGAGAGATGATACTCCCATCAGAATCCAAACAAAGAGGACTATGA 1765  
245 AGAAGATTTCTGGGATCTGAGAGTCTGTTGAGACTGTTTCAAGAGAGGATGTTGTTT 304  
1766 AGAAGATTTCTGGGATCTGAGAGTCTGTTGAGACTGTTTCAAGAGAGGATGTTGTTT 1825  
305 ACCCAAGGCTACACATCAAAAGAAATAGATAAAATAAATGAAATTAAGAGAGTCTCC 364  
1826 ACCCAAGGCTACACATCAAAAGAAATAGATAAAATAAATGAAATTAAGAGAGTCTCC 1885  
365 TGATATGATGTTTCTGAGGCTCCCTGAGATGAAGTTCTATTCCAATCAAGC 424  
1886 TGATATGATGTTTCTGAGGCTCCCTGAGATGAAGTTCTATTCCAATCAAGC 1945  
425 CTTAGAAATTTGATGGACATGCCAAACTTTCAAGCAGAGGCTCCCGAAGAGCCATCTGCCCT 484  
1946 CTTAGAAATTTGATGGACATGCCAAACTTTCAAGCAGAGGCTCCCGAAGAGCCATCTGCCCT 2005  
485 CGAGCCTGCCATTTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATGAAGATGA 544  
2006 CGAGCCTGCCATTTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATGAAGATGA 2065  
545 ACAACATTTGAGAGAGATGATGTTCCCTTCAGATCAAAACAAAGAGGTTGAAGA 604  
2066 ACAACATTTGAGAGAGATGATGTTCCCTTCAGATCAAAACAAAGAGGTTGAAGA 2125  
605 AAATCTTGGGATCTGAGAGTCTCGTGAGACTGTTTCAAGAGAGGATGTTGTTGTTACC 664  
2126 AAATCTTGGGATCTGAGAGTCTCGTGAGACTGTTTCAAGAGAGGATGTTGTTGTTACC 2185  
665 CAAGGCTACACATCAAAAGAAATGATAAATTAAGTGAAGATTTGTTGTTACTGAA 724  
2186 CAAGGCTACACATCAAAAGAAATGATAAATTAAGTGAAGATTTGTTGTTACTGAA 2245  
725 CCTATCAAAATCTTGGATACAGTTCAATCTTTGTAAGAGCAAGGGAATTTCAAAAGA 784  
2246 CCTATCAAAATCTTGGATACAGTTCAATCTTTGTAAGAGCAAGGGAATTTCAAAAGA 2305  
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2306 TCATCTGACACAGTACAGGAAATGGAACATTAAGTGAAGATTTGTTGTTACTGAA 2365  
845 AAAGAACTGTCAGAGCAAAAGAAATTAAGTGAAGATTTGTTGTTACTGAA 904  
2366 AAAGAACTGTCAGAGCAAAAGAAATTAAGTGAAGATTTGTTGTTACTGAA 2425  
905 GGAACAGAGCTCTGAGTGTGAGTTGATTTAAACCAAGAGAGAGAGAGAGAA 964  
2426 GGAACAGAGCTCTGAGTGTG----- 2447  
965 TGCCGATATATTAATGAAAAAATTAGGAGAAATTTAGGAAGATTCGAAGAGCGCATAG 1024  
2448 ----- 2447  
1025 GAAAGAGTTAGAGTGAACAAACACTTGAACAGGCTCTCAGNATCAAGATATAGAAAT 1084  
2448 ----- 2447  
1085 GAAAGGTGAGAAAGTAATTTGAATCAGGTTTCTCAGCTCATGAAAAATGAAATTTATCT 1144  
2448 -----AGGTTTCTCAGCTCATGAAAAATGAAATTTATCT 2481

1145 CTTACATGAAGATTCGATGTTGAAAAAGGAAATTCGCCATGCTAAAACTGGAATAGCCAC 1204  
2482 CTTACATGAAGATTCGATGTTGAAAAAGGAAATTCGCCATGCTAAAACTGGAATAGCCAC 2541  
1205 ACTGAAACACCAATACCAAGGAAAGGAAATTAATTAATCTTTGAGGACATTAAGATTTTAA 1264  
2542 ACTGAAACACCAATACCAAGGAAAGGAAATTAATTAATCTTTGAGGACATTAAGATTTTAA 2601  
1265 AGAAGAGATGCTGACATTCAGATGACCTTAAGAACTGGAAGAGGAAATCAATTAACATAAG 1324  
2602 AGAAGAGATGCTGACATTCAGATGACCTTAAGAACTGGAAGAGGAAATCAATTAACATAAG 2661  
1325 GGCATCTCAATATAGTGGGAGCTTTAAAGTTCTGATAGCTGAGAACACAATGCTCACTTC 1384  
2662 GGCATCTCAATATAGTGGGAGCTTTAAAGTTCTGATAGCTGAGAACACAATGCTCACTTC 2721  
1385 TAAATTAAGGAAACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1444  
2722 TAAATTAAGGAAACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 2781  
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2782 TAGACTGGCTTCTGCTGTACAAAGCACCATGATCAAAATTTGTGACATCAAGAAAAAGTCAAGA 2841  
1505 ACCTGCTTCCACATTTGAGAGGAGTCTGTTTGAAGAGGAAATTTGAATCAACATCC 1564  
2842 ACCTGCTTCCACATTTGAGAGGAGTCTGTTTGAAGAGGAAATTTGAATCAACATCC 2901  
1565 TAGTACCGATATATAAATGAGGCTCTCCATCAACCACTTTCTGAAGCTCAAGAGAAAT 1624  
2902 TAGTA-CGATATATAAATGAGGCTCTCCATCAACCACTTTCTGAAGCTCAAGAGAAAT 2960  
1625 CCANAAGCCTTAAATTAATCTCAATTTGAGGAGATGCTCTAAGAGAAATACATTCG 1684  
2961 CCAAGAGCCTTAAATTAATCTCAATTTGAGGAGATGCTCTAAGAGAAATACATTCG 3020  
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3021 TTTTCA-GAATCTGCAAAAGAGACCAACGTTGAACACAGTGTCAAAATGAAGAGAGTGA 3079  
1745 CACATGTTCAAAAGCAAGATNATGTAACAAACACACTGAGGAGAGGAGTCTCTA 1804  
3080 CACATGTTCAAAAGCAAGATNATGTAACAAACACACTGAGGAGAGGAGTCTCTA 3139  
1805 GATCAGAAATTTTCAACTACAAAGCAAAATATGTTGGCTTCAACAGCAATTAGTTTCA 1864  
3140 GATCAGAAATTTTCAACTACAAAGCAAAATATGTTGGCTTCAACAGCAATTAGTTTCA 3199  
1865 GCACATAAGGAAAGCTGACAAACAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1924  
3200 GCACATAA-GAAAGCTGACAAACAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 3258  
1925 GAAATGCT-NCATCATCTTCTTAAAGAGGAAATGAGGAGATTTTAAATGAGGAGAG 1983  
3259 GAAATGCAACATCATCTCTTAAAGAGGAAATGAGGAGATTTTAAATGAGGAGAG 3318  
1984 TTTAAAAAACCCGTATATTTCAATATGGAAGAAAAAAGAAAAAAGAAAAA 2030  
3319 TTTAAAAAACCCGTATATATCAATATGGAAGAAAAAAGAAAAAAGAAAAA 3364

## RESULT 10

US-09-620-405B-468  
; Sequence 468, Application US/09620405B  
; Patent No. 6528054  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yuguo  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Hepler, William T.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER  
; FILE REFERENCE: 210121.470C8  
; CURRENT APPLICATION NUMBER: US/09/620,405B  
; CURRENT FILING DATE: 2000-07-20  
; NUMBER OF SEQ ID NOS: 495  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 468  
; LENGTH: 2307  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-620-405B-468

Query Match 76.8%; Score 1558.8; DB 4; Length 2307;  
Best Local Similarity 89.5%; Pred. No. 0;  
Matches 1815; Conservative 0; Mismatches 23; Indels 189; Gaps 6;

Qy	5	TGCCGTTAAAGATGGTCTCTGAAGCTAACTCCGGAATGAAAGTTCTTATTCCTCACTAA	64
Db	169	TCTGTTAAAGATGGTCTCTGAAGCTAACTCCGGAATGAAAGTTCTTATTCCTCACTAA	228
Qy	65	AGCCTTAGAATTGATGACATGCAAACTTTCAAAGCAGAGCCCTCCCGAAGCCATCTGC	124
Db	229	AGCCTTAGAATTGATGACATGCAAACTTTCAAAGCAGAGCCCTCCCGAAGCCATCTGC	288
Qy	125	CTTCGAGCCTGCCATTGAATGCAAAAGCTCTGTTCCAAATAAAGCCTTCGGAATTGAAGAA	184
Db	289	CTTCGAGCCTGCCATTGAATGCAAAAGCTCTGTTCCAAATAAAGCCTTCGGAATTGAAGAA	348
Qy	185	TGAACAAACATTGAGAGCAGATGAGATATCCCATCAGAAATCAAAACAAAGGACTATGA	244
Db	349	TGAACAAACATTGAGAGCAGATGAGATATCCCATCAGAAATCAAAACAAAGGACTATGA	408
Qy	245	AGAAAGTTCTGGGATTCCTGAGAGTCTCTGAGAGTCTGTTTACAGAGAGTGTGTGTTT	304
Db	409	AGAAAGTTCTGGGATTCCTGAGAGTCTCTGAGAGTCTGTTTACAGAGAGTGTGTGTTT	468
Qy	305	ACCCAGGCTCACATCAAAAGAAATAGATAATAATAATGAAAAATTAGAAGAGTCTCC	364
Db	469	ACCCAGGCTCACATCAAAAGAAATAGATAATAATAATGAAAAATTAGAAGAGTCTCC	528
Qy	365	TGATAATGATGGTTTCTGAGAGTCTCTGAGAGTCTGTTTACAGAGAGTGTGTGTTT	424
Db	529	TGATAATGATGGTTTCTGAGAGTCTCTGAGAGTCTGTTTACAGAGAGTGTGTGTTT	588
Qy	425	CTTAGAATTGATGACATGCAAACTTTCAAAGCAGAGCCTCCCGAAGCCATCTGCCTT	484
Db	589	CTTAGAATTGATGACATGCAAACTTTCAAAGCAGAGCCTCCCGAAGCCATCTGCCTT	648
Qy	485	CGAGCTGCCATTGAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATTGAAGATGA	544
Db	649	CGAGCTGCCATTGAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATTGAAGATGA	708
Qy	545	ACAAACATTGAGAGCAGATCAGATGTTCCCTTCAAGATCAAAACAAAGAGGTTGAAGA	604
Db	709	ACAAACATTGAGAGCAGATCAGATGTTCCCTTCAAGATCAAAACAAAGAGGTTGAAGA	768
Qy	605	AAATCTTTGGGATCTCGAGAGTCTCCGAGAGTCTGTTTACAGAGAGTGTGTGTACC	664
Db	769	AAATCTTTGGGATCTCGAGAGTCTCCGAGAGTCTGTTTACAGAGAGTGTGTGTACC	828
Qy	665	CAAGCTCACATCAAAAGAAATGGAATAAATAGTGGAAATTTAGAAGATTCAACTAG	724
Db	829	CAAGCTCACATCAAAAGAAATGGAATAAATAGTGGAAATTTAGAAGATTCAACTAG	888
Qy	725	CCTATCAAAATCTTTGGATACAGTTCTTTGTTGAAAGAGCAAGGGAATCTCAAAAGA	784
Db	889	CCTATCAAAATCTTTGGATACAGTTCTTTGTTGAAAGAGCAAGGGAATCTCAAAAGA	948
Qy	785	TCAGTGTGAACCACTACAGGAAATGGAACAAATGAAAGAAAGTTTGTGTACTGAA	844
Db	949	TCAGTGTGAACCACTACAGGAAATGGAACAAATGAAAGAAAGTTTGTGTACTGAA	1008

Qy	845	AAAGAACTGTGTAGAGCAAAAGAAATATAATCACAGTTAGAGACCAAAAGATTTAAATG	904
Db	1009	AAAGAACTGTGTAGAGCAAAAGAAATATAATCACAGTTAGAGACCAAAAGATTTAAATG	1068
Qy	905	GGAAACAGAGCTCTGCAGTGTGTGAGTTGACTTTAAACCAAGAGAGAGAGAGAGAAA	964
Db	1069	GGAAACAGAGCTCTGCAGTGTGTGAGTTGACTTTAAACCAAGAGAGAGAGAGAGAAA	1090
Qy	965	TGCCGATATATTAAATGAAAAAATTAGGAAGAAATTAGGAAGAAATCGAAGAGCAGCATAG	1024
Db	1091	TGCCGATATATTAAATGAAAAAATTAGGAAGAAATTAGGAAGAAATCGAAGAGCAGCATAG	1090
Qy	1025	GAAAGAGTTAGAAAGTGAAACCAACTTGAAACAGGCTCTCAGAAATACAAGATATAGAATT	1084
Db	1091	GAAAGAGTTAGAAAGTGAAACCAACTTGAAACAGGCTCTCAGAAATACAAGATATAGAATT	1090
Qy	1085	GAAGAGTGTAGAAAGTAATTTGAATCAGGTTTCTCACACTCATGAAATGAAATTTATCT	1144
Db	1091	GAAGAGTGTAGAAAGTAATTTGAATCAGGTTTCTCACACTCATGAAATGAAATTTATCT	1124
Qy	1145	CTTACATGAAAAATTGCATGTTGAAAAAGGAAATTTGCCATGCTAAAACTGGAAATAGCCAC	1204
Db	1125	CTTACATGAAAAATTGCATGTTGAAAAAGGAAATTTGCCATGCTAAAACTGGAAATAGCCAC	1184
Qy	1205	ACTGAACACCAATACACAGAAAAAGGAAATAAATTAATTTGAGGACATTAAGATTTTAAA	1264
Db	1185	ACTGAACACCAATACACAGAAAAAGGAAATAAATTAATTTGAGGACATTAAGATTTTAAA	1244
Qy	1265	AGAAAGAGTCTGAACTTCAGATGACCTTAAACCTGAAAGAGGAATCATTTAACTAAAAG	1324
Db	1245	AGAAAGAGTCTGAACTTCAGATGACCTTAAACCTGAAAGAGGAATCATTTAACTAAAAG	1304
Qy	1325	GGCATCTCAATATATAGTGGCAGCTTAAAGTTCTGATAGTGAGAGAACAAATGCTCACTTC	1384
Db	1305	GGCATCTCAATATATAGTGGCAGCTTAAAGTTCTGATAGTGAGAGAACAAATGCTCACTTC	1364
Qy	1385	TAAATTGAGGAAAAAACAAGACAAGAAATTAATAGAGGAGAAATTAATTAACACCACTCC	1444
Db	1365	TAAATTGAGGAAAAAACAAGACAAGAAATTAATAGAGGAGAAATTAATTAACACCACTCC	1424
Qy	1445	TAGACTGCTCTCTGCTGTACAAAGACCATGATCAAAATTTGTCACATCAAGAAAAAGTCAAGA	1504
Db	1425	TAGACTGCTCTCTGCTGTACAAAGACCATGATCAAAATTTGTCACATCAAGAAAAAGTCAAGA	1484
Qy	1505	ACCTGCTTTCCACATTTGAGAGAGATGCTGTTTTCGAAAGAAATTAATGATGTTGATGTGAG	1564
Db	1485	ACCTGCTTTCCACATTTGAGAGAGATGCTGTTTTCGAAAGAAATTAATGATGTTGATGTGAG	1544
Qy	1565	TAGTACCGATATATAACCAATGAGGTGCTCCATCAACCACTTTCTGAAGCTCAAGGAAAT	1624
Db	1545	TAGTACCGATATATAACCAATGAGGTGCTCCATCAACCACTTTCTGAAGCTCAAGGAAAT	1603
Qy	1625	CCAAAGCCTAAAAATTAATCTCAATTTGAGAGAGATGCTCTTAAGAGAAATACATTTGG	1684
Db	1604	CCAAAGCCTAAAAATTAATCTCAATTTGAGAGAGATGCTCTTAAGAGAAATACATTTGG	1663
Qy	1685	TTTTCAGGAACATGCAAAAGAGACCAACGTCGAAACACAGTGTCAAATGAAAGGAGCTGAA	1744
Db	1664	TTTTCAGGAACATGCAAAAGAGACCAACGTCGAAACACAGTGTCAAATGAAAGGAGCTGAA	1722
Qy	1745	CACATGTTTCAANCGAAACAGATTTGTAACAAACACACTGANCAGCAGGAGCTCTCTA	1804
Db	1723	CACATGTTTCAANCGAAACAGATTTGTAACAAACACACTGANCAGCAGGAGCTCTCTA	1782
Qy	1805	GATCAGAAATTTTCAACTCAAAAGCAAAATATGTGGCTTCAACAGCAATTTAGTTTCAAT	1864
Db	1783	GATCAGAAATTTTCAACTCAAAAGCAAAATATGTGGCTTCAACAGCAATTTAGTTTCAAT	1842
Qy	1865	GCACATAANGAAGCTGCAACAAAGCAAGATAAATTAATGATTTTCAATTTCTTGAGAG	1924
Db	1843	GCACATAANGAAGCTGCAACAAAGCAAGATAAATTAATGATTTTCAATTTCTTGAGAG	1901
Qy	1925	GAAATGCTCCATCATCTTCTTAAAGAGAAATGAGGAGATATTTTATTACNATAACCA	1983

Db 1902 GAAATGCAACATCATCTCTTAAAGAGAAATAGAGAGATTTTAAATTACATAACCA 1961  
Qy 1984 TTTAAACCCGATATTTCAATATGGAAGAAAAAATAAAAA 2030  
Db 1962 TTTAAAAA-CCGTATATATCAATATGAAAGAGAAAGAGAGAAACA 2007

RESULT 11  
US-09-433-826B-468  
; Sequence 468, Application US/09433826B  
; Patent No. 6579973  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yuqi  
; APPLICANT: Dillon, Devin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND  
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE  
; FILE REFERENCE: 210121.470C4  
; CURRENT APPLICATION NUMBER: US/09/433,826B  
; CURRENT FILING DATE: 1999-11-03  
; NUMBER OF SEQ ID NOS: 474  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 468  
; LENGTH: 2307  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-433-826B-468

Query Match 76.8%; Score 1558.8; DB 4; Length 2307;  
Best Local Similarity 89.5%; Pred. No. 0;  
Matches 1815; Conservative 0; Mismatches 23; Indels 189; Gaps 6;

Qy 5 TGCCTTAAAGATGGTCTTCTCAAGGCTAACTGGGAATGAAAGCTTTCTATTCCAACTAA 64  
Db 169 TCCCTGTTAAAGATGGTCTTCTGAAGCTAACTGGGAATGAAAGCTTTCTATTCCAACTAA 228  
Qy 65 AGCCTGAAGATGATGACATGCAAACTTTCAAGAGAGAGGCTCCGAGAGAGCCATCTGC 124  
Db 229 AGCCTTAGAATGATGACATGCAAACTTTCAAGAGAGAGGCTCCGAGAGAGCCATCTGC 268  
Qy 125 CTTGAGGCTGCTGATGAAATGCAAAAGCTGTGTTCCAAATAAAGCTTGGAAATGGAAGAA 184  
Db 289 CTTGAGGCTGCTGATGAAATGCAAAAGCTGTGTTCCAAATAAAGCTTGGAAATGGAAGAA 348  
Qy 185 TGACAAACATGAGAGAGATGATGATCTCCATCAGAAATCCAAACAAAGGACTATGA 244  
Db 349 TGACAAACATGAGAGAGATGATGATCTCCATCAGAAATCCAAACAAAGGACTATGA 408  
Qy 245 AGAAGATTTCTGGGATTTCTGAGAGTCTCTGTGAGACTGTTTTCAGAGAGGATGTTGTTT 304  
Db 409 AGAAGATTTCTGGGATTTCTGAGAGTCTCTGTGAGACTGTTTTCAGAGAGGATGTTGTTT 468  
Qy 305 ACCCAAGGCTACACATCAAAAGAAATAGATAAAATTAATGGAATTTAGAGAGTCTCC 364  
Db 469 ACCCAAGGCTACACATCAAAAGAAATAGATAAAATTAATGGAATTTAGAGAGTCTCC 528  
Qy 365 TGATAATGATGTTTCTGAGGCTCCCTGAGAGTGAAGTTTCTATTCCAACTAAAGC 424  
Db 529 TGATAATGATGTTTCTGAGAGTCTCCCTGAGAGTGAAGTTTCTATTCCAACTAAAGC 588  
Qy 425 CTTAGAATGATGACATGCAAACTTTCAAGAGAGAGGCTCCGAGAGAGCCATCTGCCTT 484  
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Qy 485 CGAGCTGCCATGAAATGCAAAAGCTGTGTTCCAAATAAAGCTTGGAAATGGAAGATGA 544  
Db 649 CGAGCTGCCATGAAATGCAAAAGCTGTGTTCCAAATAAAGCTTGGAAATGGAAGATGA 708  
Qy 545 ACAACATGAGAGAGATGATGATCTCCCTTCAAGATCAAAACAAAGAGAGGTTGAAGA 604

Db 709 ACAAACATTGAGAGCAGATCAGATGTTCCCTTCAGAATCAAAACAAAGAACGTTGAAGA 768  
Qy 605 AATATCTTGGGATCTGAGAGTCTCCGAGAGACTGTTTTCAGAGAGGATGTTGTTGATCC 664  
Db 769 AATATCTTGGGATCTGAGAGTCTCCGAGAGACTGTTTTCAGAGAGGATGTTGTTGATCC 828  
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Db 829 CAAGGCTACACATCAAAAGAAATGATGATAAATTAAGTGGAAAAATTTAGAGATTTCAACTAG 888  
Qy 725 CCTATCAAAATCTTGGATACAGTTCTTCTGTAAGAGCAAGGAGACTTCAAAAGA 784  
Db 889 CCTATCAAAATCTTGGATACAGTTCTTCTGTAAGAGCAAGGAGACTTCAAAAGA 948  
Qy 785 TCACCTGTGAACAACTGACAGGAAAAATGGAACAAATGAAAAAGAGTTTCTGTACTGAA 844  
Db 949 TCACCTGTGAACAACTGACAGGAAAAATGGAACAAATGAAAAAGAGTTTCTGTACTGAA 1008  
Qy 845 AAGAAATCTGACAGAGCAAAAGAAATTAATCAAGTTAGAGAACCAAAAGTTAAATG 904  
Db 1009 AAGAAATCTGACAGAGCAAAAGAAATTAATCAAGTTAGAGAACCAAAAGTTAAATG 1068  
Qy 905 GGAACAAGAGCTCTGAGTGTGAGATTGACTTTAAACCAAGAGAGAGAGAGAGAA 964  
Db 1069 GGAACAAGAGCTCTGAGTGTGAGATTGACTTTAAACCAAGAGAGAGAGAGAGAA 1090  
Qy 965 TGCCGATATATTAATGAAAAATTTAGGAAGAATTAGGAAGAATCGAAGAGAGCATAG 1024  
Db 1091 ----- 1090  
Qy 1025 GAAAGATTAGAGTGAAACAACTTTGAACAGGCTCTCAGAAATACAAATATAGAAAT 1084  
Db 1091 ----- 1090  
Qy 1085 GAAGAGTGTAGAAAGTAATTTGAATCAGGTTTCTCACACTCATGAAATGAAAAATATCT 1144  
Db 1091 -----AGTTTCTCACACTCATGAAATGAAAAATATCT 1124  
Qy 1145 CTTACATGAAATTCGATGTTGAAAAAGAAATGCCATGCTAAACCTGGAATAGCCAC 1204  
Db 1125 CTTACATGAAATTCGATGTTGAAAAAGAAATGCCATGCTAAACCTGGAATAGCCAC 1184  
Qy 1205 ACTGAAACCAATACAGGAAAAAGAAAAATAAATACCTTTGAGGACATTAAGATTTTAAA 1264  
Db 1185 ACTGAAACCAATACAGGAAAAAGAAAAATAAATACCTTTGAGGACATTAAGATTTTAAA 1244  
Qy 1265 AGAAAGATGCTGAACTCAGATGACCTTAACCTGAAAGAGGAAATCATTAACCTTAAAG 1324  
Db 1245 AGAAAGATGCTGAACTCAGATGACCTTAACCTGAAAGAGGAAATCATTAACCTTAAAG 1304  
Qy 1325 GGCATCTCAATATAGTGGGCTTAAAGTTCTGATAGCTGAGAACCAATGCTCACCTTC 1384  
Db 1305 GGCATCTCAATATAGTGGGCTTAAAGTTCTGATAGCTGAGAACCAATGCTCACCTTC 1364  
Qy 1385 TAAATGAAAGAAAAAAGAAATTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1444  
Db 1365 TAAATGAAAGAAAAAAGAAATTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1424  
Qy 1445 TAGACTGGCTTCTGCTGTACAGAGCATGATCAAAATTTGTGACATCAAGAAAAAGTCAAGA 1504  
Db 1425 TAGACTGGCTTCTGCTGTACAGAGCATGATCAAAATTTGTGACATCAAGAAAAAGTCAAGA 1484  
Qy 1505 ACCTGTTTCCCATTTGAGGAGATGCTGTTTGAAGAAAAAATGAATGTTGATGAG 1564  
Db 1485 ACCTGTTTCCCATTTGAGGAGATGCTGTTTGAAGAAAAAATGAATGTTGATGAG 1544  
Qy 1565 TAGTACCGATATTAACAAATGAGGTTCTCCATCAACCACTTTCTGAAGCTCAAGAGAAAT 1624  
Db 1545 TAGTA-CGATATATACATGAGGTTCTCCATCAACCACTTTCTGAAGCTCAAGAGAAAT 1603  
Qy 1625 CCNAAAGCCTAAAAATTAATCTCAATTTAGAGGAGATGCTCTAAGAGAAAAATACATTGG 1684  
Db 1604 CCAAAAGCCTAAAAATTAATCTCAATTTAGAGGAGATGCTCTAAGAGAAAAATACATTGG 1663

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QY 1685 TTTGAGAAATGTCACAAAGAGACCAACGCTGAAACACAGTGTCAATGAGGAGCTGAA 1744
DB 1664 TTTTCA-GAAGCATGACAAAGAGACCAACGCTGAAACACAGTGTCAATGAGGAGCTGAA 1722
QY 1745 CACATGTTTCAAAAGCAAGAGATGATGAAACAAACACACAGTGTCAATGAGGAGCTGAA 1804
DB 1723 CACATGTTTCAAAAGCAAGAGATGATGAAACAAACACACAGTGTCAATGAGGAGCTGAA 1782
QY 1805 GATCAGAAATTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1864
DB 1783 GATCAGAAATTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1842
QY 1865 GCACATAAGGAGAGCTGACAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1924
DB 1843 GCACATAA-GAAGAGCTGACAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1901
QY 1925 GAAATATC-NCATCATCTTCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1983
DB 1902 GAAATATC-NCATCATCTTCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1961
QY 1984 TTTTAAAAACCCCTATATTTTCAATATGATGATGATGATGATGATGATGATGATGATGAT 2030
DB 1962 TTTTAAAAACCCCTATATCAATATGATGATGATGATGATGATGATGATGATGATGAT 2007

RESULT 12
US-09-604-287A-468
; Sequence 468, Application US/09604287A
; Patent No. 8586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yudi
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 468
; LENGTH: 2307
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-604-287A-468

Query Match 76.8%; Score 1558.8; DB 4; Length 2307;
Best Local Similarity 89.5%; Pred. No. 0;
Matches 1815; Conservative 0; Mismatches 23; Indels 189; Gaps 6;

QY 5 TCCGCTTAAAGATGGTCTTCTGAGGCTAACTGCGGAATGAAAGTTTCTATTCCAACTAA 64
DB 169 TCCTGTTAAAGATGGTCTTCTGAGGCTAACTGCGGAATGAAAGTTTCTATTCCAACTAA 228
QY 65 AGCCTTAGAATGATGACATGCAAACTTTCAAGAGAGAGCTCCCGAGAGAGCTATGTC 124
DB 229 AGCCTTAGAATGATGACATGCAAACTTTCAAGAGAGAGCTCCCGAGAGAGCTATGTC 288
QY 125 CTTCAGAGCTGCCATTTGAAATGCAAAAGTCTGTTCCAAATGAAAGCTTTGAAATTTGAAGAA 184
DB 289 CTTCAGAGCTGCCATTTGAAATGCAAAAGTCTGTTCCAAATGAAAGCTTTGAAATTTGAAGAA 348
QY 185 TGAACAAACATGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 244
DB 349 TGAACAAACATGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 408
QY 245 AGAAAGTTCTTGGGATTTGAGAGTCTCTGTGAGAGTCTGTTTCAAGAGAGAGTGTGTTT 304
DB 409 AGAAAGTTCTTGGGATTTGAGAGTCTCTGTGAGAGTCTGTTTCAAGAGAGAGTGTGTTT 468

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QY 305 ACCAAGGCTACACATCAAAAGAGAAATAGATAAATAAATGAAATTAAGAGAGTCTCC 364
DB 469 ACCAAGGCTACACATCAAAAGAGAAATAGATAAATAAATGAAATTAAGAGAGTCTCC 528
QY 365 TGATAATGATGGTTTCTGAGGCTCCCTGAGAGATGAAAGTTTCTATTCCAACTAAAGC 424
DB 529 TGATAATGATGGTTTCTGAGGCTCCCTGAGAGATGAAAGTTTCTATTCCAACTAAAGC 588
QY 425 CTTAGAAATTCATGAGACATGCAAACTTTCAAAGCAGAGCTCCCGAGAGAGCTATCTCCCTT 484
DB 589 CTTAGAAATTCATGAGACATGCAAACTTTCAAAGCAGAGCTCCCGAGAGAGCTATCTCCCTT 648
QY 485 CGAGCTTCCCATTTGAAATGCAAAAGTCTGTTCCAAATAAAGCTTGGAAATTTGAAGATGA 544
DB 649 CGAGCTTCCCATTTGAAATGCAAAAGTCTGTTCCAAATAAAGCTTGGAAATTTGAAGATGA 708
QY 545 ACAGACATTCAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 604
DB 709 ACAGACATTCAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 768
QY 505 AAATTTCTTGGGATTTCTGAGAGTCTCCGTGAGAGTCTTTCACAGAGAGTGTGTGTATCC 664
DB 769 AAATTTCTTGGGATTTCTGAGAGTCTCCGTGAGAGTCTTTCACAGAGAGTGTGTGTATCC 828
QY 565 CAAGCTTACACATCAAAAGAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 724
DB 829 CAAGCTTACACATCAAAAGAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 888
QY 725 CCTATCAAAATCTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 784
DB 889 CCTATCAAAATCTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 948
QY 785 TCATCTGTAACAGCTTCAGAGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 844
DB 949 TCATCTGTAACAGCTTCAGAGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 1008
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DB 1009 AAAGAACTGTGAGAGCAAAAGAGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATG 1068
QY 905 GGAACAAAGAGCTCTGAGAGTGTGAGATTTGATTTTAAACCAAGAGAGAGAGAGAGAGAGAG 964
DB 1069 GGAACAAAGAGCTCTGAGAGTGTG----- 1090
QY 965 TGCCGATATATTAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 1024
DB 1091 TGCCGATATATTAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATG 1090
QY 1025 GAAAGAGTTAGAGTGAAACAAACAACTTGAAACAGGCTCTCAGAAATCAAGATATGAAAT 1084
DB 1091 GAAAGAGTTAGAGTGAAACAAACAACTTGAAACAGGCTCTCAGAAATCAAGATATGAAAT 1090
QY 1085 GAAGAGTGTAGAAAGTAAATTTGAATCAGGTTTCTCAGACTCATGAAATGAAATTTATCT 1144
DB 1091 GAAGAGTGTAGAAAGTAAATTTGAATCAGGTTTCTCAGACTCATGAAATGAAATTTATCT 1124
QY 1145 CTTACATGAAATTTGATGTTGAAAGAGGAAATTTGCCATGCTAAATCTGAAATAGCCAC 1204
DB 1125 CTTACATGAAATTTGATGTTGAAAGAGGAAATTTGCCATGCTAAATCTGAAATAGCCAC 1184
QY 1205 ACTGAAACACCAATACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1264
DB 1185 ACTGAAACACCAATACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1244
QY 1265 AGAAAGAGAGTGTGAAATCTCAGATGAGAGCTTAAAGCTTAAAGAGAGAGAGAGAGAGAGAG 1324
DB 1245 AGAAAGAGAGTGTGAAATCTCAGATGAGAGCTTAAAGCTTAAAGAGAGAGAGAGAGAGAGAG 1304
QY 1325 GGCATCTCAATATAGTGGCAGCTTTAAAGTTCTGATAGTGTGAGAGAGAGAGAGAGAGAGAG 1384
DB 1305 GGCATCTCAATATAGTGGCAGCTTTAAAGTTCTGATAGTGTGAGAGAGAGAGAGAGAGAGAG 1364

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QY 1385 TAAATTGAAGGAAACAAAGCAAGAAATCTAGAGGCGAAATGGAATCACACCATCC 1444  
 Db 1365 TAAATTGAAGGAAACAAAGCAAGAAATCTAGAGGCGAAATGGAATCACACCATCC 1424  
 QY 1445 TAGACTGCTCTCTGCTGACAGACCATGATCAAAATTTGTGACATCAAGAAAGTCAAGA 1504  
 Db 1425 TAGACTGCTCTCTGCTGACAGACCATGATCAAAATTTGTGACATCAAGAAAGTCAAGA 1484  
 QY 1505 ACCTGCTTTCCACATTTGCGAGAGATGCTTGTTCGAAAGAAATGAATGTTGATGTGAG 1564  
 Db 1485 ACCTGCTTTCCACATTTGCGAGAGATGCTTGTTCGAAAGAAATGAATGTTGATGTGAG 1544  
 QY 1565 TAGTACCGATATATACAGATGCTGCTCCATCAACACATTTCTGAAGCTCAAGAGGAAT 1624  
 Db 1545 TAGTA - CGATATATACAGATGCTGCTCCATCAACACATTTCTGAAGCTCAAGAGGAAT 1603  
 QY 1625 CCNAGGCTTAAATTAATCTCAATATGAGAGATGCTCTTAAGAGAAATACATGG 1684  
 Db 1604 CCNAGGCTTAAATTAATCTCAATATGAGAGATGCTCTTAAGAGAAATACATGG 1663  
 QY 1685 TTTCCAGGACATGCAAGAGACCAAGCTGCAACACAGTCTCAAAATGAAGAGCTGAA 1744  
 Db 1664 TTTCA - GAACATGCAAGAGACCAAGCTGCAACACAGTCTCAAAATGAAGAGCTGAA 1722  
 QY 1745 CACATGTTTCAAAAGCAAGATNATGTAACAAACACACTGANCAGCAGGAGTCTCTA 1804  
 Db 1723 CACATGTTTCAAAAGCAAGATNATGTAACAAACACACTGANCAGCAGGAGTCTCTA 1782  
 QY 1805 GATCAGAAATTTTCAACTCAAGCAAGAAATATGCTGGCTTCAACAGCAATAGTTCAT 1864  
 Db 1783 GATCAGAAATTTTCAACTCAAGCAAGAAATATGCTGGCTTCAACAGCAATAGTTCAT 1842  
 QY 1865 GCACATAANGAAGCTGCAACAAAGCAAGATAAATGATNTTCAATTTCTTTGAGAG 1924  
 Db 1843 GCACATA - GAAGCTGCAACAAAGCAAGATAAATGATNTTCAATTTCTTTGAGAG 1901  
 QY 1925 GAAATGC - NCATCTCTTCAAAAGCAAGAAATGAGGAGATATTTNATACNATACCA 1983  
 Db 1902 GAAATGC - NCATCTCTTCAAAAGCAAGAAATGAGGAGATATTTNATACNATACCA 1961  
 QY 1984 TTTTAAAAACCGGTATTTTCAATATGAAAAAANAAAAA 2030  
 Db 1962 TTTTAAAAA - CGGTATATATCAATATGAAAAAGCAAGCAAGCA 2007

RESULT 13  
 US-09-834-759-468  
 ; Sequence 468, Application US/09834759  
 ; Patent No. 6680197  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jiang, Yugu  
 ; APPLICANT: Dillon, Davin C.  
 ; APPLICANT: Mitcham, Jennifer L.  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Harlocker, Susan L.  
 ; APPLICANT: Hepler, William T.  
 ; APPLICANT: Henderson, Robert A.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 ; FILE REFERENCE: 210121.470C9  
 ; CURRENT FILING DATE: 2001-04-13  
 ; NUMBER OF SEQ ID NOS: 547  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 468  
 ; LENGTH: 2307  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-834-759-468

Query Match 76.8%; Score 1558.8; DB 4; Length 2307;  
 Best Local Similarity 89.5%; Pred. No. 0;  
 Matches 1815; Conservative 0; Mismatches 23; Indels 189; Gaps 6;

QY 5 TCCCTTAAAGATGCTCTTCTGAGGCTAACTGCGGAATGAAAGTTCTTATTCACATAA 64  
 Db 169 TCCCTTAAAGATGCTCTTCTGAGGCTAACTGCGGAATGAAAGTTCTTATTCACATAA 228  
 QY 65 AGCCTTAGAATTTGATGACATGCAAACTTTCAAAGCAGAGCTCCCGAAGAGCCATCTGC 124  
 Db 229 AGCCTTAGAATTTGATGACATGCAAACTTTCAAAGCAGAGCTCCCGAAGAGCCATCTGC 288  
 QY 125 CTTGAGCTGCTGATTTGAATGCAAAAGCTCTGTTCCAAATAAAGCTTTGGAATTCAGAA 184  
 Db 289 CTTGAGCTGCTGATTTGAATGCAAAAGCTCTGTTCCAAATAAAGCTTTGGAATTCAGAA 348  
 QY 185 TGAACAAACATTTGAGAGCAGATGAGATCTCCCATCAGAATCCAAACAAAGAGCTATGA 244  
 Db 349 TGAACAAACATTTGAGAGCAGATGAGATCTCCCATCAGAATCCAAACAAAGAGCTATGA 408  
 QY 245 AGAAGCTTTCTGGGATTTCTGAGAGTCTCTGAGAGCTCTTTTCAAGAGAGTCTGCTTT 304  
 Db 409 AGAAGCTTTCTGGGATTTCTGAGAGTCTCTGAGAGCTCTTTTCAAGAGAGTCTGCTTT 468  
 QY 305 ACCCAAGGCTACACATCAAAAGAAATAGATAAATAAATGGAATAATAGAGAGTCTCC 364  
 Db 469 ACCCAAGGCTACACATCAAAAGAAATAGATAAATAAATGGAATAATAGAGAGTCTCC 528  
 QY 365 TGATAATGATGCTTTCTGAGGCTCCCTGCGAGATGAAAGTTTCTATTCACAACTAAGC 424  
 Db 529 TGATAATGATGCTTTCTGAGGCTCCCTGCGAGATGAAAGTTTCTATTCACAACTAAGC 588  
 QY 425 CTTTAGAATTTGAGAGCTCAAACTTTCAAAGCAGAGCTCCCGAAGAGCCATCTGCTTT 484  
 Db 589 CTTTAGAATTTGAGAGCTCAAACTTTCAAAGCAGAGCTCCCGAAGAGCCATCTGCTTT 648  
 QY 485 CGAGCTGCTGATTTGAAATGCAAAAGCTCTTTCAAATAAAGCTTTGGAATTCAGAAATGA 544  
 Db 649 CGAGCTGCTGATTTGAAATGCAAAAGCTCTTTCAAATAAAGCTTTGGAATTCAGAAATGA 708  
 QY 545 ACAAACATTTGAGAGCAGATGAGTCTCCCTTCAAGATCAAAACAAAGAGCTTCAAGA 604  
 Db 709 ACAAACATTTGAGAGCAGATGAGTCTCCCTTCAAGATCAAAACAAAGAGCTTCAAGA 768  
 QY 605 AAATTTCTGGGATTTCTGAGAGTCTCCGTCAGAGCTGTTTCAAGAGAGTGTGTGTAC 664  
 Db 769 AAATTTCTGGGATTTCTGAGAGTCTCCGTCAGAGCTGTTTCAAGAGAGTGTGTGTAC 828  
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 Db 829 CAAGGCTACACATCAAAAGAAATGGAATAAATAGTGAATAATAGAGAGTCTCAACTAG 888  
 QY 725 CCTATCAAAATCTTGGATACAGTTCATTTCTTGTGAAAGCAGCAAGGAACTTCAAAA 784  
 Db 889 CCTATCAAAATCTTGGATACAGTTCATTTCTTGTGAAAGCAGCAAGGAACTTCAAAA 948  
 QY 785 TCATCTGTAACAAAGTACAGGAAAAATGGAACAAATGAAAGAGCTTTTGTGTACTGAA 844  
 Db 949 TCATCTGTAACAAAGTACAGGAAAAATGGAACAAATGAAAGAGCTTTTGTGTACTGAA 1008  
 QY 845 AAAGAACTGTCAGAGCAAAAGAAATAAATCAAGTTAGAGAACCAAAAGTTAAATG 904  
 Db 1009 AAAGAACTGTCAGAGCAAAAGAAATAAATCAAGTTAGAGAACCAAAAGTTAAATG 1068  
 QY 905 GGAACACAGAGCTCTGAGTGTGAGATGACTTTTAAACCAAGAGAGAGAGAGAGAA 964  
 Db 1069 GGAACACAGAGCTCTGAGTGTGAGATGACTTTTAAACCAAGAGAGAGAGAGAGAA 1090  
 QY 965 TGCCGATATTAATTAAGAAAAATTTAGGAGAAATTTAGGAGAAATCGAAGAGCAGCATAG 1024  
 Db 1091 TGCCGATATTAATTAAGAAAAATTTAGGAGAAATTTAGGAGAAATCGAAGAGCAGCATAG 1090  
 QY 1025 GAAAGAGTTAGAAAGTGAACCAACACTTGAAAGAGCTCTCAGAAATACAGATATAGAA 1084  
 Db 1091 GAAAGAGTTAGAAAGTGAACCAACACTTGAAAGAGCTCTCAGAAATACAGATATAGAA 1090

RESULT 14	
US 05-620-405B-467	
; Sequence 467, Application US/09620405B	
; Patent No. 6528054	
; GENERAL INFORMATION:	
; APPLICANT: Jiaogang Yudiu	
; APPLICANT: Dillon, Gavin C.	
; APPLICANT: Mirzaban, Jennifer I.	
701	CCAGGCTACACATCAAAAAAGAAATGATAAATAAGTGGAAAAATTAGAAGATTCACACTAG 760
702	
725	CCATCAAAAAATCTTGGATACAGTTCATTTCTTGTGAAGAGCAAGGGAACCTTCAAAAAAGA 784
761	CCATCAAAAAATCTTGGATACAGTTCATTTCTTGTGAAGAGCAAGGGAACCTTCAAAAAAGA 820
785	TCACGTGGAACAACGTCACAGGAAAAATGGAACAAATGAAAAAGAGATTTTGTGTACTGAA 844



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Db      821 TCACGTGACCAACGTCACAGAAATGGAAACAATGAAAGAGAGTTTGTGTACTGAA 880
Qy      845 AAAGAACTGTGACAGCAAAAGAAATGAAATCAAGTTAGAGAAACAAAGTTAAATG 904
Db      881 AAAGAACTGTGACAGCAAAAGAAATGAAATCAAGTTAGAGAAACAAAGTTAAATG 940
Qy      905 GGAACAGAGCTCTGAGTGTGAGATTGACTTTAAACCAAGAGAGAGAGAGAGAA 964
Db      941 GGAACAGAGCTCTGAGTGTGAGATTGACTTTAAACCAAGAGAGAGAGAGAGAA 1000
Qy      965 TGCCGATATATTAATGAAAGAAATAGGGAAGAAATAGGGAAGAAATCGAAGAGCAGATAG 1024
Db      1001 TGCCGATATATTAATGAAAGAAATAGGGAAGAAATAGGGAAGAAATCGAAGAGCAGATAG 1060
Qy      1025 GAAGAGTTAGAGTGAACCAACCACTGACAGGCTCTCAGATCAAGATAGAAAT 1084
Db      1061 GAAGAGTTAGAGTGAACCAACCACTGACAGGCTCTCAGATCAAGATAGAAAT 1120
Qy      1085 GAAGAGTTAGAGTGAACCAACCACTGACAGGCTCTCAGATCAAGATAGAAAT 1144
Db      1121 GAAGAGTTAGAGTGAACCAACCACTGACAGGCTCTCAGATCAAGATAGAAAT 1180
Qy      1145 CTTACATGAAATTTGATGTTGAAAGAAATGCAATGCTTAAACTGGAATAGCCAC 1204
Db      1181 CTTACATGAAATTTGATGTTGAAAGAAATGCAATGCTTAAACTGGAATAGCCAC 1240
Qy      1205 ACTGAACACCAATACAGAGAAAGAAATGCAATGCTTAAACTGGAATAGCCAC 1264
Db      1241 ACTGAACACCAATACAGAGAAAGAAATGCAATGCTTAAACTGGAATAGCCAC 1300
Qy      1265 AGAAAGATGCTGAACTTCAGATGACCC 1293
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RESULT 15

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US-09-433-826B-467
; Sequence 467, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqi
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433.826B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 467
; LENGTH: 1337
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-433-826B-467

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Query Match 63.2%; Score 1282.6; DB 4; Length 1337;
Best Local Similarity 99.7%; Pred. No. 9.5e-310;
Matches 1285; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      5 TGCCGTTAAAGATGCTCTTCTGAGCGTAACTGCGGAATGAAAGTTTCTATTCCCACTAA 64
Db      41 TCCTGTTAAAGATGCTCTTCTGAGGCTAACTGCGGAATGAAAGTTTCTATTCCCACTAA 100
Qy      65 AGCCTTAGAATGATGGAACATGCAAACTTTCAAGCAGAGCTCCGAGAGAGCCATCTGC 124
Db      101 AGCCTTAGAATGATGGAACATGCAAACTTTCAAGCAGAGCTCCGAGAGAGCCATCTGC 160
Qy      125 CTTGAGAGCTGCAATGAAATGCAAAAGTCTGTTCCCAATAAAGCTTTGGAATGGAAGAA 184

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Db      161 CTTGAGAGCTGCCATTGAATGCAAAAGTCTGTTCCAAATAGAGCCTTGGAAATGAAGAA 220
Qy      185 TGAACAAACATTTGAGAGCAGATGAGATCTCCCATCAGAAATCCAAACCAAGAGGACTATGA 244
Db      221 TGAACAAACATTTGAGAGCAGATGAGATCTCCCATCAGAAATCCAAACCAAGAGGACTATGA 280
Qy      245 AGAAAGTTCTTTGGGATCTGAGAGTCTCTGTGAGAGTCTCTGTGAGAGTCTCTGTGAGT 304
Db      281 AGAAAGTTCTTTGGGATCTGAGAGTCTCTGTGAGAGTCTCTGTGAGAGTCTCTGTGAGT 340
Qy      305 ACCCAAGGCTACATCAAAAGAAATAGATAAAATAAATGGAATAATAGAGAGTCTCC 364
Db      341 ACCCAAGGCTCGCATCAAAAGAAATAGATAAAATAAATGGAATAATAGAGAGTCTCC 400
Qy      365 TGATAATGATGTTTCTGAAAGGCTCCCTGAGAGTGAAGTCTTCTATTCCAACTAAAGC 424
Db      401 TGATAATGATGTTTCTGAAAGGCTCCCTGAGAGTGAAGTCTTCTATTCCAACTAAAGC 460
Qy      425 CTTAGAAATGATGGAATGCAAACTTTTCAAGCAGAGCTCCCGAGAGAGCCATCTGCTT 484
Db      461 CTTAGAAATGATGGAATGCAAACTTTTCAAGCAGAGCTCCCGAGAGAGCCATCTGCTT 520
Qy      485 CGAGCTCCCATGGAATGCAAAAGTCTGTTCCAAATAGAGCCTTGGAAATGGAAGATGA 544
Db      521 CGAGCTCCCATGGAATGCAAAAGTCTGTTCCAAATAGAGCCTTGGAAATGGAAGATGA 580
Qy      545 ACAAACATTTGAGAGCAGATCAGATGTTCCCTTCAGAAATCAAAACAAAGAGGTTGAAGA 604
Db      581 ACAAACATTTGAGAGCAGATCAGATGTTCCCTTCAGAAATCAAAACAAAGAGGTTGAAGA 640
Qy      605 AAATTTCTTTGGGATCTGAGAGTCTCCGAGAGTCTGTTTTCAGAGAGGATGTTGTGTACC 664
Db      641 AAATTTCTTTGGGATCTGAGAGTCTCCGAGAGTCTGTTTTCAGAGAGGATGTTGTGTACC 700
Qy      665 CAAGGCTACATCAATCAAAAGAAATGGAATAAATAGTGGAAATTTAGAGATTTCAACTAG 724
Db      701 CAAGGCTACATCAATCAAAAGAAATGGAATAAATAGTGGAAATTTAGAGATTTCAACTAG 760
Qy      725 CCTATCAAAATCTTGGATCAGATCTATCTGTTGAAAGCAAGGGAACCTCAAAAGAA 784
Db      761 CCTATCAAAATCTTGGATCAGATCTATCTGTTGAAAGCAAGGGAACCTCAAAAGAA 820
Qy      785 TCACCTGTGAACCAACGTACAGGAAATGGAACAAATGAAAGAGGTTTCTGTACTGAA 844
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Qy      845 AAAGAACTGTGAGAGCAAAAGAAATGAAATCAAGTTAGAGAACCAAAAGTTAAATG 904
Db      881 AAAGAACTGTGAGAGCAAAAGAAATGAAATCAAGTTAGAGAACCAAAAGTTAAATG 940
Qy      905 GGAACAGAGCTCTGAGTGTGAGATTGACTTTAAACCAAGAGAGAGAGAGAGAA 964
Db      941 GGAACAGAGCTCTGAGTGTGAGATTGACTTTAAACCAAGAGAGAGAGAGAGAA 1000
Qy      965 TGCCGATATATTAATGAAAGAAATAGGGAAGAAATAGGGAAGAAATCGAAGAGCAGATAG 1024
Db      1001 TGCCGATATATTAATGAAAGAAATAGGGAAGAAATAGGGAAGAAATCGAAGAGCAGATAG 1060
Qy      1025 GAAGAGTTAGAGTGAACCAACCACTTGAAGGCTCTCAGATCAAGATAGAAAT 1084
Db      1061 GAAGAGTTAGAGTGAACCAACCACTTGAAGGCTCTCAGATCAAGATAGAAAT 1120
Qy      1085 GAAGAGTTAGAGTGAACCAACCACTTGAATCAGGTTTCTCAGACTCATGAAATGAAATATCT 1144
Db      1121 GAAGAGTTAGAGTGAACCAACCACTTGAATCAGGTTTCTCAGACTCATGAAATGAAATATCT 1180
Qy      1145 CTTACATGAAATTTGATGTTGAAAGAAATGCAATGCTTAAACTGGAATAGCCAC 1204
Db      1181 CTTACATGAAATTTGATGTTGAAAGAAATGCAATGCTTAAACTGGAATAGCCAC 1240
Qy      1205 ACTGAACACCAATACAGAGAAAGAAATGCAATGCTTAAACTGGAATAGCCAC 1264
Db      1241 ACTGAACACCAATACAGAGAAAGAAATGCAATGCTTAAACTGGAATAGCCAC 1300

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Qy 1265 AGAAGAGATGCTGACTTCAGATGACCC 1293  
Db 1301 AGAAGAGATGCTGACTTCAGATGACCC 1329

Search completed: May 7, 2004, 00:30:18  
Job time : 163 secs



CC gene is a tumour suppressor candidate gene. The cancer associated antigen  
 CC polynucleotides and polypeptides are useful for screening for the  
 CC possible presence of a pathological condition in a subject such as  
 CC cancer. The cancer associated antigen polypeptides are useful for  
 CC producing vaccines  
 XX

SQ Sequence 2030 BP; 827 A; 334 C; 397 G; 460 T; 0 U; 12 Other;

Query Match 99.4%; Score 2018; DB 4; Length 2030;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	1	CTCGTGCCTTAAAGATGCTCTCTGAAAGCTAACTCGGATGAAGTTCTATTCGAA	60
QY	61	CTAAAGCCTTAGAATGATGCAATGCAAACTTCAAAGCAGAGCCTCCGAGAGCCAT	120
DB	61	CTAAAGCCTTAGAATGATGCAATGCAAACTTCAAAGCAGAGCCTCCGAGAGCCAT	120
QY	121	CTGCTTTGAGCGCTGCCATTTGAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAA	180
DB	121	CTGCTTTGAGCGCTGCCATTTGAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAA	180
QY	181	AGATGAACAAACATTCAGAGCAGATGAGATATCCCATCAGATCCAAACAAAGGACT	240
DB	181	AGATGAACAAACATTCAGAGCAGATGAGATATCCCATCAGATCCAAACAAAGGACT	240
QY	241	ATGAAGAAAGTCTCTGGATTTCTGAGAGTCTCTGTGAGAGCTGTTTCAAGAGGATGT	300
DB	241	ATGAAGAAAGTCTCTGGATTTCTGAGAGTCTCTGTGAGAGCTGTTTCAAGAGGATGT	300
QY	301	GTATTACCCAGGCTACACATCAAAAGAAATAGATATAATGAAATTTAGAAGAGT	360
DB	301	GTATTACCCAGGCTACACATCAAAAGAAATAGATATAATGAAATTTAGAAGAGT	360
QY	361	CTCTGTATATGATGCTTTCTGAAGCTCCCTGCAGAAATGAAAGTTTCTATTCGAA	420
DB	361	CTCTGTATATGATGCTTTCTGAAGCTCCCTGCAGAAATGAAAGTTTCTATTCGAA	420
QY	421	AAAGCTTTAGATTTGATGCAATGCAAACTTCAAAGCAGAGCCTCCGAGAGCCATCTG	480
DB	421	AAAGCTTTAGATTTGATGCAATGCAAACTTCAAAGCAGAGCCTCCGAGAGCCATCTG	480
QY	481	CCTTTCGAGCTGCCATTTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAA	540
DB	481	CCTTTCGAGCTGCCATTTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAA	540
QY	541	ATGAACAAACATTCAGAGCAGATCAGATGTTCCCTTCAGATCAAAACAAAGAGTTG	600
DB	541	ATGAACAAACATTCAGAGCAGATCAGATGTTCCCTTCAGATCAAAACAAAGAGTTG	600
QY	601	AAGAAATTTCTGGATTTCTGAGAGTCTCCGTGAGAGCTGTTTCAAGAGGATGTGTG	660
DB	601	AAGAAATTTCTGGATTTCTGAGAGTCTCCGTGAGAGCTGTTTCAAGAGGATGTGTG	660
QY	661	TACCAAGGCTACATCAAAAGAAATGGAATTAAGTGGAAATTTAGAATTCAA	720
DB	661	TACCAAGGCTACATCAAAAGAAATGGAATTAAGTGGAAATTTAGAATTCAA	720
QY	721	CTAGGCTATCAAAATCTTGGATACAGTTCATTTCTTGTGAAAGCAAGGAACTTCAA	780
DB	721	CTAGGCTATCAAAATCTTGGATACAGTTCATTTCTTGTGAAAGCAAGGAACTTCAA	780
QY	781	AAGATCACTGTGAACAAAGTACAGAAATTTGAACAAATGAAGTTTGTGTAC	840
DB	781	AAGATCACTGTGTGAACAAAGTACAGAAATTTGAACAAATGAAGTTTGTGTAC	840
QY	841	TGAAAAAGAACTGTTCAGAGCAGAAAGAAATTAAGTTCAGAGTTCAGAGTTCAG	900
DB	841	TGAAAAAGAACTGTTCAGAGCAGAAAGAAATTAAGTTCAGAGTTCAGAGTTCAG	900
QY	901	AATGGGAAACAGAGCTCTGAGTGTGAGATTGACTTTTAAACCAAGAGAGAGAGAA	960

DB	901	AATGGGAAACAGAGCTCTGAGTGTGAGATTGACTTTTAAACCAAGAGAGAGAGAA	960
QY	961	GAAATGCCGATATATTAAATGAAAAAATTAGGAGAGAAATTAGGAGAGACAC	1020
DB	961	GAAATGCCGATATATTAAATGAAAAAATTAGGAGAGAAATTAGGAGAGACAC	1020
QY	1021	ATAGGAAAGAGTTAGAAAGTGAACCAACACTTGAACAGGCTCTCAGAAATACAGATATAG	1080
DB	1021	ATAGGAAAGAGTTAGAAAGTGAACCAACACTTGAACAGGCTCTCAGAAATACAGATATAG	1080
QY	1081	AATTGAAGAGTTAGAAAGTGAATTTGAATCAGGTTTCTCACACTCATGAAATGAAAAAT	1140
DB	1081	AATTGAAGAGTTAGAAAGTGAATTTGAATCAGGTTTCTCACACTCATGAAATGAAAAAT	1140
QY	1141	ATCTTTACATGAAATTTGCATGTTGAAAGAGAAATTTGCCATGCTTAAACTCGAAATAG	1200
DB	1141	ATCTTTACATGAAATTTGCATGTTGAAAGAGAAATTTGCCATGCTTAAACTCGAAATAG	1200
QY	1201	CCACACTGAAACACCAATACAGGAAAGGAAATTAATTAATTAATTAATTAATTAATTAAT	1260
DB	1201	CCACACTGAAACACCAATACAGGAAAGGAAATTAATTAATTAATTAATTAATTAATTAAT	1260
QY	1261	TAAAGAAAGAAATGCTGAACTTCAGATGACCTTAAACTCGAAAGAGGAAATTAATTAAT	1320
DB	1261	TAAAGAAAGAAATGCTGAACTTCAGATGACCTTAAACTCGAAAGAGGAAATTAATTAAT	1320
QY	1321	AAAGGCTATCTCAATATAGTGGGAGCTTAAAGTTCTGATAGCTGAGAAACAAATGCTCA	1380
DB	1321	AAAGGCTATCTCAATATAGTGGGAGCTTAAAGTTCTGATAGCTGAGAAACAAATGCTCA	1380
QY	1381	CTTCTTAAATTCAGGAAAGAAACAAAGAAATTAATTAATTAATTAATTAATTAATTAAT	1440
DB	1381	CTTCTTAAATTCAGGAAAGAAACAAAGAAATTAATTAATTAATTAATTAATTAATTAAT	1440
QY	1441	ATCTTAGACTGGCTTCTGCTGTACAAGCAGATGATCAATTTGTGACATCAAGAAAAAGTC	1500
DB	1441	ATCTTAGACTGGCTTCTGCTGTACAAGCAGATGATCAATTTGTGACATCAAGAAAAAGTC	1500
QY	1501	AAGAACTGCTTCCACATTCAGGAGATGCTTTGTCGAAAGAAATTAATTAATTAATTAAT	1560
DB	1501	AAGAACTGCTTCCACATTCAGGAGATGCTTTGTCGAAAGAAATTAATTAATTAATTAAT	1560
QY	1561	TGAGTAGTACCGATATATAAATGAGTGTCTCCATCAACCACTTCTGAGCTCAAGG	1620
DB	1561	TGAGTAGTACCGATATATAAATGAGTGTCTCCATCAACCACTTCTGAGCTCAAGG	1620
QY	1621	AAATCCANAAGCCTTAAATTAATTCATTAATTCAGGAGATGCTTAAAGGAAATTAATTAAT	1680
DB	1621	AAATCCANAAGCCTTAAATTAATTCATTAATTCAGGAGATGCTTAAAGGAAATTAATTAAT	1680
QY	1681	TTGGTTTCAGGAAACATGCAAGAGAGACCAAGTGAACACAGTGTCAATTAAGGAGGAGC	1740
DB	1681	TTGGTTTCAGGAAACATGCAAGAGAGACCAAGTGAACACAGTGTCAATTAAGGAGGAGC	1740
QY	1741	TGAACACATGTTTCAAAACGAAAGATGATGTAACAAACACACTGAGCAGGAGGAGTC	1800
DB	1741	TGAACACATGTTTCAAAACGAAAGATGATGTAACAAACACACTGAGCAGGAGGAGTC	1800
QY	1801	TTAGATCAGAAATTTATTTCACTCAAGCAAAATATGCTGCTTCAACAGCAATTAATTAAT	1860
DB	1801	TTAGATCAGAAATTTATTTCACTCAAGCAAAATATGCTGCTTCAACAGCAATTAATTAAT	1860
QY	1861	TCATGCAATTAAGAAAGCTGCAACAAAGCAAGATTAATTAATTAATTAATTAATTAATTAAT	1920
DB	1861	TCATGCAATTAAGAAAGCTGCAACAAAGCAAGATTAATTAATTAATTAATTAATTAATTAAT	1920
QY	1921	AGAGGAAATGNCATCATCTTCTTAAAGAGAAATTAAGGAGATATTATTAATTAATTAAT	1980
DB	1921	AGAGGAAATGNCATCATCTTCTTAAAGAGAAATTAAGGAGATATTATTAATTAATTAAT	1980
QY	1981	CAATTTAAAAAACCCTATATTTTCAATATGAAAAAANAAAAAANAAAAAANAAAAAAN	2030

Db	1981	CCATTTAAAAACCCGTATATTTCATATGGAAGAAAAA	2030
ABT33272			
RESULT 2			
ID	ABT33272	standard; DNA; 4047 BP.	
XX	AC	ABT33272;	
XX	AC	XX	
XX	DT	15-MAY-2003 (first entry)	
XX	DE	Human tumour-related DNA sequence - SEQ ID No 566.	
XX	XX	Human; ds; vaccine; gene therapy; T cell stimulation; T cell expansion;	
KW	KW	tumour; breast cancer; cancer; immune response stimulation.	
XX	OS	Homo sapiens.	
XX	XX	WO200283956-A1.	
PN	XX	24-OCT-2002.	
PD	XX	15-APR-2002; 2002WO-US012378.	
XX	XX	13-APR-2001; 2001US-00834759.	
PR	PR	07-DEC-2001; 2001US-00007805.	
XX	PR	13-FEB-2002; 2002US-00076622.	
XX	XX	(CORI-) CORIXA CORP.	
PA	XX	Houghton RL, Sleath PR, Persing DH, Jiang Y, Dillon DC;	
PI	PI	Mitcham JL, Xu J, Harlocker SL, Hepler WT, Henderson RA, Fanger GR;	
PI	PI	Vedvick TS, McNeill PD, Durham M;	
XX	XX	WPI; 2003-103376/09.	
DR	XX	New polypeptide and polynucleotide useful for stimulating and/or	
XX	PT	expanding T cells specific for a tumor protein and treating breast	
PT	PT	cancer.	
XX	XX	Example 12; Page 346-347; 375pp; English.	
PS	XX	The invention comprises a method of stimulating and/or expanding T cells	
CC	CC	specific for a tumor protein. The invention further comprises human	
CC	CC	nucleic acids and proteins that are associated with tumors (e.g. breast	
CC	CC	cancer). The method and sequences of the invention are useful for	
CC	CC	stimulating and/or expanding T cells specific for a tumor protein,	
CC	CC	detecting the presence of cancer, stimulating an immune response in a	
CC	CC	patient and treating breast cancer. The present DNA sequence represents a	
CC	CC	human tumour-related DNA sequence	
XX	SQ	Sequence 4047 BP; 1563 A; 716 C; 850 G; 918 T; 0 U; 0 Other;	
Query Match		95.6%; Score 1940; DB 7; Length 4047;	
Best Local Similarity		98.7%; Pred. No. 0;	
Matches 2001; Conservative		0; Mismatches (21) Indels 5; Gaps 5;	
QY	5	TGCCCTTAAAGATGGTCTTCTGAAGCGTAACTCGGGAATGAAGTTTCTATTCCAACTAA	64
Db	2016	TCCTGTTAAAGATGGTCTTCTGAAGCGTAACTCGGGAATGAAGTTTCTATTCCAACTAA	2075
QY	65	AGCCTTAGAATGATGGACATGCAAACTTTCAAGCAGAGCGCTCCGAGAGGCCATCTGC	124
Db	2076	AGCCTTAGAATGATGGACATGCAAACTTTCAAGCAGAGCGCTCCGAGAGGCCATCTGC	2135
QY	125	CTTCGAGCGCTGCATTGAAATGCAAAAGTCTGTTCCCAATAAAGCTTTGGAAATTGAAGAA	184
Db	2136	CTTCGAGCGCTGCATTGAAATGCAAAAGTCTGTTCCCAATAAAGCTTTGGAAATTGAAGAA	2195
QY	185	TGAACAAACATTGAGAGCAGATGAGATCTCCCATCAGAAATCCAAACAAAGGACTATGA	244
Db	2196	TGAACAAACATTGAGAGCAGATGAGATCTCCCATCAGAAATCCAAACAAAGGACTATGA	2255

Db 3336 GGCACTCTCAATATAGTGGGAGCTTAAAGTTCTGATAGCTGAGAACACAACTGCTCACITC 3395  
 QY 1385 TAAATTGAAGAAACACAGACAAAGAAATAGTGGGAGAAATGAATACACCAATCC 1444  
 Db 3396 TAAATTGAAGAAACACAGACAAAGAAATAGTGGGAGAAATGAATACACCAATCC 3455  
 QY 1445 TAGACTGGCTTCTGCTGTACAGACCAATGATCAAAATTTGTGACATCAAGAAAAAGTCAAGA 1504  
 Db 3456 TAGACTGGCTTCTGCTGTACAGACCAATGATCAAAATTTGTGACATCAAGAAAAAGTCAAGA 3515  
 QY 1505 ACTGCTTTCCATTCAGAGAGATGCTGTTTGCAGAGAAATGAATTTGATGTGAG 1564  
 Db 3516 ACTGCTTTCCATTCAGAGAGATGCTGTTTGCAGAGAAATGAATTTGATGTGAG 3575  
 QY 1565 TAGTACCGATATATAAATAGAGTGTCTCCATCAACCACTTTCTGAAGCTCAAGAGAAAT 1624  
 Db 3576 TAGTA-CGATATATAAATAGAGTGTCTCCATCAACCACTTTCTGAAGCTCAAGAGAAAT 3634  
 QY 1625 CCNAAAGCCTAAATTAATCTCAATATTCAGAGATGCTTAAAGAGAAATACATTTGG 1684  
 Db 3635 CCNAAAGCCTAAATTAATCTCAATATTCAGAGATGCTTAAAGAGAAATACATTTGG 3694  
 QY 1685 TTTCAAGAAATGACACAAAGAGACCAACGTCGAAACACAGTGTCAAAATGAAGAAAGTGA 1744  
 Db 3695 TTTCA-GAATGACACAAAGAGACCAACGTCGAAACACAGTGTCAAAATGAAGAAAGTGA 3753  
 QY 1745 CACATGNTCAANCGAACAAAGATNATGTGAACAAACACACTGACAGAGAGTGTCTTA 1804  
 Db 3754 CACATGNTCAANCGAACAAAGATNATGTGAACAAACACACTGACAGAGAGTGTCTTA 3813  
 QY 1805 GATCAGAAATTTATTTCAACTACAAAGCAAAATATGTGGCTTCAACAGCAATTAAGTTCA 1864  
 Db 3814 GATCAGAAATTTATTTCAACTACAAAGCAAAATATGTGGCTTCAACAGCAATTAAGTTCA 3873  
 QY 1865 GCACATANGAAGCTGACACAAAGCAAGCAAGATTAACAAATTTGATTTTCTTGAGAG 1924  
 Db 3874 GCACATAA-GAAAGCTGACACAAAGCAAGCAAGATTAACAAATTTGATTTTCTTGAGAG 3932  
 QY 1925 GAAATATC-NCATCATCTTCTTAAAGAGAAAAATGAGAGATATTTNATTACNATAACCA 1983  
 Db 3933 GAAATATCNCATCATCTTCTTAAAGAGAAAAATGAGAGATATTTNATTACNATAACCA 3992  
 QY 1984 TTTAAAAACCCGATATTTCAATATGAAAAAANAANAANAANA 2030  
 Db 3993 TTTAAAAA-CCGATATATCAATATGAAAAAGAGAAAGCAAGA 4038

RESULT 3  
 ID ABT07694 standard; DNA; 4458 BP.  
 AC ABT07694;  
 XX  
 DT 14-NOV-2002 (first entry)  
 XX  
 DE Breast cancer-associated gene sequence 2.  
 XX  
 XX Gene; ds; breast cancer; breast cancer-associated gene sequence;  
 KW drug development; pharmacogenetics; biosensor development.  
 XX  
 OS Unidentified.  
 XX  
 FN WO200259377-R2.  
 XX  
 PD 01-AUG-2002.  
 XX  
 XX 24-JAN-2002; 2002WO-US002242.  
 XX  
 PR 24-JAN-2001; 2001US-0263965P.  
 PR 02-FEB-2001; 2001US-0285938P.  
 PR 09-APR-2001; 2001US-00829472.  
 PR 09-APR-2001; 2001US-0282698P.

PR 04-MAY-2001; 2001US-0288590P.  
 PR 29-MAY-2001; 2001US-0294443P.  
 XX  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 XX  
 PI Mack DH, Gish KC, Afar D;  
 XX  
 DR WPI; 2002-583738/62.  
 DR N-PSDB; ABJ05537.  
 XX  
 PT Detecting a breast cancer-associated transcript in a patient's cell,  
 PT useful for diagnosing breast cancer, comprises contacting a biological  
 PT sample with a polynucleotide that selectively hybridizes with breast  
 PT cancer nucleic acids.  
 XX  
 PS Claim 9; Page 347-348; 414pp; English.  
 XX  
 CC The invention comprises a method of detecting a breast cancer-associated  
 CC transcript in a cell from a patient. The method of the invention involves  
 CC contacting a biological sample from the patient with a nucleotide that  
 CC hybridizes to one of the 69 breast cancer-associated gene sequences shown  
 CC in the specification. The method of the invention is useful in the  
 CC diagnosis or prognosis of breast cancer, and for detecting genes that are  
 CC up or down-regulated in breast cancer cells. Genes identified by the  
 CC method of the invention can be used in diagnostic purposes and also as  
 CC targets for screening for therapeutic compounds that modulate breast  
 CC cancer (e.g. hormones or antibodies). Identification of genes that are  
 CC over or under expressed in breast cancer can additionally provide high-  
 CC resolution, high-sensitivity datasets which can be used in the areas of  
 CC diagnostics, therapeutics, drug development, pharmacogenetics, protein  
 CC structure and biosensor development. DNA sequences ABT07693 - ABT07761  
 CC represent the 69 breast cancer-associated gene sequences of the invention  
 XX  
 SQ Sequence 4458 BP; 1698 A; 812 C; 931 G; 1017 T; 0 U; 0 Other;  
 Query Match 95.6%; Score 1940; DB 6; Length 4458;  
 Best Local Similarity 98.7%; Pred. No. 0;  
 Matches 2001; Conservative 0; Mismatches 21; Indels 5; Gaps 5;  
 QY 5 TCCGCTTAAAGATGCTTCTGAGGCTAACTGCGAATGAAAGTTTCTATCCAACTAA 64  
 Db 2091 TCTGTTAAAGATGCTTCTGAGGCTAACTGCGAATGAAAGTTTCTATCCAACTAA 2150  
 QY 65 AGCTTAGAATGATGACATGCAAACTTCAAGAGAGAGCTCCGAGAGGCAATCTGC 124  
 Db 2151 AGCTTAGAATGATGACATGCAAACTTCAAGAGAGAGCTCCGAGAGGCAATCTGC 2210  
 QY 125 CTTGAGCTGCCATTTGAATGCAAAAGTCTGTTCCAAATGAAAGCTTGAATGAAGAA 184  
 Db 2211 CTTGAGCTGCCATTTGAATGCAAAAGTCTGTTCCAAATGAAAGCTTGAATGAAGAA 2270  
 QY 185 TGAACAAACATTTGAGAGAGATGAGTACTCCCATCAGATCCCAACAAAGGACTATGA 244  
 Db 2271 TGAACAAACATTTGAGAGAGATGAGTACTCCCATCAGATCCCAACAAAGGACTATGA 2330  
 QY 245 AGAAAGTTCTTGGGATTTCTGAGAGTCTCTGTGAGAGTCTTTCAGAGAGATGTGTCTT 304  
 Db 2331 AGAAAGTTCTTGGGATTTCTGAGAGTCTCTGTGAGAGTCTTTCAGAGAGATGTGTCTT 2390  
 QY 305 ACCCAAGGCTACATCAATCAAAAGAAATAGATAAATAATGAAAAATAGAGAGTCTCC 364  
 Db 2391 ACCCAAGGCTACATCAATCAAAAGAAATAGATAAATAATGAAAAATAGAGAGTCTCC 2450  
 QY 365 TGATAATGATGTTTCTGAGAGGCTCCCTGAGAGTGAAGTTTCTATTCCAATGAAGC 424  
 Db 2451 TGATAATGATGTTTCTGAGAGGCTCCCTGAGAGTGAAGTTTCTATTCCAATGAAGC 2510  
 QY 425 CTTAGAATTTGATGGAATGCAAACTTTCAAGAGAGCTCCCGAGAGGCAATCTGCCTT 484  
 Db 2511 CTTAGAATTTGATGGAATGCAAACTTTCAAGAGAGCTCCCGAGAGGCAATCTGCCTT 2570  
 QY 485 CGAGCTGCCATTTGAATGCAAAAGTCTGTTCCAAATGAAGCTTGAATGAAGATGA 544

2571	CGAGCCTGCCATTGAATGCAAAAGTCTGTTCCAAATAAAGACCTTGGAAATTGGAAGTAATGA	2633
Qy	ACAAACATTGAGAGCAGATCAGATGTTTCCCTTCAGAAATCAAAACAAAGAGGTTTGAAGA	604
Db	ACAAACATTGAGAGCAGATCAGATGTTTCCCTTCAGAAATCAAAACAAAGAGGTTTGAAGA	2630
Qy	AAATTCCTGGATTCTCAGAGTCTCCGTGAGACTGTTTTCACGAAGAGTCTGTGTCTACC	664
Db	AAATTCCTGGATTCTCAGAGTCTCCGTGAGACTGTTTTCACGAAGAGTCTGTGTGTACC	2750
Qy	CAAGGCTACACATCAAAAGAAATGGATATAAAATAAGTGGAAAAATTAGAAGATTCAACTAG	724
Db	CAAGGCTACACATCAAAAGAAATGGATATAAAATAAGTGGAAAAATTAGAAGATTCAACTAG	2810
Qy	CCTATCAAAAATCTTGGATACAGTTCAATCTTGTGAAGAGCAAGGGAATCTCAAAAAGA	784
Db	CCTATCAAAAATCTTGGATACAGTTCAATCTTGTGAAGAGCAAGGGAATCTCAAAAAGA	2870
Qy	TCAGTGTGAACAACGTCACAGAAAAATGGAAACAAATGAAAAAGCAAGTTTGTGTACTGAA	844
Db	TCAGTGTGAACAACGTCACAGAAAAATGGAAACAAATGAAAAAGCAAGTTTGTGTACTGAA	2930
Qy	AAAGAAACTGTTCAGAACCAAAAGAAATAAAATCAAGTTAGAGAACCAAAAAGTTTAAATG	904
Db	AAAGAAACTGTTCAGAACCAAAAGAAATAAAATCAAGTTAGAGAACCAAAAAGTTTAAATG	2990
Qy	GGAACAAGAGCTCTGCAAGTGTGAGATTGACTTTAAACCAAGAGAGAGAGAGAGAGAA	964
Db	GGAACAAGAGCTCTGCAAGTGTGAGATTGACTTTAAACCAAGAGAGAGAGAGAGAGAA	3050
Qy	TGCCGATATATAAATGAAAAAATTAGGGAAGAAATTAGGAAGAAATGGAAGAGCAGCATAG	1024
Db	TGCCGATATATAAATGAAAAAATTAGGGAAGAAATTAGGAAGAAATGGAAGAGCAGCATAG	3110
Qy	GAAAGAGTTAGAGTGAACCAACACTTGAACAGGCTCTCAGATACAAAGATATAGAAAT	1084
Db	GAAAGAGTTAGAGTGAACCAACACTTGAACAGGCTCTCAGATACAAAGATATAGAAAT	3170
Qy	GAAAGAGTGTAGAAAGTAATTTGAATCAGGTTTCTCACACTCATGAAATGAAATTTATCT	1144
Db	GAAAGAGTGTAGAAAGTAATTTGAATCAGGTTTCTCACACTCATGAAATGAAATTTATCT	3230
Qy	CTTACATGAAAATTTGCATGTGTGAAAAAGAAATTTGCCATGCTGTAAGATAGCCAC	1204
Db	CTTACATGAAAATTTGCATGTGTGAAAAAGAAATTTGCCATGCTGTAAGATAGCCAC	3290
Qy	ACTGAAACACCAATACACAGGAAAAAGGAAATAAATACTTTGAGGACATTAAGATTTTAAA	1264
Db	ACTGAAACACCAATACACAGGAAAAAGGAAATAAATACTTTGAGGACATTAAGATTTTAAA	3350
Qy	AGAAAGAAATGCTGAACTTCAGATGACCTTAAATCTGAAAGAGAAATCAATTAACAAAG	1324
Db	AGAAAGAAATGCTGAACTTCAGATGACCTTAAATCTGAAAGAGAAATCAATTAACAAAG	3410
Qy	GGCATCTCAATATAGTGGCAGCTTAAAGTTCTGATAGCTGAGAACCAATGCTCAGTTC	1384
Db	GGCATCTCAATATAGTGGCAGCTTAAAGTTCTGATAGCTGAGAACCAATGCTCAGTTC	3470
Qy	TAAATTTGAAGGAAAAACAAGACAAAGAAATACTAGGCGAGAAATTTGAAATCAACCATCC	1444
Db	TAAATTTGAAGGAAAAACAAGACAAAGAAATACTAGGCGAGAAATTTGAAATCAACCATCC	3530
Qy	TAGACTGCTTCTGCTGTACAAGACCATGATCAAAATTTGTGACATCAAGAAAAAGTCAAGA	1504
Db	TAGACTGCTTCTGCTGTACAAGACCATGATCAAAATTTGTGACATCAAGAAAAAGTCAAGA	3590
Qy	ACCTGCTTTCCACATTTGAGGAGATGCTTGTGTCGAAAGAAAAATGAATGTTGATGTGAG	1564
Db	ACCTGCTTTCCACATTTGAGGAGATGCTTGTGTCGAAAGAAAAATGAATGTTGATGTGAG	3650
Qy	TAGTACCGATATATAACAAATGAGGTGCTTCCATCAACCACTTTCTGGAAGCTCAAGGAAAT	1624
Db	TAGTACCGATATATAACAAATGAGGTGCTTCCATCAACCACTTTCTGGAAGCTCAAGGAAAT	3709

Qy	1625	CCANAAGCCTAAATAATTAATCTCAAAATTAAGGAGAGATGCTCTTAAGAGAAATACATGG	1684
Db	3710	CCAAAAGCCTAAATAATTAATCTCAAAATTAAGGAGAGATGCTCTTAAGAGAAATACATGG	3769
Qy	1685	TTTCAGGAACATGSCACAAAGAGACCAACGCTGAAACACACAGTGTCAAATGAAGGAAGCTGAA	1744
Db	3770	TTTICA-GAACATGCAACAAGAGACCCACGCTGNAACACAGTGTCAAATGAAGGAAGCTGAA	3828
Qy	1745	CACATGTTTCAAANCGAACCAAGATWATGTGAACAAACACACCTGANCAGCAGAGTCTCTA	1804
Db	3829	CACATGTATCAAAACCAACAAGATAATGTGAACAAACACACCTGAAACAGCAGAGTCTCTA	3888
Qy	1805	GATCAGAAATATTATTTCAACTACAAAGCAAAAATATGTGGCTTCAACAGCAATTAGTTTCAT	1864
Db	3889	GATCAGAAATATTATTTCAACTACAAAGCAAAAATATGTGGCTTCAACAGCAATTAGTTTCAT	3948
Qy	1865	GCACATAAGAAAGCTGACAAACAAAGCAAGATAACAATGATNTTCAATTTCTTGAGAG	1924
Db	3949	GCACATAA-GAAAGCTGACAAACAAAGCAAGATAACAATGATNTTCAATTTCTTGAGAG	4007
Qy	1925	GAAAATGC-NCATCATCTTCTTAAAGAGAGAAAAATGAGGAGATATTTNATTACNATAACCA	1983
Db	4008	GAAAATGCACATCATCTTCTTAAAGAGAGAAAAATGAGGAGATATTTNATTACNATAACCA	4067
Qy	1984	TTTAAAAAACCCGTATATTTCAATATGMAAAAAAANAANAANAANA 2030	
Db	4068	TTTAAAAAAC-CCGTATATATCAATATGMAAAAAAAGAGAAAGCAAAAAA 4113	
RESULT 4			
ABT33271			
ID	ABT33271	standard; DNA; 4458 BP.	
AC	ABT33271;		
DT	15-MAY-2003	(first entry)	
DE	Human tumour-related DNA sequence - SEQ ID NO 564.		
XX	Human; ss; vaccine; gene therapy; T cell stimulation; T cell expansion;		
KW	tumour; breast cancer; cancer; immune response stimulation; PCR; primer.		
XX	Homo sapiens.		
OS			
PN	WO200283956-A1.		
PD	24-OCT-2002.		
XX			
PF	15-APR-2002; 2002WO-US012378.		
XX			
PR	13-APR-2001; 2001US-00834759.		
PR	07-DEC-2001; 2001US-00007805.		
PR	13-FEB-2002; 2002US-00076522.		
XX			
PA	(CORI-) CORIXA CORP.		
XX			
PI	Houghton RL, Sleath PR, Persing DH, Jiang Y, Dillon RC;		
PI	Mitcham JL, Xu J, Harlocker SL, Hepler WT, Henderson RA, Fanger GR;		
PI	Vedwick TS, McNeill PD, Durham M;		
XX			
DR	WPI; 2003-103376/09.		
XX			
PT	New polypeptide and polynucleotide useful for stimulating and/or		
PT	expanding T cells specific for a tumor protein and treating breast		
PT	cancer.		
XX			
PS	Example 9; Page 340-341; 375pp; English.		
XX			
CC	The invention comprises a method of stimulating and/or expanding T cells		
CC	specific for a tumour protein. The invention further comprises human		
CC	nucleic acids and proteins that are associated with tumours (e.g. breast		
CC	cancer). The method and sequences of the invention are useful for		

CC stimulating and/or expanding T cells specific for a tumour protein,  
CC detecting the presence of cancer, stimulating an immune response in a  
CC patient and treating breast cancer. The present DNA sequence represents a  
CC human tumour-related PCR primer  
XX  
SQ Sequence 4458 BP; 1698 A; 812 C; 931 G; 1017 T; 0 U; 0 Other;  
Query Match 95.6%; Score 1940; DB 7; Length 4458;  
Best Local Similarity 98.7%; Pred. No. 0;  
Matches 2001; Conservative 0; Mismatches 21; Indels 5; Gaps 5;  
QY 5 TGCGTTAAAGATGGCTCTCTGAAGGCTAACTCGGGAATGAAGTTCTTATTCCAACTAA 64  
Db 2091 TCCTGTTAAAGATGGCTCTCTGAAGGCTAACTCGGGAATGAAGTTCTTATTCCAACTAA 2150  
QY 65 AGCCTTAGAATTGATGACATGCAAACTTTCAAAGCAGAGCCTCCGAGAGCCATCTGC 124  
Db 2151 AGCCTTAGAATTGATGACATGCAAACTTTCAAAGCAGAGCCTCCGAGAGCCATCTGC 2210  
QY 125 CTTGAGCCTGCCATTGAAGTCAAAAGTCTGTTCMAATAAAGCCTTGGAAATGAAGAA 184  
Db 2211 CTTGAGCCTGCCATTGAAGTCAAAAGTCTGTTCMAATAAAGCCTTGGAAATGAAGAA 2270  
QY 185 TGAACAAACATTGAGACGATGATGACTCCCATCAGATCCAAACAAAGGACTATGA 244  
Db 2271 TGAACAAACATTGAGACGATGATGACTCCCATCAGATCCAAACAAAGGACTATGA 2330  
QY 245 AGAAAGTCTTGGATCTGTGAGTCTCTGTGAGACTGTTTTCAGAGAGATGTGTGTT 304  
Db 2331 AGAAAGTCTTGGATCTGTGAGTCTCTGTGAGACTGTTTTCAGAGAGATGTGTGTT 2390  
QY 305 ACCGAGCTACATCAAAAGAAATAGATAAATAAATGGAATAATTAGAAGTCTCC 364  
Db 2391 ACCGAGCTACATCAAAAGAAATAGATAAATAAATGGAATAATTAGAAGTCTCC 2450  
QY 365 TGATAATGATGGTTTTCTGAAGGCTCCCTGAGAGTGAAGTCTTCTATTCAAACCTAAAGC 424  
Db 2451 TGATAATGATGGTTTTCTGAAGGCTCCCTGAGAGTGAAGTCTTCTATTCAAACCTAAAGC 2510  
QY 425 CTTAGAAATGATGNCATGCAAACTTTCAAAGCAGAGCCTCCGAGAGCAATCTGCCTT 484  
Db 2511 CTTAGAAATGATGNCATGCAAACTTTCAAAGCAGAGCCTCCGAGAGCAATCTGCCTT 2570  
QY 485 CGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATGAAGATGA 544  
Db 2571 CGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATGAAGATGA 2630  
QY 545 ACAACATTGAGAGCAGATCAGATGTTCCCTTCAGATCAAAACAAAGAGGTTGAAGA 604  
Db 2631 ACAACATTGAGAGCAGATCAGATGTTCCCTTCAGATCAAAACAAAGAGGTTGAAGA 2690  
QY 605 AAATCTTGGGATCTGAGAGTCTCCGTGAGACTGTTTTCAGAGAGGATGTGTGTGACC 664  
Db 2691 AAATCTTGGGATCTGAGAGTCTCCGTGAGACTGTTTTCAGAGAGGATGTGTGTGACC 2750  
QY 665 CAAGGCTACATCAAAAGAAATGGATAAATAAGTGGAAAATTAGAGATTCACTAG 724  
Db 2751 CAAGGCTACATCAAAAGAAATGGATAAATAAGTGGAAAATTAGAGATTCACTAG 2810  
QY 725 CCTATCAAAATCTTGGATACAGTTCAATCTTGTGAAGAGCAAGGAACTTCAAAAAGA 784  
Db 2811 CCTATCAAAATCTTGGATACAGTTCAATCTTGTGAAGAGCAAGGAACTTCAAAAAGA 2870  
QY 785 TCAGTGTAAACGCTACAGGAAAATGGAACAAATGAAGAAGTGTGTGTACTGAA 844  
Db 2871 TCAGTGTAAACGCTACAGGAAAATGGAACAAATGAAGAAGTGTGTGTACTGAA 2930  
QY 845 AAGAACTGTGACAGAGCAAAAGAAATAAATCAGATTAGAGAACCAAAAAGTTAAATG 904  
Db 2931 AAGAACTGTGACAGAGCAAAAGAAATAAATCAGATTAGAGAACCAAAAAGTTAAATG 2990  
QY 905 GGAACAGAGCTCTGCAGTGTGAGATGTGCTTTAAACCAAGAGAGAGAGAGAA 964

Db 2991 GGAACAGAGCTCTGCAGTGTGAGATGTGCTTTAAACCAAGAGAGAGAGAGAA 3050  
QY 965 TGCCGATATATTAAATGAAAAAATTAGGGAAGAAATTAGGAAGAAATCGAAGAGCAGATAG 1024  
Db 3051 TGCCGATATATTAAATGAAAAAATTAGGGAAGAAATTAGGGAAGAAATCGAAGAGCAGATAG 3110  
QY 1025 GAAAGAGTTAGAGTGAACCAAACTTTGAACAGGCTCTCAGAAATCAGATATAGAAAT 1084  
Db 3111 GAAAGAGTTAGAGTGAACCAAACTTTGAACAGGCTCTCAGAAATCAGATATAGAAAT 3170  
QY 1085 GAAGAGTGTAGAAGTAATTTGAATCAGGTTTCTCAGCTCATGAAATGAATAATTTCT 1144  
Db 3171 GAAGAGTGTAGAAGTAATTTGAATCAGGTTTCTCAGCTCATGAAATGAATAATTTCT 3230  
QY 1145 CTTACATGAAAATTTGATGTTGAAAAAGGAAATTCCTAGCTTAAACCTGAAATAGCCAC 1204  
Db 3231 CTTACATGAAAATTTGATGTTGAAAAAGGAAATTCCTAGCTTAAACCTGAAATAGCCAC 3290  
QY 1205 ACTGAAACCACTACACAGGAAAGGAAAAATAAATCTTTGAGGACATTAAGATTTTAAA 1264  
Db 3291 ACTGAAACCACTACACAGGAAAGGAAAAATAAATCTTTGAGGACATTAAGATTTTAAA 3350  
QY 1265 AGAAAGAAATCTGAACTTCAGATGACCTTAAACCTGAAAGAGGAAATCAATTAACATAAG 1324  
Db 3351 AGAAAGAAATCTGAACTTCAGATGACCTTAAACCTGAAAGAGGAAATCAATTAACATAAG 3410  
QY 1325 GGCATCTCAATATAGTGGGCAAGCTTAAAGTTCTGATAGCTGAGAACCAATGCTCATT 1384  
Db 3411 GGCATCTCAATATAGTGGGCAAGCTTAAAGTTCTGATAGCTGAGAACCAATGCTCATT 3470  
QY 1385 TAAATGAAGGAAAAAACAAGCAAGAAATCTAGAGCGAGATTTGAATCAGACCATCC 1444  
Db 3471 TAAATGAAGGAAAAAACAAGCAAGAAATCTAGAGCGAGATTTGAATCAGACCATCC 3530  
QY 1445 TAGACTGCTCTGCTGTACAGACCATGATCAAAATTTGATGACCAAGAAAAAGTCAAGA 1504  
Db 3531 TAGACTGCTCTGCTGTACAGACCATGATCAAAATTTGATGACCAAGAAAAAGTCAAGA 3590  
QY 1505 ACCTGCTTCCACATGTCAGAGAGTCTGTTTGCAGAAAAAATGAATGTTGATGTGAG 1564  
Db 3591 ACCTGCTTCCACATGTCAGAGAGTCTGTTTGCAGAAAAAATGAATGTTGATGTGAG 3650  
QY 1565 TAGTACCGATATATAACCAATGAGGTGCTCCATCAACCACTTTCTGAAAGCTCAAGGAAAT 1624  
Db 3651 TAGTACCGATATATAACCAATGAGGTGCTCCATCAACCACTTTCTGAAAGCTCAAGGAAAT 3709  
QY 1625 CCNAAAGCCTAAAAATTAATCTCAATATGAGAGAGTCTCTTAAGAGAAAAATCATTTGG 1684  
Db 3710 CCNAAAGCCTAAAAATTAATCTCAATATGAGAGAGTCTCTTAAGAGAAAAATCATTTGG 3769  
QY 1685 TTTGAGGAAATGCAACAAAGAGCAACCAAGTGAACACACAGTGTCAAAATGAAGGAACTGAA 1744  
Db 3770 TTTGCA-GAAGATGCAACAAAGAGCAACCAAGTGAACACACAGTGTCAAAATGAAGGAACTGAA 3828  
QY 1745 CACATGTTCAAAACCAAGATNATGTGAACAAACACACCTGAGAGAGGATCTCTA 1804  
Db 3829 CACATGTTCAAAACCAAGATNATGTGAACAAACCAACCTGAGAGAGGATCTCTA 3888  
QY 1805 GATCAGAAATTTTCAACTCAAGGAAAAATATGTGCTTCAACAGCAATTAAGTTTCAAT 1864  
Db 3889 GATCAGAAATTTTCAACTCAAGGAAAAATATGTGCTTCAACAGCAATTAAGTTTCAAT 3948  
QY 1865 GCACATAAGGAAAGCTGACACAAAGAGCAAGATTAACAAATGATTTTCTTTCTTGAGAG 1924  
Db 3949 GCACATAA-GAAGCTGACAAACAAAGAGCAAGATTAACAAATGATTTTCTTTCTTGAGAG 4007  
QY 1925 GAAAAATGTC-NCATCATCTTCTAAAGAGAAAAATGAGGAGATTTTATTCNATAACCA 1983  
Db 4008 GAAAAATGCAACATCATCTCCTTAAAGAGAAAAATGAGGAGATTTTATTAACATAACCA 4067  
QY 1984 TTTAAAAAACCCGTATATTTCATATATGAAAAAATAAAAAAATAAAAAA 2030  
Db 4068 TTTAAAAAACCCGTATATATCAATATGAAAAAAGAGAGAAAGCAGAAACA 4113



Db	2211	CTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATTAAGCCCTTGAAATTGAAGAA	2270
Qy	185	TGAACAAACATTGAGAGCAGATGAGATCTCCCATCAGAAATCCAAACAAAGAGCTATGA	244
Db	2271	TGAACAAACATTGAGAGCAGATGAGATCTCCCATCAGAAATCCAAACAAAGAGCTATGA	2330
Qy	245	AGAAAGTTCTTGGGATCTGAGAGTCTCTGTGAGACTGTTTTCAGAGAGGATGTGTGTTT	304
Db	2331	AGAAAGTTCTTGGGATCTGAGAGTCTCTGTGAGACTGTTTTCAGAGAGGATGTGTGTTT	2390
Qy	305	ACCAAGGCTACACATCAAAAGAAATAGATAAAATAAATGGAATAATAGAGAGTCTCC	364
Db	2391	ACCAAGGCTACACATCAAAAGAAATAGATAAAATAAATGGAATAATAGAGAGTCTCC	2450
Qy	365	TCATAATGATGTTTCTGAGAGGCTCCCTGCAGAAATGAAAGTCTTCTATTCCAATTAAGC	424
Db	2451	TGATAATGATGTTTCTGAGAGGCTCCCTGCAGAAATGAAAGTCTTCTATTCCAATTAAGC	2510
Qy	425	CTTAGAATTGATGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAGGCAATCTGCTT	484
Db	2511	CTTAGAATTGATGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAGGCAATCTGCTT	2570
Qy	485	CGAGCTGCCATTGAAATGCAAAAGTCTGTTCCAAATTAAGCCCTTGGAATTAAGAGATGA	544
Db	2571	CGAGCTGCCATTGAAATGCAAAAGTCTGTTCCAAATTAAGCCCTTGGAATTAAGAGATGA	2630
Qy	545	ACAAACATTGAGAGCAGATCAGATGTTCCCTTCAGAAATCAAAAACAAAGAGGTTGAAGA	604
Db	2631	ACAAACATTGAGAGCAGATCAGATGTTCCCTTCAGAAATCAAAAACAAAGAGGTTGAAGA	2690
Qy	605	AAATCTTGGGATCTGAGAGTCTCCGTGAGACTGTTTCAGAGAGGATGTGTGTACC	664
Db	2691	AAATCTTGGGATCTGAGAGTCTCCGTGAGACTGTTTCAGAGAGGATGTGTGTACC	2750
Qy	665	CAAGGCTACACATCAAAAGAAATGGAATAAATAAGTGGAAATTAAGAGATTCACATAG	724
Db	2751	CAAGGCTACACATCAAAAGAAATGGAATAAATAAGTGGAAATTAAGAGATTCACATAG	2810
Qy	725	CTATCAAAATCTTGGATACAGTTCATCTTGTGAAGAGCAAGGAGGACTTCAAAAGA	784
Db	2811	CTATCAAAATCTTGGATACAGTTCATCTTGTGAAGAGCAAGGAGGACTTCAAAAGA	2870
Qy	785	TCACCTGTAACAACTCAGCAAAATGGAACAAATGAAAGAAAGTCTGTGTACTGAA	844
Db	2871	TCACCTGTAACAACTCAGCAAAATGGAACAAATGAAAGAAAGTCTGTGTACTGAA	2930
Qy	845	AAAGAACTGTGAGAGCAAAAGAAATAAATCAAGTTAGAGAACCCAAAGTTAATG	904
Db	2931	AAAGAACTGTGAGAGCAAAAGAAATAAATCAAGTTAGAGAACCCAAAGTTAATG	2990
Qy	905	GGAAACAGAGCTCTGAGTGTGAGATTCACCTTTAAACCAAGAGAGAGAGAGAA	964
Db	2991	GGAAACAGAGCTCTGAGTGTGAGATTCACCTTTAAACCAAGAGAGAGAGAGAA	3050
Qy	965	TGCCGATATATTAAATGAAATAATTTAGGGAAGAAATTAGGAAGAATCGAAGAGCAGATAG	1024
Db	3051	TGCCGATATATTAAATGAAATAATTTAGGGAAGAAATTAGGAAGAATCGAAGAGCAGATAG	3110
Qy	1025	GAAAGATTAGAGTGAACCAACAACTTTGAACAGGCTCTCAGATACAGATATAGAAAT	1084
Db	3111	GAAAGATTAGAGTGAACCAACAACTTTGAACAGGCTCTCAGATACAGATATAGAAAT	3170
Qy	1085	GAAAGATTAGAGTGAACCAACAACTTTGAACAGGCTCTCAGATACAGATATAGAAAT	1144
Db	3171	GAAAGATTAGAGTGAACCAACAACTTTGAACAGGCTCTCAGATACAGATATAGAAAT	3230
Qy	1145	CTTACATGAAATTTGATGTTGAAAGAAATTTGCCATGTCTAAATCTGGAATAGCCAC	1204
Db	3231	CTTACATGAAATTTGATGTTGAAAGAAATTTGCCATGTCTAAATCTGGAATAGCCAC	3290
Qy	1205	ACTGAAACCAACATACCAGGAAAGGAAATAAATCTTTGAGGACATTAAGATTTTAA	1264

Db	2211	CTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATTAAGCCCTTGAAATTGAAGAA	2270
Qy	185	TGAACAAACATTGAGAGCAGATGAGATCTCCCATCAGAAATCCAAACAAAGAGCTATGA	244
Db	2271	TGAACAAACATTGAGAGCAGATGAGATCTCCCATCAGAAATCCAAACAAAGAGCTATGA	2330
Qy	245	AGAAAGTTCTTGGGATCTGAGAGTCTCTGTGAGACTGTTTTCAGAGAGGATGTGTGTTT	304
Db	2331	AGAAAGTTCTTGGGATCTGAGAGTCTCTGTGAGACTGTTTTCAGAGAGGATGTGTGTTT	2390
Qy	305	ACCAAGGCTACACATCAAAAGAAATAGATAAAATAAATGGAATAATAGAGAGTCTCC	364
Db	2391	ACCAAGGCTACACATCAAAAGAAATAGATAAAATAAATGGAATAATAGAGAGTCTCC	2450
Qy	365	TCATAATGATGTTTCTGAGAGGCTCCCTGCAGAAATGAAAGTCTTCTATTCCAATTAAGC	424
Db	2451	TGATAATGATGTTTCTGAGAGGCTCCCTGCAGAAATGAAAGTCTTCTATTCCAATTAAGC	2510
Qy	425	CTTAGAATTGATGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAGGCAATCTGCTT	484
Db	2511	CTTAGAATTGATGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAGGCAATCTGCTT	2570
Qy	485	CGAGCTGCCATTGAAATGCAAAAGTCTGTTCCAAATTAAGCCCTTGGAATTAAGAGATGA	544
Db	2571	CGAGCTGCCATTGAAATGCAAAAGTCTGTTCCAAATTAAGCCCTTGGAATTAAGAGATGA	2630
Qy	545	ACAAACATTGAGAGCAGATCAGATGTTCCCTTCAGAAATCAAAAACAAAGAGGTTGAAGA	604
Db	2631	ACAAACATTGAGAGCAGATCAGATGTTCCCTTCAGAAATCAAAAACAAAGAGGTTGAAGA	2690
Qy	605	AAATCTTGGGATCTGAGAGTCTCCGTGAGACTGTTTCAGAGAGGATGTGTGTACC	664
Db	2691	AAATCTTGGGATCTGAGAGTCTCCGTGAGACTGTTTCAGAGAGGATGTGTGTACC	2750
Qy	665	CAAGGCTACACATCAAAAGAAATGGAATAAATAAGTGGAAATTAAGAGATTCACATAG	724
Db	2751	CAAGGCTACACATCAAAAGAAATGGAATAAATAAGTGGAAATTAAGAGATTCACATAG	2810
Qy	725	CTATCAAAATCTTGGATACAGTTCATCTTGTGAAGAGCAAGGAGGACTTCAAAAGA	784
Db	2811	CTATCAAAATCTTGGATACAGTTCATCTTGTGAAGAGCAAGGAGGACTTCAAAAGA	2870
Qy	785	TCACCTGTAACAACTCAGCAAAATGGAACAAATGAAAGAAAGTCTGTGTACTGAA	844
Db	2871	TCACCTGTAACAACTCAGCAAAATGGAACAAATGAAAGAAAGTCTGTGTACTGAA	2930
Qy	845	AAAGAACTGTGAGAGCAAAAGAAATAAATCAAGTTAGAGAACCCAAAGTTAATG	904
Db	2931	AAAGAACTGTGAGAGCAAAAGAAATAAATCAAGTTAGAGAACCCAAAGTTAATG	2990
Qy	905	GGAAACAGAGCTCTGAGTGTGAGATTCACCTTTAAACCAAGAGAGAGAGAGAA	964
Db	2991	GGAAACAGAGCTCTGAGTGTGAGATTCACCTTTAAACCAAGAGAGAGAGAGAGAA	3050
Qy	965	TGCCGATATATTAAATGAAATAATTTAGGGAAGAAATTAGGAAGAATCGAAGAGCAGATAG	1024
Db	3051	TGCCGATATATTAAATGAAATAATTTAGGGAAGAAATTAGGAAGAATCGAAGAGCAGATAG	3110
Qy	1025	GAAAGATTAGAGTGAACCAACAACTTTGAACAGGCTCTCAGATACAGATATAGAAAT	1084
Db	3111	GAAAGATTAGAGTGAACCAACAACTTTGAACAGGCTCTCAGATACAGATATAGAAAT	3170
Qy	1085	GAAAGATTAGAGTGAACCAACAACTTTGAACAGGCTCTCAGATACAGATATAGAAAT	1144
Db	3171	GAAAGATTAGAGTGAACCAACAACTTTGAACAGGCTCTCAGATACAGATATAGAAAT	3230
Qy	1145	CTTACATGAAATTTGATGTTGAAAGAAATTTGCCATGTCTAAATCTGGAATAGCCAC	1204
Db	3231	CTTACATGAAATTTGATGTTGAAAGAAATTTGCCATGTCTAAATCTGGAATAGCCAC	3290
Qy	1205	ACTGAAACCAACATACCAGGAAAGGAAATAAATCTTTGAGGACATTAAGATTTTAA	1264

RESULT 5  
 ACC50246  
 ID ACC50246 standard; cDNA; 4458 BP.  
 XX  
 AC ACC50246;  
 XX  
 DT 12-JUN-2003 (first entry)  
 XX  
 DE Breast cancer associated cDNA sequence SEQ ID NO:333.  
 XX  
 KW Human; breast cancer; cytostatic; gene therapy; gene, ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W02003004989-A2.  
 XX  
 PD 16-JAN-2003.  
 XX  
 PF 21-JUN-2002; 2002WO-US019669.  
 XX  
 PR 21-JUN-2001; 2001US-0299887P.  
 PR 27-JUN-2001; 2001US-0301572P.  
 PR 18-JUL-2001; 2001US-0306501P.  
 PR 25-SEP-2001; 2001US-0325002P.  
 PR 05-MAR-2002; 2002US-0362585P.  
 PR 14-MAY-2002; 2002US-0380391P.  
 XX  
 PA (MILL-) MILLENIUM PHARM INC.  
 XX  
 PI Lillie J, Gannavarapu M, Glatt K, Hoersh S, Kamatkar S;  
 PI Mertens M, Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE;  
 PI Bast RC, Hortobagyi GN, Pusztai L, Meric F, Sahin A, Mills GB;  
 XX  
 DR WPI: 2003-210381/20.  
 DR P-PSDB; ABR47548.  
 XX  
 PT Breast cancer diagnosis or treatment by comparing the level of expression  
 PT of a marker in a patient sample with that in the control non-breast  
 PT cancer sample.  
 XX  
 PS Claim 1; SEQ ID NO 333; 128pp; English.  
 XX  
 CC The present invention describes a method for assessing whether a patient  
 CC is afflicted with breast cancer. The method comprises comparing the level  
 CC of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and  
 CC ABR47386 to ABR47632) in a patient sample and the normal level of  
 CC expression of the marker in a control non-breast cancer sample, where a  
 CC significant increase in the level of expression of the marker in the  
 CC patient sample and the normal level is an indication that the patient is  
 CC afflicted with breast cancer. The breast cancer associated sequences from  
 CC the present invention have cytostatic activities and can be used in gene  
 CC therapy. The method is useful for diagnosing and treating breast cancer.  
 CC N.B. The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 4458 BP; 1698 A; 812 C; 931 G; 1017 T; 0 U; 0 Other;  
 Query Match 95.6%; Score 1940; DB 7; Length 4458;  
 Best Local Similarity 98.7%; Pred. No. 0;  
 Matches 2001; Conservative 0; Mismatches 21; Indels 5; Gaps 5;  
 Qy 5 TCCCGTTAAGATGCTCTTCTGAAAGGCTAACTGCGGATGAAGTCTTCTATTCCAACTAA 64  
 Db 2091 TCCTTTAAGATGCTCTTCTGAAAGGCTAACTGCGGATGAAGTCTTCTATTCCAACTAA 2150  
 Qy 65 AGCCTTAGAATTGATGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAGCCATCTGC 124  
 Db 2151 AGCCTTAGAATTGATGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAGCCATCTGC 2210  
 Qy 125 CTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATTAAGCCCTTGAAATGAAGA 184



Db 1614 TGAATGATGGTTTCTGAAGGCTCCCTGAGAAATGAAGTTTCTATCCAACTAAGC 1673  
 Qy 425 CTTAGAAATGATGACATGCAAACTTTCAAAGCAGAGCCCTCCGAGAGCCATCTGCCIT 484  
 Db 1674 CTTAGAAATGATGACATGCAAACTTTCAAAGCAGAGCCCTCCGAGAGCCATCTGCCIT 1733  
 Qy 485 CGAGCCTGCCATTCGAATGCAAAAGTCTGTCTCCAAATAAAGCCCTTGGAAATGAAGAATGA 544  
 Db 1734 CGAGCCTGCCATTCGAATGCAAAAGTCTGTCTCCAAATAAAGCCCTTGGAAATGAAGAATGA 1793  
 Qy 545 ACAACATGAGAGCAGATCAGATGTTCCCTTCAGAAATCAAACAAAGAGGTTGAGA 604  
 Db 1794 ACAACATGAGAGCAGATCAGATGTTCCCTTCAGAAATCAAACAAAGAGGTTGAGA 1853  
 Qy 605 AAATTTCTGGGATTTCTGAGAGTCTCCGCTGAGACTGTTTTCAGAGAGGATGTGTGTACC 664  
 Db 1854 AAATTTCTGGGATTTCTGAGAGTCTCCGCTGAGACTGTTTTCAGAGAGGATGTGTGTACC 1913  
 Qy 665 CAAGGCTACATCAAAAAGAAATGGATTAATAATAGTGGAAATTAGAAGATTCACATAG 724  
 Db 1914 CAAGGCTACATCAAAAAGAAATGGATTAATAATAGTGGAAATTAGAAGATTCACATAG 1973  
 Qy 725 CCTATCAAAATCTTGGATACAGTTTCTTGTGAAAGAGCAAGGGAACCTTCAAAAAGA 784  
 Db 1974 CCTATCAAAATCTTGGATACAGTTTCTTGTGAAAGAGCAAGGGAACCTTCAAAAAGA 2033  
 Qy 785 TCACGTGAAACAGTACAGGAAATAATGGAACAAATGAAAGAGGTTTGTGTACTGAA 844  
 Db 2034 TCACGTGAAACAGTACAGGAAATAATGGAACAAATGAAAGAGGTTTGTGTACTGAA 2093  
 Qy 845 AAAGAACTGTGAGAGCAAGAAATTAATCAAGTTAGAGAACCAAAAGTTAAATG 904  
 Db 2094 AAAGAACTGTGAGAGCAAGAAATTAATCAAGTTAGAGAACCAAAAGTTAAATG 2153  
 Qy 905 GGAAACAGAGCTTCGAGTGTGAGATTGACTTTTAAACCAAGAAAGAGAGAGAGAAA 964  
 Db 2154 GGAAACAGAGCTTCGAGTGTGAGATTGACTTTTAAACCAAGAAAGAGAGAGAGAAA 2213  
 Qy 965 TGCCCATATTAATTAATGAAATTTAGGAGAAATTAGAGAAATCGAAGAGCAGCATAG 1024  
 Db 2214 TGCCCATATTAATTAATGAAATTTAGGAGAAATTAGAGAAATCGAAGAGCAGCATAG 2273  
 Qy 1025 GAAAGAGTTAGAGTGAACCAACACTTTGAACAGGCTCTCAGAACTGGAATATAGAAAT 1084  
 Db 2274 GAAAGAGTTAGAGTGAACCAACACTTTGAACAGGCTCTCAGAACTGGAATATAGAAAT 2333  
 Qy 1085 GAAGAGTTAGAGTGAATTTGAATCAGTTTCTCAGACTCATGAAATGAAATTTATCT 1144  
 Db 2334 GAAGAGTTAGAGTGAATTTGAATCAGTTTCTCAGACTCATGAAATGAAATTTATCT 2393  
 Qy 1145 CTTACATGAAATTTGATGTTGAAAGAGAAATTCGCATGCTTAAACTGGAATATAGCCAC 1204  
 Db 2394 CTTACATGAAATTTGATGTTGAAAGAGAAATTCGCATGCTTAAACTGGAATATAGCCAC 2453  
 Qy 1205 ACTGAAACCAATACCGAGAAAGAGAAATTAATTAATCTGAGGACATTAAGATTTAAA 1264  
 Db 2454 ACTGAAACCAATACCGAGAAAGAGAAATTAATTAATCTGAGGACATTAAGATTTAAA 2513  
 Qy 1265 AGAAAGAGATGCTGAATCTCAGATGACCTTAACTGAAAGAGGAAATCAATTAATTAAG 1324  
 Db 2514 AGAAAGAGATGCTGAATCTCAGATGACCTTAACTGAAAGAGGAAATCAATTAATTAAG 2573  
 Qy 1325 GGCATCTCAATATAGTGGCAGCTTAAAGTTCTGATAGCTGAGAACAAATGCTCAGTTC 1384  
 Db 2574 GGCATCTCAATATAGTGGCAGCTTAAAGTTCTGATAGCTGAGAACAAATGCTCAGTTC 2633  
 Qy 1385 TAAATTTAGAGAAACAGAGCAAGAAATCTAGAGGAGAAATTTGAATCAGACCATCC 1444  
 Db 2634 TAAATTTAGAGAAACAGAGCAAGAAATCTAGAGGAGAAATTTGAATCAGACCATCC 2693  
 Qy 1445 TAGACTGGCTTCTGCTGTAAGAGCAGCATCAATTTGACATCAAGAAAGTCAAGA 1504

Db 2694 TAGACTGGCTTCTGCTGTAAGAGCAGCATCAAAATTTGACATCAAGAAAGTCAAGA 2753  
 Qy 1505 ACCTCTCTTCCACATTCAGGAGATGCTTGTTCGAAAGAAAAATGAATGTTGATGTGAG 1564  
 Db 2754 ACCTCTCTTCCACATTCAGGAGATGCTTGTTCGAAAGAAAAATGAATGTTGATGTGAG 2813  
 Qy 1565 TGTACCCATATATACCAATGAGGTGCTCCATCAACCACTTCTTGAGCTCAAGGGAAT 1624  
 Db 2814 TAGTA-CGATATATAAATGAGGTGCTCCATCAACCACTTCTTGAGCTCAAGGGAAT 2872  
 Qy 1625 CCANAAGCCTAAAAATTAATCTCAATTTATGAGGAGATGCTCTAAGAGAAAAATCATTGG 1684  
 Db 2873 CCANAAGCCTAAAAATTAATCTCAATTTATGAGGAGATGCTCTAAGAGAAAAATCATTGG 2932  
 Qy 1685 TTTTGGAGACATGCAAAAGAGACCAACGTGAACACAGTGTCAAATGAAGAGGAGCTGAA 1744  
 Db 2933 TTTTCA-GAATATGCAAAAGAGACCAACGTGAACACAGTGTCAAATGAAGAGGAGCTGAA 2991  
 Qy 1745 CACATGTTTCAANCGAACAAGATNATGTGAACAAACACACTGANCAGCAGGAGTCTCTA 1804  
 Db 2992 CACATGTTTCAANCGAACAAGATNATGTGAACAAACACACTGANCAGCAGGAGTCTCTA 3051  
 Qy 1805 GATCGAAATTAATTTCACTACAAAGCAAAATATATGTGGCTTCAACAGCAATTAGTTCAT 1864  
 Db 3052 GATCGAAATTAATTTCACTACAAAGCAAAATATATGTGGCTTCAACAGCAATTAGTTCAT 3111  
 Qy 1865 GCACATTAAGAAAGCTGACAAAGCAAAAGCAAAATATATGTGGCTTCAACAGCAATTAGTTCAT 1924  
 Db 3112 GCACATTAAGAAAGCTGACAAAGCAAAAGCAAAATATATGTGGCTTCAACAGCAATTAGTTCAT 3170  
 Qy 1925 GAAATATGTC-NCATCATCTTCTAATAAGAGAAAAATGAGGAGATATTTTATCAATTAACCA 1983  
 Db 3171 GAAATATGTC-NCATCATCTTCTAATAAGAGAAAAATGAGGAGATATTTTATCAATTAACCA 3230  
 Qy 1984 TTTTAAAAACCGTATATTTTCAATTTGGAATGAAAAAANAAAAA 2030  
 Db 3231 TTTTAAAAACCGTATATATTTTCAATTTGGAATGAAAAAANAAAAA 3276

RESULT 7

ABS64022  
 ID ABS64022 standard; DNA; 3288 BP.

XX ABS64022;

XX 15-NOV-2002 (first entry)

XX Human breast tumour polynucleotide #471.

XX Human; breast tumour protein; gene; ds; breast cancer; cytostatic;

XX vaccine.

XX Homo sapiens.

XX OS

XX US2002085998-A1.

XX 04-JUL-2002.

XX 13-APR-2001; 2001US-00834759.

XX 28-DEC-1998; 98US-00222575.

XX 02-APR-1999; 99US-00285480.

XX 23-JUN-1999; 99US-00339338.

XX 02-SEP-1999; 99US-00389681.

XX 03-NOV-1999; 99US-00433826.

XX 17-APR-2000; 2000US-00551621.

XX 08-JUN-2000; 2000US-00590751.

XX 22-JUN-2000; 2000US-00604287.

XX 20-JUL-2000; 2000US-00620405.

XX (CORI-) CORIXA CORP.

XX Jiang Y, Dillon DC, Mitcham JL, Xu J, Harlocker SL, Hepler WT;

PI

PI Henderson RA;  
XX WPI; 2002-635657/68.  
DR P-ESDB; ABG78924.  
XX  
PT Novel breast cancer polynucleotides and polypeptides encoded by the  
PT polynucleotides, useful for detecting the presence of breast cancer in a  
PT patient, and in pharmaceutical compositions, for treating breast cancer.  
XX Disclosure; Page 219-221; 247pp; English.  
XX  
CC The invention relates to an isolated breast tumour polynucleotide and the  
CC polypeptide it encodes. The polynucleotide and polypeptide are useful for  
CC detecting the presence of breast cancer in a patient, and in  
CC pharmaceutical compositions for treating breast cancer. The sequences are  
CC useful for stimulating an immune response in a patient and can therefore  
CC be used in production of vaccines. The sequences are also useful for  
CC detecting the presence of a cancer in a patient, by obtaining a  
CC biological sample from the patient, contacting the biological sample with  
CC a composition of the invention and detecting the amount of polynucleotide  
CC that hybridizes to the sample. This sequence represents a human breast  
CC tumour polynucleotide of the invention  
XX  
XX Sequence 3288 BP; 1293 A; 564 C; 664 G; 761 T; 0 U; 6 Other;  
Query Match 95.5%; Score 1938.4; DB 6; Length 3288;  
Best Local Similarity 98.5%; Pred. No. 0;  
Matches 1997; Conservative 4; Mismatches 21; Indels 5; Gaps 5;  
QY 5 TGCGTAAAGATGGTCTCTGAAGGCTAACTGGGAATGAAAGTTTCTATTCCAACTAA 64  
DB 1254 TCCGTGTTAAAGATGGTCTCTGAAGGCTAACTGGGAATGAAAGTTTCTATTCCAACTAA 1313  
QY 65 AGCCTAGAAATGATGACATGCAAACTTTCAAGAGAGAGCCTCCGAGAGAGCATCTGC 124  
DB 1314 AGCCTAGAAATGATGACATGCAAACTTTCAAGAGAGAGCCTCCGAGAGAGCATCTGC 1373  
QY 125 CTTGAGGCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATTGAAGAA 184  
DB 1374 CTTGAGGCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATTGAAGAA 1433  
QY 185 TGAACAAACATTTGAGAGCAGATGAGTACTCCCATCAGAAATCCAAACAAAGGACTATGA 244  
DB 1434 TGAACAAACATTTGAGAGCAGATGAGTACTCCCATCAGAAATCCAAACAAAGGACTATGA 1493  
QY 245 AGAAAGTTCTTGGGATCTCTGAGAGTCTCTGTGAGACTGTTTACAGAGAGGATGTGTTT 304  
DB 1494 AGAAAGTTCTTGGGATCTCTGAGAGTCTCTGTGAGACTGTTTACAGAGAGGATGTGTTT 1553  
QY 305 ACCCAAGGCTACATCAAAAAGAAATAGATATAAATAAATGGAATAATTAAGAGAGTCTCC 364  
DB 1554 ACCCAAGGCTACATCAAAAAGAAATAGATATAAATAAATGGAATAATTAAGAGAGTCTCC 1613  
QY 365 TGATAATGATGTTTCTGAGGCTCCCTGAGAGTGAAGTTTCTATTCCAACTAAAGC 424  
DB 1614 TGATAATGATGTTTCTGAGGCTCCCTGAGAGTGAAGTTTCTATTCCAACTAAAGC 1673  
QY 425 CTTAGAAATGATGACATGCAAACTTTCAAGAGAGAGCCTCCGAGAGAGCCTATGCTCTT 484  
DB 1674 CTTAGAAATGATGACATGCAAACTTTCAAGAGAGAGCCTCCGAGAGAGCCTATGCTCTT 1733  
QY 485 CGAGCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATGAAGATGA 544  
DB 1734 CGAGCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATGAAGATGA 1793  
QY 545 ACAACATTGAGAGCAGATCAGATGTTCCCTTTCAGAAATCAAAAACAAAGAGAGTTGAAGA 604  
DB 1794 ACAACATTGAGAGCAGATCAGATGTTCCCTTTCAGAAATCAAAAACAAAGAGAGTTGAAGA 1853  
QY 605 AAATTTCTGGGATTTCTGAGAGTCTCCGAGAGAGTCTTTACAGAGAGGATGTGTGTACC 664  
DB 1854 AAATTTCTGGGATTTCTGAGAGTCTCCGAGAGAGTCTTTACAGAGAGGATGTGTGTACC 1913

QY 665 CAAGGCTACATCAAAAAGAAATGGATAAAATAAGTGGAAAAATTAGAGATTCAACTAG 724  
DB 1914 CAAGGCTACATCAAAAAGAAATGGATAAAATAAGTGGAAAAATTAGAGATTCAACTAG 1973  
QY 725 CCTATCAAAAATCTTGGATACAGTTCACTTCTTGTGAAGAGCAAGGAACTTCAAAAAGA 784  
DB 1974 CCTATCAAAAATCTTGGATACAGTTCACTTCTTGTGAAGAGCAAGGAACTTCAAAAAGA 2033  
QY 785 TCACCTGTGAACAACAGTACAGAAAAATGGAAACAAATGAAAAAGAAAGTTTGTGTACTGAA 844  
DB 2034 TCACCTGTGAACAACAGTACAGAAAAATGGAAACAAATGAAAAAGAAAGTTTGTGTACTGAA 2093  
QY 845 AAAGAACTGTGAGAGCAAAAGAAATAAATACAGTTAGAGAACCAAAAAGCTTAAATG 904  
DB 2094 AAAGAACTGTGAGAGCAAAAGAAATAAATACAGTTAGAGAACCAAAAAGCTTAAATG 2153  
QY 905 GGAAACAGAGCTCTGCACTGTGAGATTGACCTTTAAACCAAGAGAGAGAGAGAGAA 964  
DB 2154 GGAAACAGAGCTCTGCACTGTGAGATTGACCTTTAAACCAAGAGAGAGAGAGAA 2213  
QY 965 TGCCGATATATAATGAAAAATTTAGGGAAGAAATTAGGAAGAAATCGAAGAGCAGCTAG 1024  
DB 2214 TGCCGATATATAATGAAAAATTTAGGGAAGAAATTAGGAAGAAATCGAAGAGCAGCTAG 2273  
QY 1025 GAAAGAGTTAGAGTGAAACCAACCAACTTGAACAGGCTCTCAGAAATCAAGATATAGAAAT 1084  
DB 2274 GAAAGAGTTAGAGTGAAACCAACCAACTTGAACAGGCTCTCAGAAATCAAGATATAGAAAT 2333  
QY 1085 GAAGAGTGTAGAAAGTAAATTTGAAATCAGGTTTCTCACTCATGAAATGAAATTTATCT 1144  
DB 2334 GAAGAGTGTAGAAAGTAAATTTGAAATCAGGTTTCTCACTCATGAAATGAAATTTATCT 2393  
QY 1145 CTTACATCAAAATTCATGTTTGAAGAAAGGAAATTCCTGAACTGAACTGGAATATAGCCAC 1204  
DB 2394 CTTACATCAAAATTCATGTTTGAAGAAAGGAAATTCCTGAACTGAACTGGAATATAGCCAC 2453  
QY 1205 ACTGAAACCAACCACTACAGGAAAAAGGAAATTAATATCTTTGAGACATTAAGATTAAAA 1264  
DB 2454 ACTGAAACCAACCACTACAGGAAAAAGGAAATTAATATCTTTGAGACATTAAGATTAAAA 2513  
QY 1265 AGAAAGAAATGCTGAATCTCAGATGACCCCTAAATGAAAGAGAAATCATTAATCTAAAG 1324  
DB 2514 AGAAAGAAATGCTGAATCTCAGATGACCCCTAAATGAAAGAGAAATCATTAATCTAAAG 2573  
QY 1325 GGCATCTCAATATAGTGGGAGCTTAAAGTTCTGATAGCTGAGAACCAATGCTCACTTC 1384  
DB 2574 GGCATCTCAATATAGTGGGAGCTTAAAGTTCTGATAGCTGAGAACCAATGCTCACTTC 2633  
QY 1385 TAAATTTGAAGGAAAAACAGACAAAGAAATTAAGAGGCAAGAAATGGAATCACCATTCC 1444  
DB 2634 TAAATTTGAAGGAAAAACAGACAAAGAAATTAAGAGGCAAGAAATGGAATCACCATTCC 2693  
QY 1445 TAGACTGGCTTCTGCTGTACAGACCATGATCAAAATTTGTGATCATCAAGAAAAAGTCAAGA 1504  
DB 2694 TAGACTGGCTTCTGCTGTACAGACCATGATCAAAATTTGTGATCATCAAGAAAAAGTCAAGA 2753  
QY 1505 ACTGCTTTCCACATTTGAGAGAGTCTGTTTGAAGAAAGAAATGAAATGTTGATGTGAG 1564  
DB 2754 ACTGCTTTCCACATTTGAGAGAGTCTGTTTGAAGAAAGAAATGAAATGTTGATGTGAG 2813  
QY 1565 TAGTACCGATATATAAATGAGGCTCCATCAACCACTTTCTGAAGCTCAAGGAAAT 1624  
DB 2814 TAGTA-CGATATATAAATGAGGCTCCATCAACCACTTTCTGAAGCTCAAGGAAAT 2872  
QY 1625 CCNAAAGCCTAAAAATTTAATCTCAATTTATGAGGAGATGCTCTAGAGAAATATCAATGG 1684  
DB 2873 CCNAAAGCCTAAAAATTTAATCTCAATTTATGCGGAGATGCTCTTAAGAGAAATATCAATGG 2932  
QY 1685 TTTTCAGGAACTGCAAAAAGAGACCAACGTGAAAAACACAGTGTCAATGAAGAGAGCTGAA 1744  
DB 2933 TTTTCA-GAATCTGCAAAAAGAGACCAACGTGAAAAACACAGTGTCAATGAAGAGAGCTGAA 2991  
QY 1745 CACATGTTCAAAACGAAACAAAGATNATGTGAACAAACACACCTGANCAGCAGAGTCTCTA 1804

Db	2992	CACATGATCAAAAGCAGACAGATATGTGAACACACACTGAACAGCAGGAGTCTCTA	3051
Qy	1805	GATCAGAAATATTTCCTAATCAAAAGCAAAATATATGGCTTCAACAGCAATAGTTTCAT	1864
Db	3052	GATCAGAAATATTTCCTAATCAAAAGCAAAATATATGGCTTCAACAGCAATAGTTTCAT	3111
Qy	1865	GCACATAANGAAAGCTGACACAAAGCAAGATACAAATTTGATNTTCATTNTCTTGAGAG	1924
Db	3112	GCACATAA-GAAAGCTGACACAAAGCAAGATACAAATTTGATNTTCATTNTCTTGAGAG	3170
Qy	1925	GAAATGC-NCATCATCTTCTTAAAGAGAAATATGAGGAGATATTNNATTACMNATACCA	1983
Db	3171	GAAATGCACATCATCTCTCTTAAAGAGAAATATGAGGAGATATTNNATTACMNATACCA	3230
Qy	1984	TTTAAAAAACCCTGATATTTCATATGCAAAAAAATAAATAAATAAATAAATAAATAAATAA	2030
Db	3231	TTTAAAAA-CCGTATATATCATATGAAAAAGAGAAAGCAGAAACA	3276
RESULT 8			
ABT33234			
ID	ABT33234	standard; DNA; 3288 BP.	
XX	XX	ABT33234;	
AC	15-MAY-2003	(first entry)	
DT	Human tumour-related DNA sequence - SEQ ID NO 490.		
DE	Human; ds; vaccine; gene therapy; T cell stimulation; T cell expansion;		
KW	tumour; breast cancer; cancer; immune response stimulation.		
XX	Homo sapiens.		
OS	WO200283956-A1.		
PN	24-OCT-2002.		
PD	15-APR-2002; 2002WO-US012378.		
FF	13-APR-2001; 2001US-00834759.		
XX	07-DEC-2001; 2001US-00007805.		
PR	13-FEB-2002; 2002US-00076622.		
XX	(CORI-) CORIXA CORP.		
PA	Houghton RL, Sleath PR, Persing DH, Jiang Y, Dillon DC;		
XX	Mitcham JL, Xu J, Harlocker SL, Hepler WT, Henderson RA, Fanger GR;		
PI	Vedwick TS, McNeill PD, Durham M;		
PI	WPI; 2003-103376/09.		
XX	New polypeptide and polynucleotide useful for stimulating and/or		
XX	expanding T cells specific for a tumor protein and treating breast		
PT	cancer.		
PT	Disclosure; Page 307-308; 375pp; English.		
XX	The invention comprises a method of stimulating and/or expanding T cells		
XX	specific for a tumour protein. The invention further comprises human		
CC	nucleic acids and proteins that are associated with tumours (e.g. breast		
CC	cancer). The method and sequences of the invention are useful for		
CC	stimulating and/or expanding T cells specific for a tumour protein,		
CC	detecting the presence of cancer, stimulating an immune response in a		
CC	patient and treating breast cancer. The present DNA sequence represents a		
CC	human tumour-related DNA sequence		
XX	Sequence 3288 BP; 1293 A; 564 C; 664 G; 761 T; 0 U; 6 Other;		
XX	Query Match 95.5%; Score 1938.4; DB 7; Length 3288;		
XX	Best Local Similarity 98.5%; Pred. NO. 0;		
XX	Matches 1997; Conservative 4; Mismatches 21; Indels 5; Gaps 5;		

Qy	5	TGCGTTAAAGATGGTCTTCTGAGGCTAACTGCGGAATGAAAGTTCTTATTCCAACTAA	64
Db	1254	TCTGTTAAAGATGGTCTTCTGAGGCTAACTGCGGAATGAAAGTTCTTATTCCAACTAA	1313
Qy	65	AGCCTTAGAATTTGATGACATGCAAACTTTCAAGCAGAGCCTCCGAGAGCCATCTGC	124
Db	1314	AGCCTTAGAATTTGATGACATGCAAACTTTCAAGCAGAGCCTCCGAGAGCCATCTGC	1373
Qy	125	CTTCGAGCCTCCATTTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATGAAGAA	184
Db	1374	CTTCGAGCCTCCATTTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATGAAGAA	1433
Qy	185	TGAACAAACATTTGAGAGCAGATGAGATACTCCCATCAAGATCCAAACAAAGAGCATGA	244
Db	1434	TGAACAAACATTTGAGAGCAGATGAGATACTCCCATCAAGATCCAAACAAAGAGCATGA	1493
Qy	245	AGAAAGTTCTTGGGATTTCTGAGAGTCTCTGTGAGACTGTTTTCACAGAGGAGTGTGTT	304
Db	1494	AGAAAGTTCTTGGGATTTCTGAGAGTCTCTGTGAGACTGTTTTCACAGAGGAGTGTGTT	1553
Qy	305	ACCCAAGGCTACATCAAAAGAAATAGATAAAATAAATGAAATTTAGAAAGTCTCC	364
Db	1554	ACCCAAGGCTACATCAAAAGAAATAGATAAAATAAATGAAATTTAGAAAGTCTCC	1613
Qy	365	TGATAATGATGGTCTTCTGAGGCTCCCTGAGAGTGAAGTCTTCTTATTCAACTAAGC	424
Db	1614	TGATAATGATGGTCTTCTGAGGCTCCCTGAGAGTGAAGTCTTCTTATTCAACTAAGC	1673
Qy	425	CTTAGAATTTGATGACATGCAAACTTTTCAAGCAGAGCCTCCGAGAGCCATCTGCCT	484
Db	1674	CTTAGAATTTGATGACATGCAAACTTTTCAAGCAGAGCCTCCGAGAGCCATCTGCCT	1733
Qy	485	CGAGCCTCCATTTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATGAAGAA	544
Db	1734	CGAGCCTCCATTTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATGAAGAA	1793
Qy	545	ACAAACATTTGAGAGCAGATCAGATGTTCCCTTCAAGATCAAAACAAAGAGGTTGAAGA	604
Db	1794	ACAAACATTTGAGAGCAGATCAGATGTTCCCTTCAAGATCAAAACAAAGAGGTTGAAGA	1853
Qy	605	AAATCTTGGGATTTCTGAGAGTCTCCGTGAGACTGTTTTCACAGAGGAGTGTGTGTACC	664
Db	1854	AAATCTTGGGATTTCTGAGAGTCTCCGTGAGACTGTTTTCACAGAGGAGTGTGTGTACC	1913
Qy	665	CAAGGCTACATCAAAAGAAATGGAATAAATAGTGGAAATTTAGAAAGTTCACCTAG	724
Db	1914	CAAGGCTACATCAAAAGAAATGGAATAAATAGTGGAAATTTAGAAAGTTCACCTAG	1973
Qy	725	CCTATCAAAATCTTTGGATACAGTTCATTTCTTGTGAAAGCAAGGGAACCTTCAAAAAGA	784
Db	1974	CCTATCAAAATCTTTGGATACAGTTCATTTCTTGTGAAAGCAAGGGAACCTTCAAAAAGA	2033
Qy	785	TCACCTGTAACAACTGACGAAATGGAACAAATGGAACAAATGGAACAAATGGAACAAAT	844
Db	2034	TCACCTGTAACAACTGACGAAATGGAACAAATGGAACAAATGGAACAAATGGAACAAAT	2093
Qy	845	AAAGAACTGTGCAAGCAAAAGAAATAAATCAAGTTAGAGAACCAAAAAGTTAAATG	904
Db	2094	AAAGAACTGTGCAAGCAAAAGAAATAAATCAAGTTAGAGAACCAAAAAGTTAAATG	2153
Qy	905	GGAAACAGAGCTCTCAGTGTGAGATTCGACTTAAACCAAGAGAGAGAGAGAGAGAA	964
Db	2154	GGAAACAGAGCTCTCAGTGTGAGATTCGACTTAAACCAAGAGAGAGAGAGAGAGAA	2213
Qy	965	TGCCGATATTTAAATGAAAAAATTTAGGAAAGAAATTTAGGAAAGAAATTTAGGAAAG	1024
Db	2214	TGCCGATATTTAAATGAAAAAATTTAGGAAAGAAATTTAGGAAAGAAATTTAGGAAAG	2273
Qy	1025	GAAAGGTTAGAGTGAAGCAACAACTTGAACAGGCTCTCAGATACAGATATAGATTT	1084
Db	2274	GAAAGGTTAGAGTGAAGCAACAACTTGAACAGGCTCTCAGATACAGATATAGATTT	2333

QY	1085	GAAGAGTGTAGAAGTAATTTGAAATCAGGTTCTCAGACTCATGAAATGAAATTTATCT	1144
DB	2334	GAAGAGTGTAGAAGTAATTTGAAATCAGGTTCTCAGACTCATGAAATGAAATTTATCT	2393
QY	1145	CTTACATGAAATTTGATGTTGAAAGGAAATTTGCCATGCTAAACTGGAATAGCCAC	1204
DB	2394	CTTACATGAAATTTGATGTTGAAAGGAAATTTGCCATGCTAAACTGGAATAGCCAC	2453
QY	1205	ACTGAAACACCAATACAGGAAAGGAAATTAATTTGAGGACATTAAGATTTTAA	1264
DB	2454	ACTGAAACACCAATACAGGAAAGGAAATTAATTTGAGGACATTAAGATTTTAA	2513
QY	1265	AGAAAGAAATGCTGAACTTCAGATGACCTTAAACTGAAAGAGGAATTAATTAAC	1324
DB	2514	AGAAAGAAATGCTGAACTTCAGATGACCTTAAACTGAAAGAGGAATTAATTAAC	2573
QY	1325	GGCATCTCAATATAGTGGGAGCTTAAAGTTCTGATAGCTGAGAACACATGCTC	1384
DB	2574	GGCATCTCAATATAGTGGGAGCTTAAAGTTCTGATAGCTGAGAACACATGCTC	2633
QY	1385	TAAATTCAGGAAACCAAGCAAGAAATACCTAGAGGAGAAATGAATCACACATCC	1444
DB	2634	TAAATTCAGGAAACCAAGCAAGAAATACCTAGAGGAGAAATGAATCACACATCC	2693
QY	1445	TAGACTGGCTTCTGCTGACAGACCATGATCAAAATTTGACATCAAGAAAAGTCA	1504
DB	2694	TAGACTGGCTTCTGCTGACAGACCATGATCAAAATTTGACATCAAGAAAAGTCA	2753
QY	1505	ACCTGCTTCCATGTCAGAGATGCTGTTGTCAGGAAATGAATGATGATGAG	1564
DB	2754	ACCTGCTTCCATGTCAGAGATGCTGTTGTCAGGAAATGAATGATGATGAG	2813
QY	1565	TAGTACCGATATATACAAATGAGTGTCCATCAACATTTCTGAAGCTCAAGGAAT	1624
DB	2814	TAGTACCGATATATACAAATGAGTGTCCATCAACATTTCTGAAGCTCAAGGAAT	2872
QY	1625	CCAAAGCCTTAAATTAATCTCAATTTATGTCAGGAGATGCTTAAGAGAAATACAT	1684
DB	2873	CCAAAGCCTTAAATTAATCTCAATTTATGTCAGGAGATGCTTAAGAGAAATACAT	2932
QY	1685	TTTCAGGAACATGACAAAGAGACCAAGCTGAAACACAGTGTCAAATGAAGGAAG	1744
DB	2933	TTTCAGGAACATGACAAAGAGACCAAGCTGAAACACAGTGTCAAATGAAGGAAG	2991
QY	1745	CACATGTTCAANGAACACAGATTAATGTAACAAACACACTGACAGAGGAGTCTCT	1804
DB	2992	CACATGTTCAANGAACACAGATTAATGTAACAAACACACTGACAGAGGAGTCTCT	3051
QY	1805	GATCAGAAATTTATTTCAACTACAAAGCAAAATATGTTGCTTCAACAGCAATTA	1864
DB	3052	GATCAGAAATTTATTTCAACTACAAAGCAAAATATGTTGCTTCAACAGCAATTA	3111
QY	1865	GCACATTAANGAAGCTGACACAAAGCAAGATTAATGTAATTTTCAATTTCTGAG	1924
DB	3112	GCACATTAANGAAGCTGACACAAAGCAAGATTAATGTAATTTTCAATTTCTGAG	3170
QY	1925	GAATATGC-NCATCATCTTTTAAAGAGAAATGAGGAGATTTTATTAACNATAAC	1983
DB	3171	GAATATGC-NCATCATCTTTTAAAGAGAAATGAGGAGATTTTATTAACNATAAC	3230
QY	1984	TTTTAAAAACCGTATTTTCAATGAGAAATTAATTAATTAATTAATTAATTAAT	2030
DB	3231	TTTTAAAAACCGTATTTTCAATGAGAAATTAATTAATTAATTAATTAATTAAT	3276
RESULT 9			
AAS47411			
ID	AAS47411 standard; cDNA; 3865 BP.		
XX			
AC	AAS47411;		
XX			
DT	18-DEC-2001 (first entry)		
XX			

Human cDNA encoding breast cancer protein B726P alternative splice form.  
Human; ss; breast cancer protein; tumour; cancer; cytostatic;  
gene therapy.  
Homo sapiens.  
WO200179286-A2.  
25-OCT-2001.  
12-APR-2001; 2001WO-US012164.  
17-APR-2000; 2000US-00551621.  
08-JUN-2000; 2000US-00590751.  
22-JUN-2000; 2000US-00604287.  
20-JUL-2000; 2000US-00620405.  
(CORI-) CORIXA CORP.  
Jiang Y, Dillon DC, Mitcham JL, Xu J, Harlocker SL, Hepler WT;  
WPI; 2001-611721/70.  
P-PSDB; AAU33351.  
Breast Tumor Proteins and nucleic acids useful for the prevention,  
diagnosis and treatment of breast cancer.  
Claim 1; Page 280-281; 297pp; English.  
The invention relates to isolated breast tumour proteins and nucleic  
acids that encode them, including immunogenic fragments of the proteins.  
Also included are expression vectors expressing the proteins, transformed  
cells and antibodies raised against the proteins or an antigen presenting  
cell expressing the protein. The proteins and nucleic acids may be used  
in the prevention, diagnosis and treatment of diseases associated with  
inappropriate breast tumour protein expression, i.e. breast tumours and  
breast cancer e.g by gene therapy. The nucleic acids and their  
complements may also be used as DNA probes in diagnostic assays to detect  
and quantitate the presence of similar nucleic acids in samples, and  
therefore which patients may be in need of restorative therapy. The  
proteins, nucleic acids and antibodies may be used in assays to identify  
modulators (e.g. antagonists) of breast tumour protein expression and  
activity. The antibodies and antagonists may also be used to down  
regulate expression and activity. The antibodies may also be used as  
diagnostic agents for detecting the presence of the proteins in samples  
(e.g. by enzyme linked immunosorbent assay (ELISA)) and in other immuno-  
purification diagnostic techniques. The present sequence is a cDNA from a  
breast tumour cDNA library isolated by subtractive hybridisation against  
a normal breast cDNA library and encodes a breast tumour protein of the  
invention. The present sequence is also a splice variant  
Sequence 3865 BP; 1499 A; 697 C; 801 G; 862 T; 0 U; 6 Other;  
Query Match 95.5%; Score 1938.4; DB 4; Length 3865;  
Best Local Similarity 98.5%; Pred. No. 0;  
Matches 1997; Conservative 4; Mismatches 21; Indels 5; Gaps 5;  
QY 5 TGCCCTTAAGATGCTCTTCTGAAGCTTAACCTGCGAATGAAGTTCTTATTCACATAA 64  
DB 1526 TCCTGTTAAGATGCTCTTCTGAAGCTTAACCTGCGAATGAAGTTCTTATTCACATAA 1585  
QY 65 AGCCTTAGAATTCATGACATGCAACTTCAACAGAGCTCCCGAGAGCCATCTGC 124  
DB 1586 AGCCTTAGAATTCATGACATGCAACTTCAACAGAGCTCCCGAGAGCCATCTGC 1645  
QY 125 CTTGAGAGCTGCCATTTGAAATGAAATGCTGTTCCAAATAAAGCTTTGGAATGAAGAA 184  
DB 1646 CTTGAGAGCTGCCATTTGAAATGAAATGCTGTTCCAAATAAAGCTTTGGAATGAAGAA 1705  
QY 185 TGAACAAAATTTGAGAGCAGATGAGATCTCCATCAGATCCCAACAAAAGCATATGA 244  
DB 1706 TGAACAAAATTTGAGAGCAGATGAGATCTCCATCAGATCCCAACAAAAGCATATGA 1765



Qy	245	AGAAAGTTCTTGGGATTTCTGAGAGTCTCTGTGAGACTGTTTTCACAGAGGATGTGTGTTT	304
Db	1766	AGAAAGTTCTTGGGATTTCTGAGAGTCTCTGTGAGACTGTTTTCACAGAGGATGTGTGTTT	1825
Qy	305	ACCCAAGGCTACACATCAAAAAGAAATAGATATAAATAAATGGAATTTAGAGAGTCTCC	364
Db	1826	ACCCAAGGCTACATCAAAAAGAAATAGATATAAATAAATGGAATTTAGAGAGTCTCC	1885
Qy	365	TGATATGATGGTTTCTGGAAGCTCCCTCGAAGTGAAGATTTCTATTCCAACTAAAGC	424
Db	1886	TGATATGATGGTTTCTGGAAGCTCCCTCGAAGTGAAGATTTCTATTCCAACTAAAGC	1945
Qy	425	CTTAGAATTCATGGACATGCAAACTTTCAAAGCAGAGCTCCGAGAGCCATCTCCCTT	484
Db	1946	CTTAGAATTCATGGACATGCAAACTTTCAAAGCAGAGCTCCGAGAGCCATCTCCCTT	2005
Qy	485	CGAGCTGCCATTGAATGCAAAAGTCTGTTCCAAATAAGCCCTCGAATTTGAAGATGA	544
Db	2006	CGAGCTGCCATTGAATGCAAAAGTCTGTTCCAAATAAGCCCTCGAATTTGAAGATGA	2065
Qy	545	ACAAACATTCAGAGCAGATCAGATGTTTCCCTTCAGAAATCAAAAACAAAGAGGTTGAAGA	604
Db	2066	ACAAACATTCAGAGCAGATCAGATGTTTCCCTTCAGAAATCAAAAACAAAGAGGTTGAAGA	2125
Qy	605	AAATTCCTGGGATTCGAGAGTCTCGTGAGACTGTTTACAGAGGATGTGTGTACC	664
Db	2126	AAATTCCTGGGATTCGAGAGTCTCGTGAGACTGTTTACAGAGGATGTGTGTACC	2185
Qy	665	CAAGGCTACACATCAAAAAGAAATGGATATAAATAAGTGGAATAATAGAGATTCAACTAG	724
Db	2186	CAAGGCTACACATCAAAAAGAAATGGATATAAATAAGTGGAATAATAGAGATTCAACTAG	2245
Qy	725	CCTATCAAAAATCTTGGATACAGTTTCATCTTGTGAAAGAGCAAGGGAATTCAAAAGA	784
Db	2246	CCTATCAAAAATCTTGGATACAGTTTCATCTTGTGAAAGAGCAAGGGAATTCAAAAGA	2305
Qy	785	TCACCTGTGAACAACGTCAGGAAATAATGGAACAAATGAAAAGAGTTTGTGTACTGAA	844
Db	2306	TCACCTGTGAACAACGTCAGGAAATAATGGAACAAATGAAAAGAGTTTGTGTACTGAA	2365
Qy	845	AAAGAAACTGTGAGAACAAAGAAATAAATCAAGTTAGAGAACCAAAAAGTTTAAATG	904
Db	2366	AAAGAAACTGTGAGAACAAAGAAATAAATCAAGTTAGAGAACCAAAAAGTTTAAATG	2425
Qy	905	GGAACAGAGCTCTGCAGTGTGACATTCGCTTTAAACCAAGAGAGAGAGAGAGAGAA	964
Db	2426	GGAACAGAGCTCTGCAGTGTGACATTCGCTTTAAACCAAGAGAGAGAGAGAGAGAA	2485
Qy	965	TGCCGATATATTAATGAAAAATTTAGGAGAAATAGGAAGATTCGAAGAGCAGCATAG	1024
Db	2486	TGCCGATATATTAATGAAAAATTTAGGAGAAATAGGAAGATTCGAAGAGCAGCATAG	2545
Qy	1025	GAAAGAGTTAGAGTGAACCAACACTTGAACAGGCTCTCAGATATCAAGATATAGNATT	1084
Db	2546	GAAAGAGTTAGAGTGAACCAACACTTGAACAGGCTCTCAGATATCAAGATATAGNATT	2605
Qy	1085	GAAGAGTCTAGAAAGTAAATTTGAATCAGGTTTCTCACACTCATGAAAATGAAAATTTATCT	1144
Db	2606	GAAGAGTCTAGAAAGTAAATTTGAATCAGGTTTCTCACACTCATGAAAATGAAAATTTATCT	2665
Qy	1145	CTTACATGAAAATTTGCATGTTGAAAAAGGAAATTCGATGCTAAAACCTGGAATATGCCAC	1204
Db	2666	CTTACATGAAAATTTGCATGTTGAAAAAGGAAATTCGATGCTAAAACCTGGAATATGCCAC	2725
Qy	1205	ACTGAAACCAATACACAGGAAAAAGGAAAAATAAATACTTTTCAGGACATTAAGATTTTAAA	1264
Db	2726	ACTGAAACCAATACACAGGAAAAAGGAAAAATAAATACTTTTCAGGACATTAAGATTTTAAA	2785
Qy	1265	AGAAAAGAAATGCTGAACCTTCAGATGACCTTAAAACTGAAAGAGGAATCATTAACATAAAG	1324
Db	2786	AGAAAAGAAATGCTGAACCTTCAGATGACCTTAAAACTGAAAGAGGAATCATTAACATAAAG	2845

Qy	1325	GGCATCTCAATATAGTGGGAGCTTTAAAGTTCTGTAGTGTGAGAAACAATGCTCACTTC	1384
Db	2846	GGCATCTCAATATAGTGGGAGCTTTAAAGTTCTGTAGTGTGAGAAACAATGCTCACTTC	2905
Qy	1385	TAAATTGAAGGAAACACAGACAAAGAAATACCTAGAGGCGAGAAATTCATCACACCATCC	1444
Db	2906	TAAATTGAAGGAAACAAAGACAAAGAAATACCTAGAGGCGAGAAATTCATCACACCATCC	2965
Qy	1445	TAGACTGGCTTCTGCTGTACAAGACCATGATCAAAATTTGTGCATCAAGAAAAAGTCAAGA	1504
Db	2966	TAGACTGGCTTCTGCTGTACAAGACCATGATCAAAATTTGTGCATCAAGAAAAAGTCAAGA	3025
Qy	1505	ACCTGCTTCCACATTCGAGGAGATGCTGTTTGCAGAGGAAATGAATGATCTGATGTGAG	1564
Db	3026	ACCTGCTTCCACATTCGAGGAGATGCTGTTTGCAGAGGAAATGAATGATCTGATGTGAG	3085
Qy	1565	TAGTACCGATATATAACAATACAGGTGCTCCATCAACACACTTCTTGAAGCTCAAGAGGAAT	1624
Db	3086	TAGTA-CGATATATAACAATACAGGTGCTCCATCAACACACTTCTTGAAGCTCAAGAGGAAT	3144
Qy	1625	CCAAAGCCTAAATAATTAATCTCAATTCGAGGAGATGCTCTTAAGGAAATACATTTGG	1684
Db	3145	CCAAAGCCTAAATAATTAATCTCAATTCGAGGAGATGCTCTTAAGGAAATACATTTGG	3204
Qy	1685	TTTCAGGAACATGACACAAAGAGACCAACGCTGAAACACAGTCTCAAAATGAAAGGAGCTGAA	1744
Db	3205	TTTCA-GAAATGACACAAAGAGACCAACGCTGAAACACAGTCTCAAAATGAAAGGAGCTGAA	3263
Qy	1745	CACATGNTCAAANCAGAACCAAGATNATGTGAAACAAACACACTGANCAGCAGGAGTCTCTA	1804
Db	3264	CACATGNTCAAANCAGAACCAAGATNATGTGAAACAAACACACTGANCAGCAGGAGTCTCTA	3323
Qy	1805	GATCAGAAATTTATTTCAACTACAAAGCAAAATATATGTGGCTTCAACACAGCAATTAGTTTCAT	1864
Db	3324	GATCAGAAATTTATTTCAACTACAAAGCAAAATATATGTGGCTTCAACACAGCAATTAGTTTCAT	3383
Qy	1865	GCAATTAANGAAAGCTGACAAACAAAGCAAGATTAACAAATTCATNTTCTTGAGAG	1924
Db	3384	GCAATAA-GAAAGCTGACAAACAAAGCAAGATTAACAAATTCATNTTCTTGAGAG	3442
Qy	1925	GAAATGC-NCATCATCTCTCTTAAAGAGAAAAATGAGGAGATATTTNATTACNATAACCA	1983
Db	3443	GAAATGCACATCATCTCTCTTAAAGAGAAAAATGAGGAGATATTTNATTACNATAACCA	3502
Qy	1984	TTTTAAAAACCCCGTATATTTCAATATATGAAAAAATAAAAAA	2030
Db	3503	TTTTAAAAA-CCGTATATATCAATATGAAAAAGAAAAAGCAGAAACA	3548
RESULT 10			
ABS64012			
ID	ABS64012	standard; cDNA; 3865 BP.	
XX	AC	ABS64012;	
XX	DT	15-NOV-2002 (first entry)	
XX	DE	Human breast tumour polynucleotide #464.	
XX	DE	Human breast tumour protein; gene; ss; breast cancer; cytostatic;	
XX	KW	Human; breast tumour vaccine.	
XX	OS	Homo sapiens.	
XX	XX	US2002085998-A1.	
XX	PN	04-JUL-2002.	
XX	PD	13-APR-2001; 2001US-00834759.	
XX	PF	28-DEC-1998; 98US-00222575.	
XX	PR	02-APR-1999; 99US-00285480.	
XX	PR	23-JUN-1999; 99US-00339338.	

RESULT 10

ABS6401  
TD AB

ID ABS64012 standard; cDNA; 3865 BP.

AC ABS64012;

XX  
DT 15-NOV-2002 (first entry)

XX  
DE Human breast tumour polynucleotide #464.

XX  
KW Human: breast tumour protein; gene: ss: breast cancer; cytostatic;

KW vaccine.

XX  
OS  
Homo sapiens.

XX  
PN US2002085998-A1.

XX  
PD 04-JUL-2002.

XX  
PE 13-APR-2001: 2001HS-00834759

[illegible]

PR 28-DEC-1998; 98US-00222575.  
PR 02-APR-1999; 99US-00285480.

PR 23-JUN-1999; 99US-00339338.



PR 02-SEP-1999; 99US-00389681.  
PR 03-NOV-1999; 99US-00433826.  
PR 17-APR-2000; 2000US-00551621.  
PR 08-JUN-2000; 2000US-00590751.  
PR 22-JUN-2000; 2000US-00604287.  
PR 20-JUL-2000; 2000US-00620405.  
XX (CORI-) CORIXA CORP.  
FA  
XX Jiang Y, Dillon DC, Mitcham JL, Xu J, Harlocker SL, Hepler WT;  
PI Henderson RA;  
PI  
XX WPI; 2002-635657/68.  
DR P-PSDB; ABG78918.  
DR  
XX Novel breast cancer polynucleotides and polypeptides encoded by the  
PT polynucleotides, useful for detecting the presence of breast cancer in a  
PT patient, and in pharmaceutical compositions, for treating breast cancer.  
XX  
XX Claim 1; Page 207-208; 247pp; English.  
XX  
CC The invention relates to an isolated breast tumour polynucleotide and the  
CC polypeptide it encodes. The polynucleotide and polypeptide are useful for  
CC detecting the presence of breast cancer in a patient, and in  
CC pharmaceutical compositions for treating breast cancer. The sequences are  
CC useful for stimulating an immune response in a patient and can therefore  
CC be used in production of vaccines. The sequences are also useful for  
CC detecting the presence of a cancer in a patient, by obtaining a  
CC biological sample from the patient, contacting the biological sample with  
CC a composition of the invention and detecting the amount of polynucleotide  
CC that hybridizes to the sample. This sequence represents a human breast  
CC tumour polynucleotide of the invention  
XX  
SQ Sequence 3865 BP; 1499 A; 697 C; 801 G; 862 T; 0 U; 6 Other;  
Query Match 95.5%; Score 1938.4; DB 6; Length 3865;  
Best Local Similarity 98.5%; Pred No 0;  
Matches 1997; Conservative 4; Mismatches 21; Indels 5; Gaps 5;  
  
QY 5 TGGCGTTAAAGATGGTCTTCTGAAGGCTAACTCGGAATGAAAGTTTCTATTCCAACTAA 1585  
DB 1526 TCCTGTTAAAGATGGTCTTCTGAAGGCTAACTCGGAATGAAAGTTTCTATTCCAACTAA 1585  
QY 65 AGCCTTAGAATGATGACATGCAACTTTCAAGCAGAGCCCTCCGAGAGCCATCTCG 124  
DB 1586 AGCCTTAGAATGATGACATGCAACTTTCAAGCAGAGCCCTCCGAGAGCCATCTCG 1645  
QY 125 CTTGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATTAAGCCCTTGGAAATGAAGAA 184  
DB 1646 CTTGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATTAAGCCCTTGGAAATGAAGAA 1705  
QY 185 TGAACAAACATTGAGACAGATGAGATCTCCCATGAGATCCAAACAAAGGACTATGA 244  
DB 1706 TGAACAAACATTGAGACAGATGAGATCTCCCATGAGATCCAAACAAAGGACTATGA 1765  
QY 245 AGAAAGTTCTTGGGATCTTGAGAGTCTCTGTGAGCTGTTTTCACAGAGGATGTGTGTTT 304  
DB 1766 AGAAAGTTCTTGGGATCTTGAGAGTCTCTGTGAGCTGTTTTCACAGAGGATGTGTGTTT 1825  
QY 305 ACCCAAGGCTACATCAAAAAGAAATAGATAAATAAATGAAATTAAGAGAGTCTCC 364  
DB 1826 ACCCAAGGCTACATCAAAAAGAAATAGATAAATAAATGAAATTAAGAGAGTCTCC 1885  
QY 365 TGATAATGATGTTTCTGAAAGGCTCCCTGAGAGTGAAGTTTCTATTCCAACTAAAGC 424  
DB 1886 TGAATAATGATGTTTCTGAAAGGCTCCCTGAGAGTGAAGTTTCTATTCCAACTAAAGC 1945  
QY 425 CTTAGAAATGATGACATGCAAACTTTCAAGCAGAGCCCTCCGAGAGCCATCTGCTTT 484  
DB 1946 CTTAGAAATGATGACATGCAAACTTTCAAGCAGAGCCCTCCGAGAGCCATCTGCTTT 2005  
QY 485 CGAGCCTCCCAATGAAATGCAAAAGTCTGTTCCAAATTAAGCCCTTGGAAATGAAGATGA 544

DB 2006 CGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATTAAGCCCTTGGAAATGAAGATGA 2065  
QY 545 ACAAACATTGAGAGCAGATCAGATGTTCCCTTCAGAAATCAAAACAAAGAGGTTGAAGA 604  
DB 2066 ACAAACATTGAGAGCAGATCAGATGTTCCCTTCAGAAATCAAAACAAAGAGGTTGAAGA 2125  
QY 605 AAATTTCTTGGGATCTGAGAGTCTCGGTGAGACTGTTTTCACAGAGGATGTGTGTACC 664  
DB 2126 AAATTTCTTGGGATCTGAGAGTCTCGGTGAGACTGTTTTCACAGAGGATGTGTGTACC 2185  
QY 665 CAAGGCTACACATCAAAAAGAAATGATAAATAAGTGGAAATTAAGAGATCAACTAG 724  
DB 2186 CAAGGCTACACATCAAAAAGAAATGATAAATAAGTGGAAATTAAGAGATCAACTAG 2245  
QY 725 CCTATCAAAAATCTTGGATACAGTTCATTTCTGTAAGAGCAAGGGAATCTTCAAAAAGA 784  
DB 2246 CCTATCAAAAATCTTGGATACAGTTCATTTCTGTAAGAGCAAGGGAATCTTCAAAAAGA 2305  
QY 785 TCACGTGGAACAACGTACAGGAAAAATGGAACAAATGAAAAAGAGTTTTGTGTACTGAA 844  
DB 2306 TCACGTGGAACAACGTACAGGAAAAATGGAACAAATGAAAAAGAGTTTTGTGTACTGAA 2365  
QY 845 AAGAAACTCTCAGAGCAAAAGAAATAAATCACAGTTTAGAGAACCAAAAAGTTAAATG 904  
DB 2366 AAGAAACTCTCAGAGCAAAAGAAATAAATCACAGTTTAGAGAACCAAAAAGTTAAATG 2425  
QY 905 GGAACAAGAGCTCTGAGTGTGAGTGTGATTTAAACCAAGAGAGAGAGAGAGAGAAA 964  
DB 2426 GGAACAAGAGCTCTGAGTGTGAGTGTGATTTAAACCAAGAGAGAGAGAGAGAGAAA 2485  
QY 965 TGCCGATATATTAATGAAAAAATTAGGGAAGAAATAGGAAGAAATCGAAGAGCAGCATAG 1024  
DB 2486 TGCCGATATATTAATGAAAAAATTAGGGAAGAAATCGAAGAGCAGCATAG 2545  
QY 1025 GAAAGAGTTAGAGTGAAGCAACCACTTGAACAGGCTCTCAGAAATCAAGATATAGAAAT 1084  
DB 2546 GAAAGAGTTAGAGTGAAGCAACCACTTGAACAGGCTCTCAGAAATCAAGATATAGAAAT 2605  
QY 1085 GAAAGAGTTAGAGTGAAGCAACCACTTGAACAGGTTTCTCACACTCATGAAATGAAATATCT 1144  
DB 2606 GAAAGAGTTAGAGTGAAGCAACCACTTGAACAGGTTTCTCACACTCATGAAATGAAATATCT 2665  
QY 1145 CTTACATGAAAAATTCATGTTGAAAAAGGAAATTCGCATGCTAAAACTGGAATAGCCAC 1204  
DB 2666 CTTACATGAAAAATTCATGTTGAAAAAGGAAATTCGCATGCTAAAACTGGAATAGCCAC 2725  
QY 1205 ACTGAAACCAACATACCAAGGAAAGAAATAAATCTTTGAGACATTAAGATTTTAAA 1264  
DB 2726 ACTGAAACCAACATACCAAGGAAAGGAAATAAATACTTTGAGACATTAAGATTTTAAA 2785  
QY 1265 AGAAAGAAATCTGAACTTCAAGTGAACCTAAAACTGAAAGAGGAATCATTAACCTAAAG 1324  
DB 2786 AGAAAGAAATCTGAACTTCAAGTGAACCTAAAACTGAAAGAGGAATCATTAACCTAAAG 2845  
QY 1325 GGCATCTCAATATAGTGGGAGCTTAAAGTTCTGATAGCTGAGACACATGCTCACTTC 1384  
DB 2846 GGCATCTCAATATAGTGGGAGCTTAAAGTTCTGATAGCTGAGACACATGCTCACTTC 2905  
QY 1385 TAAATTTGAAGCAAAAAAACAAGCAAAAGAAATACTAGAGCGAGAAATTGAATCACCCTCC 1444  
DB 2906 TAAATTTGAAGCAAAAAAACAAGCAAAAGAAATACTAGAGCGAGAAATTGAATCACCCTCC 2965  
QY 1445 TAGACTGCTTCTGCTGTACAGACCATGATCAAAATTTGTGACATCAAGAAAAAGTCAAGA 1504  
DB 2966 TAGACTGCTTCTGCTGTACAGACCATGATCAAAATTTGTGACATCAAGAAAAAGTCAAGA 3025  
QY 1505 ACCTGCTTTTCCACATGTCAGGAGATGCTTGTGTCGAAAGAAAAAATGAATGTGTGTGAG 1564  
DB 3026 ACCTGCTTTTCCACATGTCAGGAGATGCTTGTGTCGAAAGAAAAAATGAATGTGTGTGAG 3085  
QY 1565 TAGTACCGATATATAAATGAGGTGCTCCATCAACCACTTTCTGAGCTCAAGAGAAAT 1624  
DB 3086 TAGTA -CGATATATAAATGAGGTGCTCCATCAACCACTTTCTGAGCTCAAGAGAAAT 3144



Db 2426 GGAACAAGAGCTCGCAGTGTGAGATTGACTTTAAACCAAGAGAGAGAGAGAGAA 2485  
Qy 965 TGCCGATATATTAATGAAAAAATAGGGAAGAAATAGGAAGAAATCGAAGAGCAGCATAG 1024  
Db 2486 TGCCGATATATTAATGAAAAAATAGGGAAGAAATAGGAAGAAATCGAAGAGCAGCATAG 2545  
Qy 1025 GAAAGAGTTAGAGTGAAGCAACAACTTGAACAGGCTCTCAGAAATCAAGATATAGATT 1084  
Db 2546 GAAAGAGTTAGAGTGAAGCAACAACTTGAACAGGCTCTCAGAAATCAAGATATAGATT 2605  
Qy 1085 GAAAGAGTTAGAGTGAAGCAACAACTTGAACAGGCTCTCAGAAATCAAGATATAGATT 1144  
Db 2606 GAAAGAGTTAGAGTGAAGCAACAACTTGAACAGGCTCTCAGAAATCAAGATATAGATT 2665  
Qy 1145 CTTACATGAAATGCAATGTTGAAAGAAAGAAATGCAATGCTTAAACTGGAATAGCCAC 1204  
Db 2666 CTTACATGAAATGCAATGTTGAAAGAAAGAAATGCAATGCTTAAACTGGAATAGCCAC 2725  
Qy 1205 ACTGAAACACCAATACAGGAAAGAAATTAATTAATTTGAGCAATTAAGATTTTAA 1264  
Db 2726 ACTGAAACACCAATACAGGAAAGAAATTAATTAATTTGAGCAATTAAGATTTTAA 2785  
Qy 1265 AGAAAGAAATGCTGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1324  
Db 2786 AGAAAGAAATGCTGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2845  
Qy 1325 GGCATCTCAATATAGTGGGAGCTTAAAGTTCTGATAGCTGAGAACACCAATGCTCACTTC 1384  
Db 2846 GGCATCTCAATATAGTGGGAGCTTAAAGTTCTGATAGCTGAGAACACCAATGCTCACTTC 2905  
Qy 1385 TAAATTGAAGAAACAAAGCAAGAAATGCTGAGGAGGAGAAATGCAATCAACCATCC 1444  
Db 2906 TAAATTGAAGAAACAAAGCAAGAAATGCTGAGGAGGAGAAATGCAATCAACCATCC 2965  
Qy 1445 TAGACTGGCTTCTGCTGACAGACCATGATCAATTTGTGACATCAAGAAAGTCAAGA 1504  
Db 2966 TAGACTGGCTTCTGCTGACAGACCATGATCAATTTGTGACATCAAGAAAGTCAAGA 3025  
Qy 1505 ACTGCTTTCCATGTCGAGAGAGTGTCTTTGCAAGAAAGAAATGAATGTTGATGTAG 1564  
Db 3026 ACTGCTTTCCATGTCGAGAGAGTGTCTTTGCAAGAAAGAAATGAATGTTGATGTAG 3085  
Qy 1565 TAGTACCGATATATAAATGAGTGTCTCCATCAACCCATTTCTGAGCTCAAGAGAAAT 1624  
Db 3086 TAGTATCGATATATAAATGAGTGTCTCCATCAACCCATTTCTGAGCTCAAGAGAAAT 3144  
Qy 1625 CCNAAAGCTTAAATTAATCTCAATATGACGAGATGCTTAAGAGAAATPACATTGG 1684  
Db 3145 CCAAAAGCTTAAATTAATCTCAATATGACGAGATGCTTAAGAGAAATPACATTGG 3204  
Qy 1685 TTTGAGGAGATGACAAAGAGCCACGTTGAACACAGTGTCAATGAGGAGCTGA 1744  
Db 3205 TTTCA-GAATGACAAAGAGCCACGTTGAACACAGTGTCAATGAGGAGCTGA 3263  
Qy 1745 CACATGNTCAAAACGAAAGATNATGTGAACAAACACACTGACGAGGAGTCTCTA 1804  
Db 3264 CACATGNTCAAAACGAAAGATNATGTGAACAAACACACTGACGAGGAGTCTCTA 3323  
Qy 1805 GATCAGAAATTTTCACTCAAGCAAAATATGTTGCTTCAAGCAATTTAGTTTAT 1864  
Db 3324 GATCAGAAATTTTCACTCAAGCAAAATATGTTGCTTCAAGCAATTTAGTTTAT 3383  
Qy 1865 GCACATGAAGAAAGCTGACACAAAGCAAGATATAAATTAATTTCAATTTCTTGAGAG 1924  
Db 3384 GCACATGAAGAAAGCTGACACAAAGCAAGATATAAATTAATTTCAATTTCTTGAGAG 3442  
Qy 1925 GAAATGTC-NCATCATCTTTTAAAGAGAAATATGAGGAGATATTTTATTAATCAACCA 1983  
Db 3443 GAAATGTC-NCATCATCTTTTAAAGAGAAATATGAGGAGATATTTTATTAATCAACCA 3502  
Qy 1984 TTTTAAAAACCGGTATATTTTCAATATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 2030  
Db 3503 TTTTAAAAACCGGTATATTTTCAATATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 3548

RESULT 12  
ADE44426  
ID ADE44426 standard; cDNA; 3865 BP.

AC ADE44426;  
XX 29-JAN-2004 (first entry)  
XX Human cDNA associated with breast cancer #464.

DE human; ss; gene; breast tumour; cancer; vaccine; T cell stimulator;  
KW T cell expander.  
XX Homo sapiens.

OS Homo sapiens.  
XX US2003104366-A1.  
XX 05-JUN-2003.

XX 17-APR-2000; 2000US-00551621.  
XX 28-DEC-1998; 98US-0022575.  
XX 02-APR-1999; 99US-00285480.

XX 23-JUN-1999; 99US-00339338.  
XX 02-SEP-1999; 99US-00389681.  
XX 03-NOV-1999; 99US-00433826.

XX (JIAN/) JIANG Y.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (XUJ/) XU J.  
PA (HARL/) HARLOCKER S L.

Jiang Y, Dillon DC, Mitcham JL, Xu J, Harlocker SL;  
WPI: 2004-020270/02.  
P-PSDB; ADE44427.

Novel isolated polypeptide comprising immunogenic portion of breast tumor protein or its variant, useful for formulating vaccines for inhibiting cancer development in a patient.

Claim 5; SEQ ID NO 474; 217bp; English.

The invention relates to an isolated polypeptide comprising at least an immunogenic portion of a breast tumour protein. The polynucleotide, its polypeptide, its antibody, a pharmaceutical composition comprising the fusion protein or the polynucleotide encoding it, a vaccine comprising the fusion protein or the polynucleotide encoding it, an isolated T cell population comprising T cells specific for a breast tumour protein, and a method for removing tumour cells from a biological sample is useful for inhibiting the development of a cancer in a patient. The polypeptide is useful for stimulating and/or expanding T cells specific for a breast tumour protein. Stimulating and/or expanding T cells specific for a breast tumour protein is useful for inhibiting the development of a cancer in a patient. The method additionally involves the step of cloning at least one proliferated cell and then administering the cloned T cells to the patient. The present sequence represents a cDNA associated with breast cancer.

Sequence 3865 BP; 1499 A; 697 C; 801 G; 862 T; 0 U; 6 Other;

Query Match 95.5%; Score 1938.4; DB 10; Length 3865;

Best Local Similarity 98.5%; Pred. No. 0;

Matches 1997; Conservative 4; Mismatches 21; Indels 5; Gaps 5;

Qy 5 TGCCGTTAAAGATGCTTCTTGAAGGCTTAAGGCTTAAGGCTTCTTATTCACCTAA 64

Db 1526 TCCTGTTAAAGATGCTTCTTGAAGGCTTAAGGCTTCTTATTCACCTAA 1585

Qy 65 ABCCTTAGAATTGATGGACATGCAAACTTTCAAAGCAGAGCTCCCGAGAGCCATCTGC 124

1586	AGCCTTAGAATTGATGACATGCAAACTTTCAAGCAGAGCCTCCCGAGAGCCATCTGC	1645
125	CTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTCTGGAATTTGAAGAA	184
1646	CTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTCTGGAATTTGAAGAA	1705
185	TGACAAACATTTGAGAGCAGATGAGTACTCCATCAGATCCAAACAAAGAGCTATCA	244
1706	TGAACAAACATTTGAGAGCAGATGAGTACTCCATCAGATCCAAACAAAGAGCTATCA	1765
245	AGAAAGTTCTTGGGATTTCTGAGAGTCTCTGTGAGACTGTTTTCACAGAGGATGTGTGTTT	304
1766	AGAAAGTTCTTGGGATTTCTGAGAGTCTCTGTGAGACTGTTTTCACAGAGGATGTGTGTTT	1825
305	ACCCAGGCTACATCAAAAGAAATAGATAAATAAATGGAATTTAGAGGCTCTCC	364
1826	ACCCAGGCTACATCAAAAGAAATAGATAAATAAATGGAATTTAGAGGCTCTCC	1885
365	TGATAATGATGTTTCTGAAGGCTCCCTGAGAGTCTGTTTCAAACTAAAGC	424
1886	TGATAATGATGTTTCTGAAGGCTCCCTGAGAGTCTGTTTCAAACTAAAGC	1945
425	CTTAGAATTGATGACATGCAAACTTTCAAGCAGAGCCTCCGAGAGCCATCTGCTT	484
1946	CTTAGAATTGATGACATGCAAACTTTCAAGCAGAGCCTCCGAGAGCCATCTGCTT	2005
485	CGAGCCTGCCATTGAAATGCAAAAGTCTGTTTCAAACTAAAGCCTTGAATTTGAAGATGA	544
2006	CGAGCCTGCCATTGAAATGCAAAAGTCTGTTTCAAACTAAAGCCTTGAATTTGAAGATGA	2065
545	ACAAACATTTGAGAGCAGATGATGTTCCCTTCAGAAATCAAAACAAAGAGTTGAGA	604
2066	ACAAACATTTGAGAGCAGATGATGTTCCCTTCAGAAATCAAAACAAAGAGTTGAGA	2125
605	AAATCTTGGGATTTCTGAGAGTCTCCGAGAGTCTGTTTTCAGAGAGGATCTGTGTACC	664
2126	AAATCTTGGGATTTCTGAGAGTCTCCGAGAGTCTGTTTTCAGAGAGGATCTGTGTACC	2185
665	CAAGGCTACATCAAAAGAAATGGAATAAATGGAATTTGAAGATTTAGAACTCACTAG	724
2186	CAAGGCTACATCAAAAGAAATGGAATAAATGGAATTTGAAGATTTAGAACTCACTAG	2245
725	CCTATCAAAATCTTGATACAGTTCTCTGTTGAAAGAGCAGGGAATTTCAAAAGA	784
2246	CCTATCAAAATCTTGATACAGTTCTCTGTTGAAAGAGCAGGGAATTTCAAAAGA	2305
785	TCACCTGTGAACAACGTACAGGAAATTTGGAACAAATGGAATTTGTTGTACTGAA	844
2306	TCACCTGTGAACAACGTACAGGAAATTTGGAACAAATGGAATTTGTTGTACTGAA	2365
845	AAAGAACTGTGAGAGCAAAAGAAATTAATCACTGAGTACAGTACCAAAAGCTTAATG	904
2366	AAAGAACTGTGAGAGCAAAAGAAATTAATCACTGAGTACAGTACCAAAAGCTTAATG	2425
905	GGAAACAGAGCTCTGAGAGTCTGAGATTTGACCTTTAAACCAAGAGAGAGAGAGAA	964
2426	GGAAACAGAGCTCTGAGAGTCTGAGATTTGACCTTTAAACCAAGAGAGAGAGAGAA	2485
965	TGCCGATATTAATGAAATTTAGGAGAGATTTAGGAGATTTAGGAGAGAGCTAG	1024
2486	TGCCGATATTAATGAAATTTAGGAGAGATTTAGGAGATTTAGGAGAGAGCTAG	2545
1025	GAAGAGTTAGAGTGAACCAACCTTTGAACAGGCTCTCAGAAATACAGATATAGAAAT	1084
2546	GAAGAGTTAGAGTGAACCAACCTTTGAACAGGCTCTCAGAAATACAGATATAGAAAT	2605
1085	GAAGAGTTAGAGTGAATTTGAATGATGTTTCTCAGCTCATGAAATGAAATTTATCT	1144
2606	GAAGAGTTAGAGTGAATTTGAATGATGTTTCTCAGCTCATGAAATGAAATTTATCT	2665
1145	CTTATGAAATTTGATGTTGAAAGAGAAATTTGCCATGCTAAATCTGGAATAGCCAC	1204

2666	CTTACATGAAATTTGATGTTGAAAGAGAAATTTGCCATGCTAAACTGGAATAGCCAC	2725
1205	ACTGAAACCAATACCAAGGAAAGGAAATTAATCTTTTGGAGACATTAAGATTTTAAA	1264
2726	ACTGAAACCAATACCAAGGAAAGGAAATTAATCTTTTGGAGACATTAAGATTTTAAA	2785
1265	AGAAAAGAAATCTGAACTTCAGATGACCCCTAAATCTGAAAGAGAAATCAATTAACAAAG	1324
2786	AGAAAAGAAATCTGAACTTCAGATGACCCCTAAATCTGAAAGAGAAATCAATTAACAAAG	2845
1325	GGCATCTCAATATATAGTGGCAGCTTAAAGTTCTGATAGCTGAGAACACATGCTCACTTC	1384
2846	GGCATCTCAATATATAGTGGCAGCTTAAAGTTCTGATAGCTGAGAACACATGCTCACTTC	2905
1385	TAAATTTGAAGGAAAGAAACAAAGCAAGAAATACTAGAGCGAGAAATGAATCAACCCATCC	1444
2906	TAAATTTGAAGGAAAGAAACAAAGCAAGAAATACTAGAGCGAGAAATGAATCAACCCATCC	2965
1445	TAGACTGCTCTCTGCTGATCAAGACCATGATCAAAATTTGACATCAAGAAAAGCTCAAGA	1504
2966	TAGACTGCTCTCTGCTGATCAAGACCATGATCAAAATTTGACATCAAGAAAAGCTCAAGA	3025
1505	ACCTGCTTTCCACATTTGAGAGATGCTTTGTTTCCAAAGAGAAATGAATGTTGTGTGAG	1564
3026	ACCTGCTTTCCACATTTGAGAGATGCTTTGTTTCCAAAGAGAAATGAATGTTGTGTGAG	3085
1565	TAGTACCATATATATCAATGAGGTCTCATCAACCACTTTCTGAAAGCTCAAGAGAAAT	1624
3086	TAGTACCATATATATCAATGAGGTCTCATCAACCACTTTCTGAAAGCTCAAGAGAAAT	3144
1625	CCANAAGCCTAAATTAATCTCAATATGACAGAGATGCTCTTAAGAGAAATACATTTG	1684
3145	CCANAAGCCTAAATTAATCTCAATATGACAGAGATGCTCTTAAGAGAAATACATTTG	3204
1685	TTTTCAGGAACTGCAACAAAGAGACCAACGTCGAAACACAGTCTCAAAATGAAGAGCTGAA	1744
3205	TTTTCAGGAACTGCAACAAAGAGACCAACGTCGAAACACAGTCTCAAAATGAAGAGCTGAA	3263
1745	CACATGTTTCAANCGACAGATTAATGTAACCAACACACACTGACAGCAGAGTCTCTA	1804
3264	CACATGTTTCAANCGACAGATTAATGTAACCAACACACACTGACAGCAGAGTCTCTA	3323
1805	GATCAGAAATTTATTTCAACTACAAAGCAAAATATGTCGCTTCAACAGCAATTTAGTTCAT	1864
3324	GATCAGAAATTTATTTCAACTACAAAGCAAAATATGTCGCTTCAACAGCAATTTAGTTCAT	3383
1865	GCACATTAAGAAAGCTGACACAAAGCAAGATTAATGTAACCAATTTGATTTCTTTGAGAG	1924
3384	GCACATTAAGAAAGCTGACACAAAGCAAGATTAATGTAACCAATTTGATTTCTTTGAGAG	3442
1925	GAAATGTC-NCATCATCTTTTAAAGAGAGAAATGAGGAGATATTTTATTAACCAACCA	1983
3443	GAAATGTC-NCATCATCTTTTAAAGAGAGAAATGAGGAGATATTTTATTAACCAACCA	3502
1984	TTTAAAGAAACCGTATATTTTCAATATGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAA	2030
3503	TTTAAAGAAACCGTATATTTTCAATATGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAA	3548

RESULT 13

ABT33258 standard; DNA; 3045 BP.

ID ABT33258

AC ABT33258;

XX 15-MAY-2003 (first entry)

DE Human tumour-related DNA sequence - SEQ ID No 548.

XX Human; ds; vaccine; gene therapy; T cell stimulation; T cell expansion;

XX tumour; breast cancer; cancer; immune response stimulation.

OS Homo sapiens.

XX PN W0200283956-A1.  
XX PD 24-OCT-2002.  
XX PF 15-APR-2002; 2002WO-US012378.  
XX PR 13-APR-2001; 2001US-00834759.  
XX PR 07-DEC-2001; 2001US-00007805.  
XX PR 13-FEB-2002; 2002US-00076622.  
XX PA (CORI-) CORIXA CORP.  
XX PI Houghton RL, Sleath PR, Persing DH, Jiang Y, Dillon DC;  
XX PI Mitcham JL, Xu J, Harlocker SL, Hepler WT, Henderson RA, Fanger GR;  
XX PI Vedvick TS, McNeill PD, Durham M;  
XX DR WPI; 2003-103376/09.  
XX PT New polypeptide and polynucleotide useful for stimulating and/or  
XX PT expanding T cells specific for a tumor protein and treating breast  
XX PT cancer.  
XX PS Example 8; Page 329-330; 375pp; English.  
XX CC The invention comprises a method of stimulating and/or expanding T cells  
XX CC specific for a tumor protein. The invention further comprises human  
XX CC nucleic acids and proteins that are associated with tumors (e.g. breast  
XX CC cancer). The method and sequences of the invention are useful for  
XX CC stimulating and/or expanding T cells specific for a tumor protein, in  
XX CC detecting the presence of cancer, stimulating an immune response in a  
XX CC patient and treating breast cancer. The present DNA sequence represents a  
XX CC human tumour-related DNA sequence  
XX SQ Sequence 3045 BP; 1222 A; 521 C; 613 G; 689 T; 0 U; 0 Other;  
Query Match 94.9%; Score 1927.2; DB 7; Length 3045;  
Best Local Similarity 98.3%; Pred. No. 0;  
Matches 1993; Conservative 0; Mismatches 29; Indels 5; Gaps 5;  
QY 5 TGCGGTTAAGATGCTCTCTGAGGCTAACTGGGGAATGAAAGTTTCTATTCCAACTAA 64  
Db 1008 TCCTGGTAAAGATGGTCTCTTAAGGCTAACTGGGGAATGAAAGTTTCTATTCCAACTAA 1067  
QY 65 AGCCTTAGAATGATGGACATGCAAACTTTCAAGAGAGAGGCTCCGAGAGGCAATCTGC 124  
Db 1068 AGCCTTAGAATGATGGACATGCAAACTTTCAAGAGAGAGGCTCCGAGAGGCAATCTGC 1127  
QY 125 CTTGAGGCTGCCATTTGAATGCAAAAGTCTGTTCCTAAATAAAGCCTTGGAAATTTGAAGAA 184  
Db 1128 CTTGAGGCTGCCATTTGAATGCAAAAGTCTGTTCCTAAATAAAGCCTTGGAAATTTGAAGAA 1187  
QY 185 TGAAACAAACATTGAGAGCAGATGATATCTCCATCAGAAATCCAAACAAAGGACTATGA 244  
Db 1188 TGAAACAAACATTGAGAGCAGATGATATCTCCATCAGAAATCCAAACAAAGGACTATGA 1247  
QY 245 AGAAAGTTCTGGGATTTGAGAGTCTCTGTGAGACTGTTTTCACAGAGGATGTGTTT 304  
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QY 305 ACCCAAGGCTACACATCAAAAGAAATAGATAAAATTAATGGAAATTTAGAAGAGTCTCC 364  
Db 1308 ACCCAAGGCTGGCATCAAAAGAAATAGATAAAATTAATGGAAATTTAGAAGAGTCTCC 1367  
QY 365 TGATATGATGTTTTCTGAGGCTCCCTCGAGATGAAAGTTTCTATTCCAACTAAAGC 424  
Db 1368 TGATATGATGTTTTCTGAGGCTCCCTCGAGATGAAAGTTTCTATTCCAACTAAAGC 1427  
QY 425 CTTAGAAATGATGGACATGCAAACTTTCAAGAGAGAGGCTCCGAGAGGCAATCTGCCTT 484  
Db 1428 CTTAGAAATGATGGACATGCAAACTTTCAAGAGAGAGGCTCCGAGAGGCAATCTGCCTT 1487  
QY 485 CGAGCCTGCCATTTGAAATGCAAAAGTCTGTTCCTCAATTAAGCCTTGGAAATTTGAAGATGA 544

Db 1488 CGAGCCTGCCATTTGAAATGCAAAAGTCTGTTCCTCAATTAAGCCTTGGAAATTTGAAGATGA 1547  
QY 545 ACAAAACATTGAGAGCAGATCAGATGTTCCCTTCAGAAATCAAAACAAAGAGGTTCAAGA 604  
Db 1548 ACAAAACATTGAGAGCAGATCAGATGTTCCCTTCAGAAATCAAAACAAAGAGGTTCAAGA 1607  
QY 605 AAATTCTTGGATTTCTGAGAGTCTCGGTGAGACTGTTTTCACAGAGGATGTGTGTGTACC 664  
Db 1608 AAATTCTTGGATTTCTGAGAGTCTCGGTGAGACTGTTTTCACAGAGGATGTGTGTGTACC 1667  
QY 665 CAAGGCTACACATCAAAAGAAATGGATAAAATTAAGTGGAAATTTAGAAGATTTCAACTAG 724  
Db 1668 CAAGGCTACACATCAAAAGAAATGGATAAAATTAAGTGGAAATTTAGAAGATTTCAACTAG 1727  
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Db 2208 ACTGAAACACCAATACCAAGGAAAGGAAATAAATACTTTGAGGACATTTAGATTTTAA 2267  
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Db 2268 AGAAAGAGTGTGAACTTCCAGATGACCTTAAACTGAAAGAGGAAATCATTTAACTTAAAG 2327  
QY 1325 GGCATCTCAATATAGTGGGAGCTTTAAAGTTCTGATAGCTGAGAAACAACTGCTCCTTC 1384  
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Db 2388 TAAATTTGAGGAAAGCAAGACAAAGAAATCTAGAGGACAGAAATTTGAATCACACATCC 2447  
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Db 2448 ----- 2447  
QY 1025 GAAAGAGTTAGAAAGTGAACCAACAACTTGAACAGGCTCTCAGAAATACAGATATAGAAATT 1084  
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Db 2482 CTTACATGAAATTTGCATGTTGAAAGAGAAATGCGCATGCTAAACTGAAATAGCCAC 2541  
QY 1205 ACTGAAACCAATACAGAGAAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1264  
Db 2542 ACTGAAACCAATACAGAGAAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2601  
QY 1265 AGAAAGAAATGCTGAACTTCAGATGACCTTAAACTGAAAGAGAAATTAATTAATTAATTAAT 1324  
Db 2602 AGAAAGAAATGCTGAACTTCAGATGACCTTAAACTGAAAGAGAAATTAATTAATTAATTAAT 2661  
QY 1325 GGCATCTCAATATAGTGGGAGCTTAAGTTCTGATAGCTGAGAACACAAATGCTCACTTC 1384  
Db 2662 GGCATCTCAATATAGTGGGAGCTTAAGTTCTGATAGCTGAGAACACAAATGCTCACTTC 2721  
QY 1385 TAAATTGAAGGAAACCAAGCAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1444  
Db 2722 TAAATTGAAGGAAACCAAGCAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2781  
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Db 2782 TAGACTGGTCTGCTGTAAGACCAATGATCAAAATGTCATCAAGAAAGAAATGCTCAAG 2841  
QY 1505 ACCTGCTTTCCATGTCAGAGAGATGCTTTGTCAGAGAAATTAATTAATTAATTAATTAAT 1564  
Db 2842 ACCTGCTTTCCATGTCAGAGAGATGCTTTGTCAGAGAAATTAATTAATTAATTAATTAAT 2901  
QY 1565 TAGTACCGATATATACAAATGAGTGTCTCCATCAACCACTTTCTGAGCTCAAGGAAAT 1624  
Db 2902 TAGTA-CGATATATACAAATGAGTGTCTCCATCAACCACTTTCTGAGCTCAAGGAAAT 2960  
QY 1625 CCNAAAGCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1684  
Db 2961 CCNAAAGCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3020  
QY 1685 TTTGAGGAAATGCAACAAAGAGACCAACGTTGAAACACAGTGTCAAAATGAAAGGAGCTGAA 1744  
Db 3021 TTTGCA-GAATGCAACAAAGAGACCAACGTTGAAACACAGTGTCAAAATGAAAGGAGCTGAA 3079  
QY 1745 CACATGTTTCAATGACAGATGATGTAACCAACACAGTGTGACAGAGAGCTCTTA 1804  
Db 3080 CACATGTTTCAATGACAGATGATGTAACCAACACAGTGTGACAGAGAGCTCTTA 3139  
QY 1805 GATCAGAAATTAATTTCAACTACAAAGCAAAATATGCTTCAACAGCAATTAATTTCAAT 1864  
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QY 1865 GCACATTAAGAGCTGACACAAAGCAAGATCAATTAATTTCAATTTCTTTGAGAG 1924  
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QY 1925 GAAATGTC-NCATCATCTTTCTTAAAGAGAAATGAGGAGATATTTTATACNATACCA 1983  
Db 3259 GAAATGTC-NCATCATCTTTCTTAAAGAGAAATGAGGAGATATTTTATACNATACCA 3318  
QY 1984 TTTTAAACCCGTTATTTCAATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2030  
Db 3319 TTTTAAACCCGTTATTTCAATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3364

RESULT 15  
AAI67218

ID AAI67218 standard; cDNA; 3681 BP.  
XX AC AAI67218;  
XX DT 11-FEB-2002 (first entry)  
XX DE B726P splice variant encoding cDNA.  
XX KW Genetic subtraction; DNA microarray analysis; polymerase chain reaction;  
XX KW cancer; B726P; ss.  
XX OS Homo sapiens.  
XX PN WC200175171-A2.  
XX PD 11-OCT-2001.  
XX PF 02-APR-2001; 2001WO-US010631.  
XX PR 03-APR-2000; 2000US-0194241P.  
XX PR 20-JUL-2000; 2000US-0219862P.  
XX PR 27-JUL-2000; 2000US-0221300P.  
XX PR 18-DEC-2000; 2000US-0256592P.  
XX PA (CORI-) CORIXA CORP.  
XX PI Houghton RL, Dillon DC, Molesh DA, Xu J, Zehentner B, Persing DH;  
XX DR P-PSDB; AAG65983.  
XX PT Identifying tissue (tumor)-specific polymucleotides overexpressed in  
XX PT tissue of interest as compared to control tissue, for detecting cancer  
XX PT cells in patient, comprises DNA microarray analysis or quantitative  
XX PT polymerase chain reaction.  
XX PS Claim 4; Page 104-105; 127pp; English.  
XX CC The invention relates to identifying tissue-specific polymucleotides (P)  
XX CC that involves performing a genetic subtraction to identify pool of (P)  
XX CC from tissue of interest (TI), performing DNA microarray analysis to  
XX CC identify first subset of polymucleotides (SP1) at least 2-fold over  
XX CC expressed in TI, and performing quantitative polymerase chain reaction  
XX CC (PCR) analysis on SP1 to identify second subset of (P). The method is  
XX CC useful for determining the presence or absence of a cancer cell in a  
XX CC patient, monitoring the progression of cancer in a patient using a  
XX CC biological sample such as blood, serum, lymph nodes, bone marrow, sputum,  
XX CC urine or a tumour biopsy sample. The methods are useful for determining  
XX CC the presence or absence of or monitoring progression of prostate, breast,  
XX CC colon, ovarian, lung, head and neck, lymphoma, leukemia, melanoma, liver,  
XX CC gastric, kidney, bladder, pancreatic or endometrial cancer. Sequences  
XX CC AAI67218-223 represent determined cDNA sequences of splice variants of  
XX CC B726P  
SQ Sequence 3681 BP; 1411 A; 680 C; 758 G; 826 T; 0 U; 6 Other;  
Query Match 76.9%; Score 1560.4; DB 4; Length 3681;  
Best Local Similarity 89.4%; Pred. No. 6.7e-312;  
Matches 1813; Conservative 4; Mismatches 21; Indels 189; Gaps 6;  
QY 5 TCCGCTTAAGAGTGTCTTCTGAGGCTTAAGTGGGATGAAGTTCTTATTCACACTAA 64  
Db 1526 TCTGTGAAGATGCTCTTCTGAGGCTTAAGTGGGATGAAGTTCTTATTCACACTAA 1595  
QY 65 AGCCTTAGAATTTGATGGACATGCAAACTTCAAGCAGAGCTCCGAGAGCCATCTGC 124  
Db 1586 AGCCTTAGAATTTGATGGACATGCAAACTTCAAGCAGAGCTCCGAGAGCCATCTGC 1645  
QY 125 CTTGAGGCTGCAATGAAATGCAAAAGTCTGTTCCAAATGAAGCTTGGATTGAAGAA 184  
Db 1646 CTTGAGGCTGCAATGAAATGCAAAAGTCTGTTCCAAATGAAGCTTGGATTGAAGAA 1705  
QY 185 TGAACAAACATTTGAGAGCAGATGATATCTCCCATCAGAAATCCAAACAAAGGACTATGA 244



2602	AGAAAGAAATGCTGAACCTT	CAGATGACCTTAAACTGAAAGAGGAATCA	TAACTAAAG	2661
1325	GGCATCTCAATATAGTGGCAGCTTAAAGTTCT	GATAGCTGAGAACAAATGCTCACTTC	1384	
2662	GGCATCTCAATATAGTGGCAGCTTAAAGTTCT	GATAGCTGAGAACAAATGCTCACTTC	2721	
1385	TAAATTTGAGGAAAAACAAGCAAGAAATACT	TAGGGCGAGAAATGGAATCACACCATCC	1444	
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1445	TAGACTGGCTTCTGCTGTACAGACCATGATCAAA	TGTGCATCAAGAAAAAGTCAAGA	1504	
2782	TAGACTGGCTTCTGCTGTACAGACCATGATCAAA	TGTGCATCAAGAAAAAGTCAAGA	2841	
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2842	ACCTGCTTTCACATTCGAGGAGTGCTTGTGTC	CAAGAAAAAATGAAATGTGATGTCAG	2901	
1565	TAGTACCGATATATAACAAATGAGGTGCTCCAT	CAACCACTTTCTGAAAGCTCAAAAGGAAAT	1624	
2902	TAGTA-CGATATATAACAAATGAGGTGCTCCAT	CAACCACTTTCTGAAAGCTCAAAAGGAAAT	2960	
1625	CCANAAAGCTTAAANATTAATCTCAATTTATG	CGAGGAGTGCTCTAAGAGAAATACATGG	1684	
2961	CCANAAAGCTTAAANATTAATCTCAATTTATG	CGAGGAGTGCTCTAAGAGAAATACATGG	3020	
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3080	CACATGTTTCAANCGAACAGATTAATGTGAACA	ACACATGTGCAAAATGAAGGAAAGCTGCTCTA	3139	
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3140	GATCAGAAATTTATTCACACTCAAAAGCAAAA	ATATGTGGCTTCAACAGCAATTTAGTTTCAT	3199	
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3200	GCACATAANGAAAGCTGACAAACAAAGACGAG	TAACAATTTGATTTTCATTTCTTGAGAG	3258	
1925	GAAATATGC-NCATTCATCTTTCTTAAAGAG	AAAAAATGAGGAGATATTTNATTACNATAACCA	1983	
3259	GAAATATGCACATCATCTCTTAAAGAGAAAA	ATGAGGAGATATTTNATTACNATAACCA	3318	
1984	TTTAAAAAACCCGTATATTTCAATATGGA	AAAAAATAAAAAA	2030	
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QY 965 TGCCGATATATTAAATGAAAAATTAGCGAAGATTAGCAAGATCGAAGACGAGCATAG 1024.

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OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 17:03:44 ; Search time 7879 Seconds  
(without alignments)  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

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Maximum DB seq length: 2000000000

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Maximum Match 100%  
Listing first 45 summaries

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- 2: gb\_hcg.\*
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- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_or.\*
- 21: em\_ov.\*
- 22: em\_pat.\*
- 23: em\_ph.\*
- 24: em\_pl.\*
- 25: em\_ro.\*
- 26: em\_sts.\*
- 27: em\_sy.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_hcg\_hum.\*
- 31: em\_hcg\_inv.\*
- 32: em\_hcg\_other.\*
- 33: em\_hcg\_mus.\*
- 34: em\_hcg\_pln.\*
- 35: em\_hcg\_rod.\*
- 36: em\_hcg\_mam.\*
- 37: em\_hcg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_hgo\_hum.\*
- 40: em\_hgo\_mus.\*
- 41: em\_hgo\_other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2018	99.4	2030	6	AX367056 Sequence
2	1940	95.6	4458	6	AX829110 Sequence
3	1940	95.6	4458	9	AF269087 Homo sapi
4	1938.4	95.5	3288	6	AR283467 Sequence
5	1938.4	95.5	3288	6	AX303170 Sequence
6	1938.4	95.5	3865	6	AR283457 Sequence
7	1938.4	95.5	3865	6	AR351426 Sequence
8	1938.4	95.5	3865	6	AX303154 Sequence
9	1560.4	76.9	3681	6	AR283451 Sequence
10	1560.4	76.9	3681	6	AR344219 Sequence
11	1560.4	76.9	3681	6	AR351420 Sequence
12	1560.4	76.9	3681	6	AX282970 Sequence
13	1560.4	76.9	3681	6	AX303143 Sequence
14	1558.8	76.8	2307	6	AR283456 Sequence
15	1558.8	76.8	2307	6	AR344224 Sequence
16	1558.8	76.8	2307	6	AR351425 Sequence
17	1558.8	76.8	2307	6	AX282975 Sequence
18	1558.8	76.8	2307	6	AX303148 Sequence
19	1557.2	76.7	2683	6	BD271311 Reagents
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21	1282.6	63.2	1337	6	AR283455 Sequence
22	1282.6	63.2	1337	6	AR344223 Sequence
23	1282.6	63.2	1337	6	AR351424 Sequence
24	1282.6	63.2	1337	6	AX282974 Sequence
25	1282.6	63.2	1337	6	AX303147 Sequence
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27	1197.6	59.0	1681	6	AR283169 Sequence
28	1197.6	59.0	1681	6	AR341942 Sequence
29	1197.6	59.0	1681	6	AR351138 Sequence
30	1197.6	59.0	1681	6	AX352904 Sequence
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32	1197.6	59.0	1681	6	AX302860 Sequence
33	1197.6	59.0	1681	6	AR280672 Sequence
34	1116.2	55.0	1665	6	AR283168 Sequence
35	1116.2	55.0	1665	6	AR341941 Sequence
36	1116.2	55.0	1665	6	AR351137 Sequence
37	1116.2	55.0	1665	6	AR343936 Sequence
38	1116.2	55.0	1665	6	AX352903 Sequence
39	1116.2	55.0	1665	6	AX282966 Sequence
40	1116.2	55.0	1665	6	AX302858 Sequence
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ALIGNMENTS

RESULT 1	AX367056	AX367056	2030 bp	DNA	linear	PAT 16-FEB-2002
LOCUS	AX367056	Sequence 15 from Patent WO0147959.				
DEFINITION	AX367056	AX367056				
ACCESSION	AX367056.1	GI:18855278				
VERSION						
KEYWORDS						
SOURCE						
ORGANISM		Homo sapiens (human)				
		Homo sapiens				
		Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE						
AUTHORS		Jager, D., Stockert, E., Scanlan, M., Knuth, A., Old, L., Gure, A. and Chen, Y.T.				
TITLE		Isolated nucleic acid molecules encoding cancer associated				

Pred. No. is the number of results predicted by chance to have a

JOURNAL		FEATURES		source		ORIGIN	
antigens, the antigens per se, and uses thereof		Location/Qualifiers		1..2030			
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LUDWIG INSTITUTE FOR CANCER RESEARCH (US) ; MEMORIAL		/mol_type="unassigned DNA"					
SLOAN-KETTERING CANCER CENTER (US) ; Cornell Research Foundation		/db_xref="taxon:9606"					
(US)							
Query Match		99.4% ; Score 2018; DB 6; Length 2030;					
Best Local Similarity		100.0% ; Pred. No. 0;					
Matches 2030; Conservative		0; Mismatches 0; Indels 0; Gaps 0;					
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QY	61	CTAAGACCTTAGAATTGATGGACATGCAAACTTTCAAAGCAGAGCTCCCGAGAAGCCAT	120				
DB	61	CTAAGACCTTAGAATTGATGGACATGCAAACTTTCAAAGCAGAGCTCCCGAGAAGCCAT	120				
QY	121	CTGCGCTTGGAGCTGCCATTCAATGCAAGATCTGTTCCAAATAAAGCCTTTGGAATTGA	180				
DB	121	CTGCGCTTGGAGCTGCCATTCAATGCAAGATCTGTTCCAAATAAAGCCTTTGGAATTGA	180				
QY	181	AGAATGAACAAACATTGGAGCAGATGAGATATCCCATCAGAAATCCAAACAAAAGGACT	240				
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QY	241	ATGAAGAAAGTTCTTGGGATCTGAGAGTCTCTGTGAGACTGTTTCCACAGAGGAGTGTG	300				
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QY	361	CTCCTGATAATGATGGTCTTCTGGAAGGCTCCCTGCAGAAATGAAAGTTTCTATTCCAACTA	420				
DB	361	CTCCTGATAATGATGGTCTTCTGGAAGGCTCCCTGCAGAAATGAAAGTTTCTATTCCAACTA	420				
QY	421	AAGCCTTAGAATTGATGGACATGCAAACTTTTCAAAGCAGAGCTCCCGAGAAGCCATCTG	480				
DB	421	AAGCCTTAGAATTGATGGACATGCAAACTTTTCAAAGCAGAGCTCCCGAGAAGCCATCTG	480				
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LOCUS AX829110 4458 bp DNA linear PAT 12-DEC-2003  
DEFINITION Sequence 3 from Patent WO02059377.  
ACCESSION AX829110  
VERSION AX829110.1 GI:39838904  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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REFERENCE  
1 Mack,D.H., Gish,K.C. and Afar,D.  
TITLE Methods for diagnosis of breast cancer, compositions and methods of  
screening for modulators of breast cancer  
JOURNAL Patent: WO 02059377-A 3 01-AUG-2002;  
EOS Biotechnology, Inc. (US)  
FEATURES  
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Best Local Similarity 98.7%; Pred. No. 0;  
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LOCUS Homo sapiens breast cancer antigen NY-BR-1 mRNA, complete cds.
ACCESSION AF269087
VERSION AF269087.1 GI:13469728
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4458)
Jager, D., Stockert, E., Gure, A.O., Scanlan, M.J., Karbach, J.,
Jager, E., Knuth, A., Old, L.J. and Chen, Y.T.
Identification of a tissue-specific putative transcription factor
in breast tissue by serological screening of a breast cancer
library
Cancer Res. 61 (5), 2055-2061 (2001)
21174979
PUBMED 11280766
REFERENCE 2 (bases 1 to 4458)
Jager, D., Stockert, E., Gure, A.O., Scanlan, M.J., Karbach, J.,
Jager, E., Knuth, A., Old, L.J. and Chen, Y.T.
Direct Submission
Submitted (18-MAY-2000) Pathology, Cornell Medical Center, 1300
York Avenue, New York, NY 10021, USA
FEATURES
Location/Qualifiers
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Best Local Similarity 98.7%; Pred. No. 0;
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LOCUS Sequence 490 from patent US 6528054.  
DEFINITION AR283467  
ACCESSION AR283467  
VERSION AR283467.1 GI:29720294  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 3288)  
AUTHORS Jiang, Y., Dillon, D.C., Mitcham, J.L., Xu, J., Harlocker, S.L. and Hepler, W.T.  
TITLE Compositions and methods for the therapy and diagnosis of breast cancer  
JOURNAL Patent: US 6528054-A 490 04-MAR-2003;  
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Db	2634	TAAATTTGAAGGAAAAACAAGCAAAAGAAATACTAGAGCGAGAAATTTGAATCACACCATCC	2693
Qy	1445	TAGACTGGCTTCTGCTGTAACAAGACCATGATCAAAATTTGTGACATCAAGAAAAAGTCAAGA	1504
Db	2694	TAGACTGGCTTCTGCTGTAACAAGACCATGATCAAAATTTGTGACATCAAGAAAAAGTCAAGA	2753
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LOCUS	AX303170	3288 bp DNA linear	PAT 30-NOV-2001
DEFINITION	Sequence 490 from Patent WO0179286.		
ACCESSION	AX303170		
VERSION	AX303170.1 GI:17383660		
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Jiang,Y., Dillon,D.C., Mitcham,J.L., Xu,J., Harlocker,S.L. and Hepler,W.T.		
TITLE	Compositions and methods for the therapy and diagnosis of breast cancer		
JOURNAL	Patent: WO 0179286-A 490 25-OCT-2001;		
FEATURES	CORIXA CORPORATION (US)		
source	location/Qualifiers		
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Query Match	95.5%;	Score 1938.4;	DB 6; Length 3288;
Best Local Similarity	98.5%;	Pred. No. 0;	
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RESULT 6  
AR283457 LOCUS AR283457 3865 bp DNA linear PAT 10-APR-2003  
DEFINITION Sequence 474 from patent US 6528054.  
ACCESSION AR283457  
VERSION AR283457.1 GI:29720284  
KEYWORDS Unknown.  
SOURCE ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 3865)  
AUTHORS Jiang, Y., Dillon, D.C., Mitcham, J.L., Xu, J., Harlocker, S.L. and Hepler, W.T.  
TITLE Compositions and methods for the therapy and diagnosis of breast cancer  
JOURNAL Patent: US 6528054-A 474 04-MAR-2003;  
FEATURES Location/Qualifiers  
source 1. 3865  
/organism="unknown"  
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ORIGIN  
Query Match 95.5%; Score 1938.4; DB 6; Length 3865;  
Best Local Similarity 98.5%; Pred. No. 0;  
Matches 1997; Conservative 4; Mismatches 21; Indels 5; Gaps 5;

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RESULT 7  
AR351426  
LOCUS  
DEFINITION  
SEQUENCE 474 from patent US 6586572.  
AR351426  
ACCESSION  
VERSION  
AR351426.1 GI:33753105  
KEYWORDS  
SOURCE  
Unknown.

3855 bp DNA linear PAT 17-AUG-2003

ORGANISM	Unknown:	Unclassified:
REFERENCE	1 (bases 1 to 3865)	
AUTHORS	Jiang, Y., Dillon, D.C., Mitcham, J.L., Xu, J., Harlocker, S.L. and Repler, W.T.	
TITLE	Compositions and methods for the therapy and diagnosis of breast cancer	
JOURNAL	Patent: US 6586572-A 474 01-JUL-2003;	
FEATURES	source 1..3865 Location/Qualifiers /organism="unknown" /mol_type="genomic DNA"	
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Query Match	95.5%;	Score 1938.4; DB 6; Length 3865;
Best Local Similarity	98.5%;	Pred. No. 0;
Matches 1997;	Conservative	4; Mismatches 21; Indels 5; Gaps 5;
Qy	5	TGCGTTAAAGATGGTCTTCTGAAGGCTAACTCGCGAATCAAGATTCTATTCCCACTAA 64
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LOCUS			
DEFINITION		Sequence 474 from Patent WO0179286.	
ACCESSION		AX303154	
VERSION		AX303154.1 GI:17383650	
KEYWORDS			
SOURCE			
ORGANISM		Homo sapiens (human)	
REFERENCE			
AUTHORS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
TITLE		Jiang, Y., Dillon, D.C., Mitcham, J.L., Xu, J., Harlocker, S.L. and Hepler, W.T.	
JOURNAL		Compositions and methods for the therapy and diagnosis of breast cancer	
FEATURES			
source		Patent: WO 0179286-A 474 25-OCT-2001; CORIXA CORPORATION (US)	
ORIGIN			
Query Match		95.5%; Score 1938.4; DB 6; Length 3865;	
Best Local Similarity		98.5%; Pred. No. 0;	
Matches 1997; Conservative		4; Mismatches 21; Indels 5; Gaps 5;	
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Qy	365	TGATAATGATGGTTTCTGAAGGCTCCCTGCAGAAATGAAAGTTTCTATTCCAACTAAAGC	424
Db	1886	TGATAATGATGGTTTCTGAAGGCTCCCTGCAGAAATGAAAGTTTCTATTCCAACTAAAGC	1945
Qy	425	CTTAGAATTGATGACATGCAAACTTTCAAGCAGAGCCTCCGAGAACCCATCTGCCTT	484
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Qy	485	CGAGCCTCCATGAAATGCAAAAGTCGTGTTCCAAATAAAGCCTTGAAATTGAAGATGA	544
Db	2006	CGAGCCTCCATGAAATGCAAAAGTCGTGTTCCAAATAAAGCCTTGAAATTGAAGATGA	2065

QY	545	ACAAACATTGAGAGCAGATCAGATGTTCCCTTCAGATCAAAACAAAAGAGGTTGAAGA	604
DB	2066	ACAAACATTGAGAGCAGATCAGATGTTCCCTTCAGATCAAAACAAAAGAGGTTGAAGA	2125
QY	605	AAATTCCTGGGATTCCTGAGAGTCTCGTGAGACTGTGTTACAGAAAGGATGTGTGTACC	664
DB	2126	AAATTCCTGGGATTCCTGAGAGTCTCGTGAGACTGTGTTACAGAAAGGATGTGTGTACC	2185
QY	665	CAAGGCTACACATCAAAAGAGAAATCGATAAATAAGTGGAAATTTAGAAAGATTTCAACTAG	724
DB	2186	CAAGGCTACACATCAAAAGAGAAATCGATAAATAAGTGGAAATTTAGAAAGATTTCAACTAG	2245
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DB	2366	AAAGAACTGTCAAGACAAAAGAAATAAATCACAGTTAGAGAACCAAAAAGTTAAATG	2425
QY	905	GGACACAGAGCTCTGACGTGTGAGATTGACTTTAAACCAAGAGAGAGAGAGAGAGAAA	964
DB	2426	GGACACAGAGCTCTGACGTGTGAGATTGACTTTAAACCAAGAGAGAGAGAGAGAGAAA	2485
QY	965	TGCCGATATATTAAATCAAAAAATTTAGGGAAGAAATTAGAGAGAAATCGAAGAGCAGATAG	1024
DB	2486	TGCCGATATATTAAATCAAAAAATTTAGGGAAGAAATTAGAGAGAAATCGAAGAGCAGATAG	2545
QY	1025	GAAAGAGTTAGAGCTGAAACCAACCACTTGAAACAGGCTCTCAGAAATCAAGATATAGAAAT	1084
DB	2546	GAAAGAGTTAGAGCTGAAACCAACCACTTGAAACAGGCTCTCAGAAATCAAGATATAGAAAT	2605
QY	1085	GAAGAGTGTAGAAAGTAATTTGGAATCATAGGTTTCTCAGCTGTGAAATGAAATTTATCT	1144
DB	2606	GAAGAGTGTAGAAAGTAATTTGGAATCATAGGTTTCTCAGCTGTGAAATGAAATTTATCT	2665
QY	1145	CTTACATCAAAATTCGATGTTTGAAAAAGGAAATTGCCATGCTGAAAACTGGAATAGCCAC	1204
DB	2666	CTTACATCAAAATTCGATGTTTGAAAAAGGAAATTGCCATGCTGAAAACTGGAATAGCCAC	2725
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DB	2726	ACTGAAACCAATACACGAGAAAGGAAATTAATTAATCTTTGAGGACATTAAGATTTTAAA	2785
QY	1265	AGAAAAGAAATCTGAATTCAGATGACCTTAAACTGAAAAGAGAAATCAATTAACATAAAG	1324
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QY	1385	TAAATTTGAAGGAAAAACAAGCAAGAAATACTAGAGCGAGAAATTTGAATCACACCAATCC	1444
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QY	1505	AAGCTGTTTCCACATTTGAGGAGATGCTTTGTTCCAAAGAAAAATGAATGTGATGTGAG	1564
DB	3026	AAGCTGTTTCCACATTTGAGGAGATGCTTTGTTCCAAAGAAAAATGAATGTGATGTGAG	3085
QY	1565	TAGTACCGATATATAACAAATGAGGTGCTCCATCAACCACTTCTGGAAGCTCAAGAGGAAT	1624
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1806		
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AUTHORS		
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JOURNAL		
FEATURES		
source		
ORIGIN		
Query Match		
Best Local Similarity		
Matches 1813; Conservative		
4; Mismatches 21; Indels 189; Gaps 6;		
QY	5	TGCGGTAAAGATGGTCTTCTGAAGGCTAACTGCGGAATGAAAGTTTCTATTCCAACATAA 64
DB	1526	TCCTGTTAAAGATGGTCTTCTGAAGGCTAACTGCGGAATGAAAGTTTCTATTCCAACATAA 1585
QY	65	AGCCTTAGAATTCATGGACATGCAAACTTTCAAGACGAGCGCTCCGAGAGCGCATCTGC 124
DB	1586	AGCCTTAGAATTCATGGACATGCAAACTTTCAAGACGAGCGCTCCGAGAGCGCATCTGC 1645
QY	125	CTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATTAAGCCCTTGAATTGAAGAA 184
DB	1646	CTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATTAAGCCCTTGAATTGAAGAA 1705
QY	185	TGAACAAACATTGAGACGATGAGTACTCCCATCAGATCCAAACAAAGGACTATGA 244
DB	1706	TGAACAAACATTGAGACGATGAGTACTCCCATCAGATCCAAACAAAGGACTATGA 1765
QY	245	AGAAAGTCTCTGGGATTCAGAGATCTCTGTGAGACTGTTTTCACAGAAGGATGTGTTTT 304

1766	AGAAAGTCTTGGGATTCTGAGAGTCTCTGTGAGAGCTGTTTTCACAGAGGATGTGTGTTT	1825
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365	TGATAATGATGGTTTCTGAAAGCTCCCTGCGAATGAAAGTTTCTATTCCAACTAAAGC	424
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 RESULT 13  
 AX303143 3681 bp DNA linear PAT 30-NOV-2001  
 LOCUS AX303143  
 DEFINITION Sequence 463 from Patent WO0179286.  
 ACCESSION AX303143  
 VERSION AX303143.1 GI:17383644  
 KEYWORDS Homo sapiens (human)  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Jiang, Y., Dillon, D.C., Mitcham, J.L., Xu, J., Harlocker, S.B. and Hepler, W.T.  
 TITLE Compositions and methods for the therapy and diagnosis of breast cancer  
 JOURNAL Patent: WO 0179286-A 463 25-OCT-2001;  
 CORIXA CORPORATION (US)  
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 ORIGIN  
 Query Match 76.9%; Score 1560.4; DB 6; Length 3681;  
 Best Local Similarity 89.4%; Pred. No. 7.2e-275;  
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RESULT 15  
AR344224  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

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Sequence 468 from patent US 6579973.  
AR344224  
AR344224.1      GI:33740124

REFERENCE	1 (bases 1 to 2307)	
AUTHORS	Yudin, J., Dillion, D.C., Mitcham, J.L., Xu, J. and Harlocker, S.L.	
TITLE	Compositions for the treatment and diagnosis of breast cancer and methods for their use	
JOURNAL	Patent: US 6579973-A 468 17-JUN-2003;	
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Db	1843	GCATATTAAGAAAGCTGCAACAAAGAGCAAGATTAATGATGATTTTCAATTTCTTGAGAG	1901
Qy	1925	GAAATATGC-NCATCATCTTTCTTAAAGAGAAAAATGAGGAGATATTNATTAATCAATCA	1983
Db	1901	GAAATATGC-NCATCATCTTTCTTAAAGAGAAAAATGAGGAGATATTNATTAATCAATCA	1961

Fri May 7 09:17:22 2004

Qy 1984 TTTAAAAAACCCGTATATTTTCAATATCGAAAAAANAAAAA 2030  
Db 1962 TTTAAAAA-CCGTATATATCAATATGAAAAAGAGAAAGCAGAAACA 2007

Search completed: May 6, 2004, 21:03:15  
Job time : 7892 secs

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	870	33.5	574	10	BF328582	BF328582 RC5-BN019
2	809	31.1	490	9	AI951118	AI951118 wx63905.x
3	771	29.7	565	10	AW373574	AW373574 QV4-BT053
4	717	27.6	630	10	BE177744	BE177744 RCI-HT059
5	716.5	27.6	3443	11	BC028407	BC028407 Homo sapi
6	646	24.9	3794	11	BC036210	BC036210 Homo sapi
7	540.5	20.8	596	13	BQ429618	BQ429618 AGENCOURT
8	520	20.0	443	10	BF746270	BF746270 RCI-BT025
9	520	20.0	443	10	BF746340	BF746340 RCI-BT025
10	458	17.6	904	12	BG539426	BG539426 602568046
11	437.5	16.8	862	12	BG431116	BG431116 602498742
12	433.5	16.7	821	12	BG622779	BG622779 602647567
13	431.5	16.6	684	14	CA394381	CA394381 cs50108.1
14	427.5	16.4	683	14	CF181571	CF181571 818415 MA
15	416.5	16.0	638	13	BU678550	BU678550 UI-CF-DUI
16	389.5	15.0	1105	13	BQ071543	BQ071543 AGENCOURT
17	385	14.8	546	10	BE929777	BE929777 RC3-GN004
18	375.5	14.4	519	9	AL711745	AL711745 DKEZp686L
19	365.5	14.1	700	14	CB527418	CB527418 UI-M-FY0-
20	354.5	13.6	751	14	CD000265	CD000265 AGENCOURT
21	351.5	13.5	574	14	CB298280	CB298280 220016 re
22	351.5	13.5	630	14	CB298279	CB298279 220016 re
23	346.5	13.3	774	14	CA324174	CA324174 UI-M-FY0-
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38	271	10.4	386	10	AW614036	AW614036 hg73f10.x
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41	265.5	10.2	886	13	BQ437838	BQ437838 AGENCOURT
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ALIGNMENTS

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LOCUS RC5-BN0192-010900-025-E09 BN0192 Homo sapiens cDNA, mRNA linear EST 22-NOV-2000  
DEFINITION BF328582  
ACCESSION BF328582  
VERSION BF328582.1 GI:11299317  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1. (bases 1 to 574)  
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 6, 2004, 13:47:23 ; Search time 3855 Seconds  
(without alignments)  
3966.131 Million cell updates/sec

Title: US-09-451-739H-16  
Perfect score: 2599  
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Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*



Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J., and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

10737800

PubMed

COMMENT

CONTACT: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922  
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=RC5&t2=RC5-BN0192-010900-025-E09&t3=2000-09-01&t4=1)

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High quality sequence start: 25

High quality sequence stop: 525.

Location/Qualifiers

1..574

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/dev\_stage="Adult"

/clone\_lib="BN0192"

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## FEATURES

source

RESULT 2

AI9511118/c

LOCUS

DEFINITION

wx63905.x1 NCI\_CGAP\_Br18 Homo sapiens cDNA clone IMAGE:2548376 3', mRNA sequence.

AI9511118

VERSION

AI9511118.1 GI:5743428

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 490)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

TITLE

Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: cgapsb@mail.nih.gov  
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed By: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing By: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

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High quality sequence stop: 423.

Location/Qualifiers

1..490

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/notes="Organ: breast; Vector: pCMV-SPORT6; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies."

## FEATURES

source

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Score: 809.00 Matches: 157

Percent Similarity: 97.55% Conservative: 2

Best Local Similarity: 96.32% Mismatches: 4

Query Match: 31.13% Indels: 0

DB: 9 Gaps: 0

## ORIGIN

US-09-451-739H-16 (1-512) x AI9511118 (1-490)

94 GlnLysGluLeuAspLysIleAsnGlnLysLeuGluSerProAspAsnAspGlyPhe 113

489 CAAAAGAAATAGATAAATAATGAAATAGAGAGTCTCCTGATAATGATGGTTT 430

## ORIGIN

Alignment Scores:

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Score: 870.00 Matches: 173

Percent Similarity: 97.22% Conservative: 2

Best Local Similarity: 96.11% Mismatches: 4

Query Match: 33.47% Indels: 1

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37 TTGAGACAGATGATGATCTCCCATCAGATCCAAACAAAGACTATGAGAAAGTTCT 96

72 TrpAspSer-GluSerLeuGlnLysGluThrValSerGlnLysAspValCysLeuProLys 91

97 TGGGGGGCGTGAGAGTCTCTGTGAGACTGTTTCACAGAGGATGTGTGTTTACCCCAAGGC 156

91 aThrHisGlnLysGluLeuAspLysIleAsnGlnLysLeuGluSerProAspAsnAs 111

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111 pGlyPheLeuLysAlaProCysArgMetLysValSerIleProThrLysAlaLeuGluLe 131

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151 aileGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGlnThrLe 171

114 LeuLysAlaProCysArgMetLysValSerIleProThrLysAlaLeuGluLeuMetAsp 133  
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154 MetGlnLysSerValProAsnLysAlaLeuGluLysAsnGluGlnThrLeuArgAla 173  
309 ATGCAAAAGTCTGTTCCAAATGAAGCTTGAATTCGAGATGAACAAACATTGAGACA 250  
174 AspGlnMetPheProSerGluSerLysGlnLysValGluGlnLysSerTrpAspSer 193  
249 GATCAGATGTTCCCTTCAGAAATCAAAACAAAGAACGTTGAGAGAAATTTCTGGGATCT 190  
194 GluSerLeuArgGluThrValSerGlnLysAspValCysValProLysAlaThrHisGln 213  
189 GAGAGTCTCCGTCAGACTGTTTCACAGAGAGTGTGTGTATCCCAAGGCTACACATCA 130  
214 LysGluMetAspLysIleSerGlyLysLeuGluAspSerThrSerLeuSerLysIleLeu 233  
129 AAGAAATGGAATAAATAAGTGAATAATAGAGATTCAACTAGCTTATCAAAAATCTTG 70  
234 AspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHisCysGluGlnArg 253  
69 GATCAGTTCATTCTTGTGAAGAAGCAAGGAACTTCAAAAGAGACCCCTGTGACCCAGT 10  
254 ThrGlyLys 256  
9 TCAGAGAAA 1

RESULT 3  
AW373574  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLES  
JOURNAL  
COMMENT

AW373574 565 bp mRNA linear EST 04-FEB-2000  
QV4-BT0534-281299-053-a01 BT0534 Homo sapiens cDNA, mRNA sequence.  
AW373574  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 565)  
HCGP <http://www.ludwig.org.br/ORESTES>.  
The FAPESP/LICR Human Cancer Genome Project  
Unpublished (1999)  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV4t2-QV4-BT0534-281299-053-a01&t3=1999-12-28&t4=1>)  
Seq primer: puc 18 forward  
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/note="Organ: breast; Vector: puc18; Site 1: SmaI; Site 2:  
SmaI; A mini-library was made by cloning products derived  
from ORESTES PCR (U.S. Letters Patent application No.  
196,716 - Ludwig Institute for Cancer Research) profiles  
into the pUC 18 vector. Reverse transcription of tissue

mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Alignment Scores:  
Pred. No.: 1,37e-63 Length: 565  
Score: 771.00 Matches: 153  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 29.67% Indels: 0  
DB: 10 Gaps: 0

US-09-451-739H-16 (1-512) x AW373574 (1-565)

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Db 13 GTTCTCATCTCATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 72  
QY 378 GluIleAlaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrluGlnLysGlu 397  
Db 73 GAANTGCCATGCTAAATAGCAATAGCAATAGCAATAGCAATAGCAATAGCAATAGCAATAG 132  
QY 398 AsnLysTyrluPheGluAspIleLysIleLysLysLysLysLysLysLysLysLysLys 417  
Db 133 AATAAATACTTTGAGGACATTAAGATTTTAAAGAGAAAGAAATGCTGAACCTTCAGATGACC 192  
QY 418 LeuLysLysLysGluLysSerLysThrLysArgAlaSerGlnTyrluSerGlyLysLys 437  
Db 193 CTAAACTGGAAGAGAGATCAATTAACATAAGGGCATCTCAATATAGTGGCAGCTTAAA 252  
QY 438 ValLeuIleAlaGluAsnThrMetLeuThrSerLysLysLysLysLysLysLysLysLys 457  
Db 253 GTTCTCATAGCTGAGACACACATGCTCACTTTCTAAATGAAAGGAAAGAAACAAAGCAAGAA 312  
QY 458 IleLeuGluAlaGluIleGluSerHisProArgLeuAlaSerAlaValGlnAspHis 477  
Db 313 ATACTAGAGGCGAAGAAATGAAATCAACCATCTCTAGACTGGCTTCTGCTGTACAGACCAT 372  
QY 478 AspGlnIleValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAla 497  
Db 373 GATCAATTTGTGACATCAAGAAAAGTCAAGAACTGCTTCCATTCACATTCGAGGAGATGCT 432  
QY 498 CysLeuGlnArgLysMetAsnValAspValSerSerThr 510  
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RESULT 4  
BE177744/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLES  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

BE177744 650 bp mRNA linear EST 22-JUN-2000  
RC1-H70598-140300-021-b02 HT0598 Homo sapiens cDNA, mRNA sequence.  
BE177744  
BE177744.1 GI:8656896  
EST.  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 650)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,  
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,  
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
10737800  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,



```

/tissue_type="Testis"
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/note="Vector: pBluescript"

ORIGIN
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Best Local Similarity: 46.22% Mismatches: 105
Query Match: 27.57% Indels: 48
DB: 11 Gaps: 8

US-09-451-739H-16 (1-512) X BC028407 (1-3443)

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DB 1598 CAAGTGTGTATACCTGAGTCTATGATATCAAGAAAGTAATGAGATAAATAGAGAAGTAGAA 1657

QY 21 GluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSerValPro 40
DB 1658 GAGTTCCTGAGAGCACTCTCCCTTCAGCTCGCGTTGAATGCATAAAGACTGTTCCA 1717

QY 41 AsnLysAlaLeuGluLysLysGlnThrLeuArgAlaAspGluLeuLeuProSer 60
DB 1718 AATAAGCCTTTGAATTGAAGATGAACAACATTGAGAGCAGCTCAGATGTTCCCATCA 1777

QY 61 GluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGluSerLeuGluThr 80
DB 1778 GATCCAAACAAAGACGATGAAGAAATTTCTGGATTCTGAGAGTCCCTGTGAGAG 1837

QY 81 ValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLeuAspLysIle 100
DB 1838 GTTTCACAGAGGATGTGATTATCCCAAGCTACACATCAAAAGAATTCGATACCTTA 1897

QY 101 AsnGlyLysLeuGlu----- 105
DB 1898 AGTGGAAATTAAGACCTTACCTGTGGAAGAAAGTTTCTCTTCCAAATAAAGCCTTAGA 1957

QY 106 -----GluSerProAspAsnAspGlyPheLeuLysAl 116
DB 1958 ATTAAAGGACAGAGAAACATTCAAAGCAGAGTCTCTGATAAAGATGGTCTTCTCAAGCC 2017

QY 116 aProCysArgMetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnTh 136
DB 2018 TACCTGTGAAGAAAGTTTCTCTTCCAAATAAAGCCTTAGAATTAAGGACAGAGAAC 2077

QY 136 rPheLysAlaGluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLys 156
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QY 156 sSerValProAsnLysAlaLeuGluLysLysGlnThrLeuArgAlaAspGlnMe 176
DB 2138 TTCTCTTCCAAATAAAGCTTTGAATTGAAGACAGAGAAACATTCAAAGCAGCTCAGAT 2197

QY 176 tPheProSerGluSerLysGlnLysLysValGluGluAsnSerTrpAspSerGluSerIle 196
DB 2198 GTTCCCATCAGATCCAAACAAAGGATGATGAGAAATTTCTGGATTCTGAGAGTTT 2257

QY 196 uArgGluThrValSerGlnLysAspValCysValProLysAlaThrHisGlnLysGluMe 216
DB 2258 CCTTGAGGCTCTCTTACAGAAATGATGGGTGTTTACCACAGGCTACACATCAAAAGAAAT 2317

QY 216 tAspLysIleSerGlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrVa 236
DB 2318 CGATACCTTAAGTGGAAATTTAGAGAGTCTCTGTGATAAGATGGTCTTCTGAGCCT-- 2375

QY 236 lHisSerCysGluArg-----AlaArgGluLeuGluAspHi 249
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Db 2424 ----GACAGAGAAACACTCAAGCAGAGTCTCTGTATAAGATGGTCTTCTGAGCCTAC 2479
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Db 2480 CTGTGTAAGGAAAGTTTCTCTTCCAAATAAAGCCTTAGAATTAAG-----GACAG 2530
QY 283 nGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuThrLeuAsnGlnGlu 303
Db 2531 AGAAACATTAAAGACGCTCAGATGTTCCCATCAGAAATCAAAACAAAGATGATGAGA 2590
QY 303 uGluLysArgArgAsnAlaAspIleLeuAsnGluLysIleArgGluGluLeuGlyArgI 323
Db 2591 AAATTTCTGGATTTTGAAGATTTCTCTGAGAGTCTCTTACAGAAATGATGTGTGTACC 2650
QY 323 eGluGluGlnHisArgLysGluLeuGlu 332
Db 2651 CAAGGCTACACATCAAAAGAAATTCGAT 2678

RESULT 6
BC036210 3794 bp mRNA linear HTC 20-SEP-2002
LOCUS Homo sapiens, clone IMAGE:5265638, mRNA.
ACCESSION BC036210
VERSION BC036210.1 GI:23242519
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3794)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: gcgaps-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www.sngc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 63 Row: e Column: 18
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis
This clone has the following problem: frame shifted.
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Location/Qualifiers
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Pred. No.: 646.00 Matches: 191
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QY	220	SerGlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThrValHisSerCys	239
Db	297	-----GATCACTACCTTCAAAAATCTGGATGCACCTTCCTTCCTGT	341
QY	240	GluArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGln	259
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QY	260	MetLysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLysGluLysSer	279
Db	402	ACAAAAATAAGTTTGTGTACTACAAAGGAAGTGTGAGAGCGAAAGAAATAAATCA	461
QY	280	GlnLeuGluAenGlnLysValLysTrpGluGlnGluLeuCysSerValArgLeuThrIleu	299
Db	462	CAGTTAGTAGACACCAAAAGCTAAATCGGAACAGAGCTCTGCAGTGTGAGATTGACTTTA	521
QY	300	AenGlnGluGluGluLysArgAGAsnAlaAspIle	311
Db	522	ATCAAGAGAGAGAGAGAGAGAAATGTCGATATA	557

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 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 HOMO SAPIENS  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE  
 1 (bases 1 to 443)  
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P.,  
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,  
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
 Simpson,A.J.  
 Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 200202663  
 10737800  
 COMMENT  
 Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?l=Rc1&t2=RC1-BT0254-1>)  
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 High quality sequence start: 9  
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/clone lib="BT0254"  
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ORIGIN

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Best Local Similarity: 96.15% Mismatches: 1  
Query Match: 20.01% Indels: 0  
DB: 10 Gaps: 0

US-09-451-739H-16 (1-512) x BF746270 (1-443)

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130 CAATCAGAGCTCCGAGAGCCATCTGCTCGAGCTGCCATTGAAATGCAAAAGTCT 189  
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QY 79 GluThrValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLysGluLeu 98  
Db 310 GAGACTGTTTCACAGAGGATGTGTTTCCCAAGTCTACATCAAAAGAAATAGAT 369  
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DEFINITION BF746340  
ACCESSION BF746340  
VERSION BF746340.1 GI:12073016  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 443)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
10737800  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922

TITLE

JOURNAL  
MEDLINE  
PUBMED

COMMENT

Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCI&t2=RCI-BT0254-081100-119-a03&t3=2000-11-08&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 9  
High quality sequence stop: 439.  
Location/Qualifiers  
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/note="Organ: breast; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

FEATURES

source

ORIGIN

Alignment Scores: 1.01e-39 Length: 443  
Pred. No.: 520.00 Matches: 100  
Score: 520.00  
Percent Similarity: 99.04% Conservatives: 3  
Best Local Similarity: 96.15% Mismatches: 1  
Query Match: 20.01% Indels: 0  
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US-09-451-739H-16 (1-512) x BF746340 (1-443)

QY 19 LysAlaGluProGluLysProSerAlaPheGluProAlaIleGluMetGlnLysSer 38  
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130 CAATCAGAGCTCCGAGAGCCATCTGCTCGAGCTGCCATTGAAATGCAAAAGTCT 189  
QY 39 ValProSerLysAlaLeuGluLysAsnGluGlnThrLeuArgAlaAspGluLeu 58  
Db 190 GTTCCAAATGAAGCTTTGGAATGAAGATGAACAAACATTGAGAGCAGATGACTC 249  
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RESULT 10

LOCUS

DEFINITION

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BG539426  
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VERSION BG539426.1 GI:13531659  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE

1 (bases 1 to 904)  
NIH-MGC http://mgc.nci.nih.gov/.

AUTHORS

BG539426 904 bp mRNA linear EST 03-APR-2001  
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BG539426  
BG539426  
VERSION BG539426.1 GI:13531659  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 904)  
NIH-MGC http://mgc.nci.nih.gov/.



TITLE JOURNAL COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgaabbs-remail.nih.gov Tissue Procurement: CLONTECH Laboratories, Inc. cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LCM1513 row: 1 column: 12 High quality sequence stop: 608.	
	FEATURES source 1. 904 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clones="IMAGE:4692635" /lab_host="DH10B (T1 phage-resistant)" /clone_lib="NIH MGC 77" /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site: 1: SfiI (ggccattatggcc); Site 2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGCGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC library."	
ORIGIN	Alignment Scores: Pred. No.: 2.22e-33 Length: 904 Score: 458.00 Matches: 109 Percent Similarity: 68.27% Conservative: 61 Best Local Similarity: 43.78% Mismatches: 72 Query Match: 17.62% Indels: 7 DB: 12 Gaps: 3 US-09-451-739H-16 (1-512) x BG539426 (1-904)	
	QY 244 GluLeuGlnLysAspHisCysGluGlnArgThrGlyLysMetGluGlnMetLysLysLys 263 DB 6 AAATTAAAGTAATCACTGTGAGCACTTGTAGTAAATTCGAAATCGAAATGAAATG 65 QY 264 PheCysValLysLysLysLysSerGluAlaLysGluLysSerGlnLeuGluAsn 283 DB 66 GCTAGTGTAACAAAGAGAATCTGAAAGAGAAATATAATCGCAGTTAAAGCAT 125 QY 284 GlnLysValLysTrpGluGlnLysCysSerValArgLeuThrLeuAsnGlnGlu 303 DB 126 GAATACTTGTAATTTGAAAGAAAGAACTGTGTAGTTGAGATTGGCATAACGAAAGAAA 185 QY 304 GluLysArgArgAsnAlaAspIleLeuAsnGlnLysLysLysLysLysLysLys 323 DB 186 AAGAAAGAGAAATGTTGAAGAGTTGCACCAAAAGTAGTGGAAAGATTAAGATACAA 245 QY 324 GluGlnGlnHisArgLysGluGluValLysGlnGlnLeuGluGlnAlaLeuArgIle 343 DB 246 GAAGAGCAATATAGATAGAGCTGATGTGACAAACCAATTAACCGGCTCTCAATCA 305 QY 344 GlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnValSerHisThrHisGlu 363 DB 306 GCAGAGGTGGATTCAGACAGAGGAGAAATTAATCAATCAGTTTGTAACTGATCAA 365 QY 364 AsnGluAsnThrLeuLeuHisGluAsnCysMetLeuLysLysGluIleAlaMetLeuLys 383 DB 366 AAAGAGAC---CTGCTCATGAAACCGCTTGTATGCAAGATGAATTCAGGCTCAGG 422 QY 384 LeuGluIleAlaThrLeuLysHisGlnTrpGlnGlnLysGluAsnLysThrPhe-GluAs 403	
Db	423 CTGGAAAAAGACACAAATAAAAAACCAAAACCTGGAAAAG-----AAATACTTAACAAGA 476	
	QY 403 pileLysIleLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLysLeuLysGluG 423	
Db	477 CTTTGAATTTGAAAAAGAAAGACATGAAGACCTTCAAAAGGCTCTAAAAACGGAATGGGA 536	
	QY 423 uSerLeuThr-LysArgAlaSerGlnTyrSerGlyGlnLeuLysValLeuIleAlaGluA 443	
Db	537 ACATTTAGCAAAACAGATAGCTGCTGTAATAGTGGACAGCTAGCTCTCTGCAGATGACA 596	
	QY 443 snThrMetLeuThrSerLysLysLysGluLysGlnAspLysGlu---IleLeu-GluAla 461	
Db	597 ACACAACGCTCGTTACAACTGGAGAAAGCAAGAGCGAAGCAGGCAACGATGGGAACA 656	
	QY 462 GluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAspGlnIleVal 481	
Db	657 GAAGGCAATCATACCTGCTGACTGAAGGCTGCCAAAGGACCATGACCAAGGAT 716	
	QY 482 ThrSerArgLysSerGlnGlu 488	
Db	717 CCATCAGAGAGAGACAAA 737	
RESULT 11	BG431116 862 bp mRNA linear EST 14-MAR-2001	
	LOCUS 602498742F1 NTH_MGC_75 Homo sapiens cDNA clone IMAGE:4612186 5',	
DEFINITION	mRNA sequence.	
	ACCESSION BG431116	
KEYWORDS	EST..	
	SOURCE BG431116.1 GI:13337622	
ORGANISM	Homo sapiens (human)	
	Homo sapiens	
REFERENCE	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	1 (bases 1 to 862)	
AUTHORS	NIH-MGC http://mgi.nci.nih.gov/	
	National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL	Unpublished (1999)	
	COMMENT Contact: Robert Strausberg, Ph.D. Email: cgaabbs-remail.nih.gov Tissue Procurement: CLONTECH Laboratories, Inc. cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LCM1360 row: d column: 11 High quality sequence stop: 730.	
FEATURES	Location/Qualifiers	
	1. 862 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:4612186" /lab_host="DH10B (T1 phage-resistant)" /clone_lib="NIH MGC 75" /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGCGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC library."	
ORIGIN	Alignment Scores: Pred. No.: 1.91e-31 Length: 862 Score: 437.50 Matches: 108 Percent Similarity: 65.62% Conservative: 39	

Best Local Similarity: 48.21% Mismatches: 62  
 Query Match: 16.83% Indels: 15  
 DB: 12 Gaps: 5

US-09-451-739H-16 (1-512) x BG431116 (1-862)

QY 291 GluLeuCysSerValArgLeuThrLeuAenGlnGluGluLysArgAsnAlaasp 310  
 Db 2 GAATTCAGGACTGTAAGAAAGTAATTTGAATCAGGTCCTTCAAGAGCGAATGAGCCT--- 58  
 QY 311 IleLeuAsnGluLysIleArgGluLeuGluGlyArgIleGluGluGlnHisArgLysGlu 330  
 Db 59 -----CAGAGGCAACTTTCTCA-----GAACAAATGCCAGAAATG 94  
 QY 331 LeuGluValLysGlnGlnLeuGluGlnAlaLeuArgIleGlnAspIleGluLeuLysSer 350  
 Db 95 TTACAGATGGAATTCGACCAATCACCTTCCAAACAAAGGAGATTAATGGCTCAA 154  
 QY 351 ValGluSerAsnLeuAsnGlnValSerHisThrHisGluAsnGluAsnTyLeuLeuHis 370  
 Db 155 AAGAAATGAAT---TCTCAGAAATTCATAGTCATGAAGAAGAAAGAAAGACTATCGCAT 211  
 QY 371 GluAsnCysMetLeuLysGluIleAlaMetLeuLysLeuGluIleAlaThrLeuLys 390  
 Db 212 AAAATATAGCATGTTCAGGAAGAAATTCGTATGCTAAGACTAGAAATAGACACATATAA 271  
 QY 391 HisGlnTyThrGlnGluLysGluAsnLysTyPheGluAspIleLysIleLeuLysGluLys 410  
 Db 272 ATCAAAACAGGAAAGAAAGAAATGTTCTGAGGACCTTAAATTTGTAAGAAAGAAAG 331  
 QY 411 AsnAlaGluLeuGlnMetThrLeuLysLeuLysGluGluSerLeuThrLysArgAlaSer 430  
 Db 332 AATGAAGACTTTCAGAAAGACTATAAAACAGAAATGAGGAAACATTAACACAAATATCC 391  
 QY 431 GlnTySerGlyGlnLeuLysValLeuIleAlaGluAsnThrMetLeuThrSerLysLeu 450  
 Db 392 CAGTAAATGAGCGGTGATGTTCTGACAGCTGAGATGCAATGCTAAATTCATAACTG 451  
 QY 451 Lys---GluLysGlnAspLysGluIleLeuGluAlaGluIleGluSerHisHisProArg 469  
 Db 452 GAGAATGAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 511  
 QY 470 LeuAlaSerAlaValGlnAspHisSerGlnIleValThrSerArgLysSerGln---GluP 489  
 Db 512 TGGGCTGCTGCTATCATCATCTGATCAAGTGAAGATCAATCAAAAGAAAGAAAGCTAGAAC 571  
 QY 489 rolapheHisIleAlaGlyAspAlaCys-----LeuGlnArgLysMetAsnValaAspV 507  
 Db 572 TTGCTTTCCAGAGAGCAAGAGATGAATGTTCTCGTTTACAGACAAATGAATTTTGTATG 631  
 QY 507 alSerSer 509  
 Db 632 TGCTAAC 639-

RESULT 12  
 BG622779  
 LOCUS 602647567F1 NIH\_MGC\_79 Homo sapiens cDNA clone IMAGE:476891.2 5',  
 DEFINITION mRNA sequence.

ACCESSION BG622779.1 GI:13674150  
 VERSION  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 821)  
 NIH-MGC http://mgs.nci.nih.gov/  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs@mail.nih.gov  
 Tissue Procurement: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLCM1633 row: f column: 17  
 High quality sequence stop: 818.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:476891.2"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NIH\_MGC\_79"  
 /note="Orxan: Placenta; Vector: pDNR-LIB (Clontech);  
 Site\_1: Sfil (ggcgctcgcc); Site\_2: Sfil  
 (ggcgctcgcc); 5' and 3' adaptors were used in cloning  
 as follows: 5' adaptor sequence: 5'-CAGGCCATTAATGGCC-3'  
 and 3' adaptor sequence:  
 5'-ATTCTAGAGCGGCGGCGGCATG-dt(30)BN-3' (where B = A,  
 C, or G and N = A, C, G, or T). Average insert size 1.3  
 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts  
 by PCR. This library was enriched for full-length clones  
 and was constructed by Clontech Laboratories (Palo Alto,  
 CA). Note: this is a NIH\_MGC Library."

ORIGIN

Alignment Scores:  
 Pred. No.: 4,31e-31 Length: 821  
 Score: 433.50 Matches: 117  
 Percent Similarity: 65.56% Conservative: 60  
 Best Local Similarity: 43.33% Mismatches: 84  
 Query Match: 16.68% Indels: 12  
 DB: 12 Gaps: 5

US-09-451-739H-16 (1-512) x BG622779 (1-821)

QY 216 MetAspLysIleSerGlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThr 235  
 Db 20 ATTGATCAACATGAAATCAAGTGAAGATTGTTCACCTATTGAATTAAGAGACA 79  
 QY 236 ValHisSerCysGluArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGly 255  
 Db 80 TTGTG-TTATGTAAGAGATTAAACAGAACTTAAAGATAATCACTGTGAGCAACTTAGAGTA 138  
 QY 256 LysMetGluGlnMetLysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLys 275  
 Db 139 AAAATTCGAAACTGAAATAATAGCTAGTGTACTACAAAGAGACTATCTGAAAGAA 198  
 QY 276 GluIleLysSerGlnLeuGluAsnGlnLysValLysTrpGluGlnLysSerVal 295  
 Db 199 GAAATTAATCGCAGTTAAAGCATGAACACACTGAATGGGAAAAGAACTCTGTAGTTTG 258  
 QY 296 ArgLeuThrLeuAsnGlnGluLysArgAsnAlaAspIleLeuAsnGluLys 315  
 Db 259 AGATTGTCATACAGCAGAGAAAAGAAAGAAAGAAATGTTCAAGAGTTGCACCAAAA 318  
 QY 316 IleArgGluGluLeuGlyArgIleGluGluGlnHisArgLysGluLeuValLysGln 335  
 Db 319 GTTAGGAAAGATTGAAGATTCACAGAGAGCAATATAGGATAGAGCTGATGTGACAAA 378  
 QY 336 GlnLeuGluGlnAlaLeuArgIleGlnAspIleGlnLysSerValGluSerAsnLeu 355  
 Db 379 CCAATTAACC-GGCTCTCAATCAGCAGAGGTGAATTTGAAGACAGAGGAAATATTCA 437  
 QY 356 AsnGlnValSerHisThrHisGluAsnGluAsnTyLeuLeuHisGluAsnCysMetLeu 375  
 Db 438 AATCAGGTTCTGAAACTGATGAAGAAAGAGAC---CTGCTGATGAAACCG-TTGATG 493  
 QY 376 LysLysGluIleAlaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyGlnGlu 395

Db 494 CAAGATGAATTCAGCGCTCGGCTGGAAGACACACACATAAACAACCAACCAACCTGGAA 553  
 Qy 396 LysGluAsnLysTyrPheGluAspIleLysLeuLysGluLysAsnAlaGluLeuGln 415  
 Db 554 AAG-----AAATACCTTAAAGACTTTGAAATTGTGAAAGAAAGCATGAAGACCTTCAA 607  
 Qy 416 MetThrLeuLysLeuLysGluLysLeuThrLysArgAlaSerGlnTyrSer-GlyG1 435  
 Db 608 AAGGCTCTAAACCGAATGAGAAACATTAGCAGAAACGATAGCTCTTATAGTGGACA 667  
 Qy 435 nLeuLysValLeuLeuAlaGluAsnThrMetLeuThrSerLys-LeuLysGlu---LysG 454  
 Db 668 AGTTGCTGCTCTGACGGATGAAACACA-----ACCTCCGCTTCTAAACCGGGAGAGC 721  
 Qy 454 nAspLysGluLeuLeuGluAlaGluLeuGluSerHisHisProArgLeuAlaSer---A 473  
 Db 722 AAAGAGAGAGCGGGCAAGACTGGAACACAGAAATGATCATACCGTGTGACTGAATGTG 781  
 Qy 473 laValGlnAspHisAspGlnIleVal 481  
 Db 782 CTCATGTGATCCTGATCAAGTCCTC 807  
 RESULT 13  
 CA394381  
 LOCUS  
 DEFINITION  
 cs50h08.Y1 Human Retinal pigment epithelium/choroid cDNA  
 (Un-normalized, unamplified): cs Homo sapiens cDNA clone cs50h08  
 5', mRNA sequence.  
 ACCESSION  
 CA394381  
 VERSION  
 CA394381.1 GI:24728876  
 SOURCE  
 EST.  
 ORGANISM  
 Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 684)  
 Wistow,G., Bernstein,S.L., Wyatt,M.K., Farris,R.N., Behal,A.,  
 Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.  
 Expressed sequence tag analysis of human RPE/choroid for the  
 NEIBank Project: Over 6000 non-redundant transcripts, novel genes  
 and splice variants  
 Mol. Vis. 8 (4), 205-220 (2002)  
 JOURNAL  
 MEDLINE  
 22103450  
 PUBMED  
 12107410  
 COMMENT  
 Contact: Wistow G  
 Section on Molecular Structure and Function  
 National Eye Institute  
 6/331, NIH, Bethesda, MD 20892-2740, USA  
 Tel: 301 402 3452  
 Fax: 301 496 0078  
 Email: graeme@helix.nih.gov  
 Plate: 50 row: h column: 08  
 Seq primer: M13RPI reverse primer (ABI).  
 Location/Qualifiers  
 1..684  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="cs50h08"  
 /tissue\_type="RPE/choroid"  
 /dev\_stage="Adult"  
 /lab\_host="EMDH108"  
 /clone\_lib="Human Retinal pigment epithelium/choroid cDNA  
 (Un-normalized, unamplified): cs"  
 /note="Organ: Eye; Vector: pCMVSPORT6; Two different donor  
 eyes (75-80 years old) yielded approximately 600 mg of  
 dissected RPE/choroid tissue. This in turn yielded 340 ug  
 of total RNA and 7 ug of mRNA. A directionally cloned cDNA  
 library in the pCMVSPORT6 vector was constructed at Life  
 Technologies (Rockville, MD; now part of Invitrogen Corp),  
 essentially following the protocols of the SuperScript  
 Plasmid System (Invitrogen Corp.  
 <http://www.invitrogen.com/>). The library code

designation was cs. For this library, cDNA inserts were  
 cloned into the NotI/MluI sites of the vector. EST  
 analysis was performed on the unamplified library at the  
 NIH Intramural Sequencing Center (NISC)."

## ORIGIN

Alignment Scores:  
 Pred. No.: 5,26e-31 Length: 684  
 Score: 431.50 Matches: 95  
 Percent Similarity: 68.04% Conservative: 54  
 Best Local Similarity: 43.38% Mismatches: 67  
 Query Match: 16.60% Indels: 3  
 DB: 14 Gaps: 2

US-09-451-739H-16 (1-512) x CA394381 (1-684)

Qy 216 MetAspLysIleSerGlyLysLeuLysAspSerThrSerLysLysLeuAspThr 235  
 Db 36 ATGTATCAACATGAATGAAGTGTAAAGATTGTGTTCACCTATTGAAAATTAATAACA 95  
 Qy 236 ValHisSerCysGluArgAlaArgGluLeuGlnLysAspHisCysGluGlnArgThrGly 255  
 Db 96 TTTTGTATTATGAAAAGAGATTATAAACTTAAAGTAACCACTGTGACCAACTTAGATA 155  
 Qy 256 LysMetGluGlnMetLysLysPheCysValLeuLysLysLysLeuSerGluAlaLys 275  
 Db 156 AAAATTCGAAACTGAAAATAAGCTAGTGTACTACAAAAGAGAATATCTGAAAAGAA 215  
 Qy 276 GluIleLysSerGlnLeuGlnLysValLysTrpGluGlnGluLysCysSerVal 295  
 Db 216 GAAATAAAATCGAGTTAAAGCATGAAATCTGTAATTTGGAATAAAAGAACTCTGTAGTTG 275  
 Qy 296 ArgLeuThrLeuAsnGlnGluGluLysArgAspAlaAspIleLeuAsnGluLys 315  
 Db 276 AGATTTCCTATACAGCAAGAAAAGAAAAGAAAGAAATGTTGAAGAGTTGCCACCAAAA 335  
 Qy 316 IleArgGluGluLeuGlyArgIleGluGluGlnHisArgLysGluLeuGluValLysGln 335  
 Db 336 GTTAGGAAAAGTTAAGAATAACAGAAAGACGAATATAGGATAGAAGCTGTGTGACAAA 395  
 Qy 336 GlnLeuGluGlnAlaLeuArgIleGlnAspIleGluLysSerValGluSerAsnLeu 355  
 Db 396 CCAATTAAACCGGCTCTCAATCAGCAGAGGTGGAAATTCAGACAGAGGAATAATTCTCA 455  
 Qy 356 AsnGlnValSerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeu 375  
 Db 456 AATCAGGTTTCTGAAACTGATGAAAAGAAAGAC---CTGCTGATGAAAACCGCTTGATG 512  
 Qy 376 LysLysGluLeuAlaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGlu 395  
 Db 513 CAAGATGAAATTCGCCAGGCTTCAGGCTGGAAAAGACACAAATAAAACCAAAACCTGGAA 572  
 Qy 396 LysGluAsnLysTyrPheGluAspIleLysIleLysLysGluLysAsnAlaGluLeuGln 415  
 Db 573 AAG-----AAATACITAAAGACTTTGAAATTGTGAAAAGAAAGCATGAAGACCTTCAA 626  
 Qy 416 MetThrLeuLysLeuLysGluLysLeuThrLysArgAlaSerGlnTyrSerGly 434  
 Db 627 AAGGCTCTAAACCGAATGCGGAACATTAGCAAAAACGATAGCTGCTTATATAGTGA 683

## RESULT 14

CF181571  
 LOCUS  
 DEFINITION  
 818415 MARC 3PIG Sus scrofa cDNA 5', mRNA sequence.  
 ACCESSION  
 CF181571  
 VERSION  
 CF181571.1 GI:33293347  
 KEYWORDS  
 EST.  
 SOURCE  
 Sus scrofa (pig)  
 ORGANISM  
 Sus scrofa  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 1 (bases 1 to 683)  
 Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Fox,J.,  
 AUTHORS

418	QY	GAGTTTAGACAGCAAAAGAAAGAGCTGATGATAAGAGCTGAAATGAAACACACACACTTGAA	477
339	QY	GlnAlaLeuArgIleGlnAspIleGluLeuLysSerValGluSerAsnLeuAsnGlnVal	358
478	Db	CTGACTGTCCAAAGCAGCTGGACATGGAAATTGAGGGCGTGGAGAAATAATCTGAACACAGGT	533
339	QY	SerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGlu	378
538	Db	GATGAGATCTCGAAAAAGCAAAAGAACTGTGTGCTTAAPAAACCATGTCACAGAATGAA	597
379	QY	IleAlaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLysGluAsn	398
598	Db	ATTGCATGTTAAACACAGAAATAGAGCGCAGTGGAAATCATACACAGGAATGAGGAAG	657
399	QY	LysTyrPheGluAspIleLysIle	406
658	Db	AAATATTTTATGGACATGAAAAAT	681

D<sub>0</sub> 658 AATAATTTATGGACATGAAATT 681

658 AAATATTTTATGGACATGAAAATT 681

RESULT 15

BU678550/c

**DEFINITION** UI-CF-DU1-aar-o-16-0-UI.s1 UI-CF-DU1 Homo sapiens cDNA clone

ACCESSION BU678550

VERSION BU678550.1 GI:23525612  
KEYWORD DCE

SOURCE Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 638)

**AUTHORS**  
 Ronaldo, M.F., Lennon, G. and Soares, M.B.  
 Wastewater treatment and substitution have contributed to feedlot contamination

discovery

**MEDLINE 97044477**

PUBMED	8883348	Contact: McCray	DR
COMMENT			

McCray Lab  
Vancouver, BC, Canada

2024 University of Iowa Med Labs, Iowa City, IA 52242, USA

**Fax: 319 356 7171**

Email: [paul-mccray@uiowa.edu](mailto:paul-mccray@uiowa.edu)  
 Title: Procurement, Dr. M. J. Welch, University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

CLONE DISTRIBUTION: RESEARCHERS MAY OBTAIN CLONES FROM REGENERATION GENETICS ([www.reggen.com](http://www.reggen.com)) OR FROM OPEN BIOSYSTEMS

(www.openbiosystems.com).

POLYA=Yes.

source	1. .638
--------	---------

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/organism="Homo sapiens"
/mol_type="mRNA"

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/db_xref="taxon:9606"
/seq_id="17225"

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/tissue_type="Primary Lung Epithelial Cells"
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/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
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/clone_ID="OI-CF-DUI"
/rote="Organ: lung; Vector: pT7T3-pac (pharmacia) with a

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```
modified polylinker; Site_1: EcoR I; Site_2: Not I;
```

following tissue(s): Primary Lung Epithelial Cells The

Soares. Genome Research, 6:791-806, 1996. First strand

cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated

to an EcoR I adaptor, digested with Not I, and cloned

\_\_\_\_\_

used to prime the synthesis of first-strand cDNA contains  
a library tag sequence that is located between the Not I  
site and the (dr)18 tail. The sequence tag for this  
library is GGCTGTAGGC.  
TAG TISSUE=Lung Epithelial Cells Tissue nos 359-368  
TAG\_LIB=UI-CF-DUI  
TAG\_SEQ=GGCTGTAGGC"

ORIGIN

Alignment Scores:

Pred. No.: 1.31e-29 Length: 638  
Score: 416.50 Matches: 91  
Percent Similarity: 74.68% Conservative: 24  
Best Local Similarity: 59.09% Mismatches: 35  
Query Match: 16.03% Indels: 4  
DB: 13 Gaps: 2

US-09-451-739H-16 (1-512) x BUG78550 (1-638)

Qy 360 HistHrHisGluAnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluile 379  
Db 636 CATAGTCATGAGAGAGAAAGACCTATCGCATATAAATAGCATGGTCAGAGAAAT 577  
Qy 380 AlaMetLeuLysLeuGluileAlaThrLeu-LysHisGlnTyr-GlnGluLysGluasny 399  
Db 576 GCTATGCTAGACTAGAAATAGACACAATATAAAAAATCAAACCCAGGAAAAAGAA 517  
Qy 399 sTyrPheGluAspLeuLysLeuLysGluLysAsnAlaGluLeuMetThrLeuLy 419  
Db 516 ATGTTTTCAGGACCTTAATTTGPAAGAGAAAGATGAGACCTTCAGAGACTATAA 457  
Qy 419 sLeuLysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeuLysValle 439  
Db 456 ACAGATGAGGAAACATTAACACAAATATCCAGTATATGAGCGGCTTAGTGTCT 397  
Qy 439 uileAlaGluAsnThrMetLeuThrSerLysLeuLys--GluLysGlnAspLysGluil 458  
Db 396 GACAGCTGAGAAATGCAATGCTTAATTTCTAACTGGAGAAATGAAAGCAAGCAAGGAAG 337  
Qy 458 eLeuGluAlaGluileGluSerHisHisProArgLeuAlaSerAlaValGlnAspHisAs 478  
Db 336 ACTGGAACGACAGAGTGAATCATACCATTCATGATTGGCTGCTGCTATACATGCTGA 277  
Qy 478 pGlnIleValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCy 498  
Db 276 TCAAAGTGAGACATCAAAAGAGAACTAGAACTTGCTTTCCAGAGAGAGAGATGAATG 217  
Qy 498 s-----LeuGlnArgLysMetAsnValAspValSerSer 509  
Db 216 TTCTCGTTTACAGGACAAATGAATTTTGATGTGTCTAAC 177

Search completed: May 6, 2004, 17:01:19  
Job time : 3866 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 07:44:53 ; Search time 81.0178 Seconds

(without alignments)  
5870.227 Million cell updates/sec

Title: US-09-451-739H-4

Perfect score: 857  
Sequence: 1 cctccgagacgggtccat.....tcataaacccaagggaagt 857

Scoring table: IDENTITY NUC

Gapop 10'0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*

1: /cgn2\_6/ptodata/2/ina/5A COMB.seq.\*  
2: /cgn2\_6/ptodata/2/ina/5B COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/6A COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	605.4	70.8	873	US-09-006-783A-4	Sequence 4, Appli
2	605.6	70.7	1902	US-09-258-257-1	Sequence 1, Appli
3	605.6	70.7	1902	US-09-258-371-1	Sequence 1, Appli
4	605.6	70.7	1902	US-08-569-721A-1	Sequence 1, Appli
5	605.6	70.7	1902	US-08-751-230-1	Sequence 1, Appli
6	605.6	70.7	1902	US-09-499-082-1	Sequence 1, Appli
7	605.6	70.7	1902	US-09-258-372-1	Sequence 1, Appli
8	605.6	70.7	2061	US-09-258-371-9	Sequence 9, Appli
9	605.6	70.7	2061	US-08-751-230-9	Sequence 9, Appli
10	605.6	70.7	2061	US-09-499-082-9	Sequence 9, Appli
11	605.6	70.7	2061	US-09-258-372-9	Sequence 9, Appli
12	604	70.5	2061	US-09-006-783A-2	Sequence 2, Appli
13	604.4	70.3	2061	US-09-159-871-1	Sequence 1, Appli
14	534.4	62.4	633	US-09-006-783A-6	Sequence 6, Appli
15	355	41.4	451	US-09-370-838-146	Sequence 146, App
16	142.6	16.6	840	US-09-601-478-6	Sequence 6, Appli
17	142.6	16.6	1078	US-09-601-478-7	Sequence 7, Appli
18	142	16.6	1154	US-09-484-970B-81	Sequence 81, Appli
19	96.4	11.2	678	US-09-195-286-3	Sequence 3, Appli
20	96.4	11.2	699	US-09-195-286-2	Sequence 2, Appli
21	73.4	8.6	7218	US-08-232-463-14	Sequence 14, Appli
22	65.6	7.8	1864	US-09-620-312D-435	Sequence 435, App
23	61.4	7.2	1926	US-09-249-585A-4	Sequence 4, Appli
24	61.4	7.2	1931	US-09-130-114-2	Sequence 2, Appli
25	59.6	7.0	1926	US-09-249-585A-2	Sequence 2, Appli
26	59.6	7.0	1926	US-09-410-399-3	Sequence 3, Appli
27	59.6	7.0	2580	US-09-050-863-2	Sequence 2, Appli

28 59.6 7.0 2580 4 US-09-359-081-2 Sequence 2, Appli  
C 29 59.6 7.0 5452 2 US-09-130-114-1 Sequence 1, Appli  
C 30 59.6 7.0 8705 4 US-09-647-344A-14 Sequence 14, Appli  
31 59.6 7.0 9600 3 US-08-910-647-1 Sequence 1, Appli  
32 59.6 7.0 9600 4 US-09-620-925-1 Sequence 1, Appli  
33 59.6 7.0 10596 1 US-07-884-811-15 Sequence 15, Appli  
34 59.6 7.0 10596 1 US-07-885-971-15 Sequence 15, Appli  
35 59.6 7.0 10596 1 US-08-087-783A-15 Sequence 15, Appli  
36 59.6 7.0 10596 1 US-08-194-088B-15 Sequence 15, Appli  
37 59.6 7.0 10596 2 US-08-194-087-15 Sequence 15, Appli  
38 59.6 7.0 10596 5 PCT-US93-04648-15 Sequence 15, Appli  
C 39 59.6 7.0 18080 4 US-09-724-566A-48 Sequence 48, Appli  
40 58 6.8 9551 1 US-08-056-200-93 Sequence 93, Appli  
41 58 6.8 9551 2 US-08-800-644-93 Sequence 93, Appli  
42 53.8 6.3 423 4 US-09-252-991A-10032 Sequence 10032, A  
43 53.8 6.3 426 4 US-09-252-991A-10158 Sequence 10158, A  
C 44 53.8 6.3 669 4 US-09-252-991A-9916 Sequence 9916, Ap  
45 53 6.2 2793 1 US-08-209-747-1 Sequence 1, Appli

## ALIGNMENTS

RESULT 1  
US-09-006-783A-4  
; Sequence 4, Application US/09006783A  
; Patent No. 6297366  
; GENERAL INFORMATION:  
; APPLICANT: Gudkov, Andrey V  
; APPLICANT: Garkavstev, Igor  
; APPLICANT: Riabowol, Karl  
; TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling  
; TITLE OF INVENTION: Pathway  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
; STREET: 300 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/006,783A  
; FILING DATE: 15-JAN-1998  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6297366nan, Kevin E  
; REGISTRATION NUMBER: 35,303  
; REFERENCE/DOCKET NUMBER: 97,837  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-913-0001  
; TELEFAX: 312-913-0002  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 873 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 7..813  
; US-09-006-783A-4

Query Match 70.8%; Score 606.4; DB 3; Length 873;  
Best Local Similarity 99.0%; Pred. No. 1.2e-124;  
Matches 610; Conservative 0; Mismatches 6; Indels 0; Gaps 0;





GENERAL INFORMATION:  
APPLICANT: Garkavtsev, Igor  
APPLICANT: Riabowol, Karl  
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR  
TITLE OF INVENTION: SUPPRESSOR GENE INGI  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: 699 Prince Street  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/258,371  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/751,230  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Mool, Leslie A.  
REGISTRATION NUMBER: 37,047  
REFERENCE/DOCKET NUMBER: 028722-144  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-7400  
TELEFAX: 415-854-8275  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1902 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 109..741  
US-09-258-371-1

Query Match 70.7%; Score 605.6; DB 2; Length 1902;  
Best Local Similarity 95.6%; Pred. No. 2.1e-124;  
Matches 623; Conservative 0; Mismatches 29; Indels 0; Gaps 0;  
Qy 206 CTAGGCTGCTCGGAGTGTGTGTCGCGCGCGGAGTGGAGATCTTGAAGGAGCTAGACGAG 265  
Db 1 CTGACCCGAGGCTGGGCGCGCGTGGCGTGAACACAGATCTCTGAAGGAGCTAGACGAG 60  
Qy 266 TGCTACGAGCGCTTCAGTCGCGAGACAGCGGGCGCGAGCGCGGATGCTGCACTGT 325  
Db 61 TGCTACGAGCGCTTCAGTCGCGAGACAGCGGGCGCGAGCGCGGATGCTGCACTGT 120  
Qy 326 GTGACGCGCGCGCTGATCCGCGAGCAGAGCTGGCGCGACAGAGATCCAGATCGTGAGC 385  
Db 121 GTGACGCGCGCGCTGATCCGCGAGCAGAGCTGGCGCGACAGAGATCCAGATCGTGAGC 180  
Qy 386 CAGATGTTGAGCTGTTGAGAAACCGACCGCGGAGAGTGGACGCCAGCTGTTTC 445  
Db 181 CAGATGTTGAGCTGTTGAGAAACCGACCGCGGAGAGTGGACGCCAGCTGTTTC 240  
Qy 446 GAGCGCGAGAGGAGCTGGGCGACACAGCGCGGCAACAGCGGAGGCTGGCGCGGACAGG 505  
Db 241 GAGCGCGAGAGGAGCTGGGCGACACAGTGGCGACAGCGGAGGTTGGCGCGGACAGG 300  
Qy 506 CCAAGCGGAGCGCGGAGCGCGAGCTGACAAAGCCCAACAGCAAGCGCTCACGCGCGCAG 565  
Db 301 CCAATGCGGATGCGGTAGCGCAGCTGTGACAAAGCCCAACAGCAAGCGCTCACGCGCGCAG 360  
Qy 566 CGCAACACGAGACCGGTGAGAACCGCTCCAGCAACACCGACACGACGAGCGCGCGCTCG 625

Db 361 CGCAACACGAGACCGTGAGAACCGGTCCAGCAACACCGACGACGACGCGCGCTCG 420  
Qy 626 GGCACACCCAGGAGAGAGAGCGGCGGAGACCTCCAGAGAGAGAGCGCTCCAGGCGCAAG 685  
Db 421 GGCACACCCAGGAGAGAGAGCGGCGGAGACCTCCAGAGAGAGAGCGCTCCAGGCGCAAG 480  
Qy 686 GGGAGCGAGAGGCGTCCCTGCGGACCTCCCGCATCGACCCCAACGACCCACGCTACTGT 745  
Db 481 GGGAGCGAGAGGCGTCCCTGCGGACCTCCCGCATCGACCCCAACGACCCACGCTACTGT 540  
Qy 746 CTGTGCAACCGAGTCTCTATGCGGAGATGATCGGTGCGGACGAGAGTGGCCCATC 805  
Db 541 CTGTGCAACCGAGTCTCTATGCGGAGATGATCGGTGCGGACGAGAGTGGCCCATC 600  
Qy 806 GAGTGTTCCTACTTCTGCTGCGTGGGCTCAATCATAAACCCAAAGGGCAAGT 857  
Db 601 GAGTGTTCCTACTTCTGCTGCGTGGGCTCAATCATAAACCCAAAGGGCAAGT 652

## RESULT 4

US-08-569-721A-1

Sequence 1, Application US/08569721A

Patent No. 6037121

GENERAL INFORMATION:

APPLICANT: GARKAVTSEV, Igor

APPLICANT: RIABOWOL, Karl

TITLE OF INVENTION: DNA SEQUENCE ENCODING A TUMOR

TITLE OF INVENTION: SUPPRESSOR GENE

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Burns, Doane, Swecker &amp; Mathis

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/569,721A

FILING DATE: 08-DEC-1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Mool, Leslie A.

REGISTRATION NUMBER: 37,047

REFERENCE/DOCKET NUMBER: 028722-128

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 854-7400

TELEFAX: (650) 854-8275

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1902 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 109..738

US-08-569-721A-1

Query Match 70.7%; Score 605.6; DB 3; Length 1902;

Best Local Similarity 95.6%; Pred. No. 2.1e-124;

Matches 623; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 206 CTAGGCTGCTCGGAGTGTGTGTCGCGCGCGGAGTGGAGATCTTGAAGGAGCTAGACGAG 265

Db 1 CTGACCCGAGGCTGGGCGCGCGTGGCGTGGAAACAGATCTCTGAGGAGCTAGACGAG 60

266 TGCTACAGGCTTCACTCGCGAGACAGACGGGGCCAGAGCGGGCGGATGCTGCACTGT 325  
Db TGCTACAGGCTTCACTCGCGAGACAGACGGGGCCAGAGCGGGCGGATGCTGCACTGT 120  
QY GTCCAGCGGCGCTGTATCCGACACAGGAGCTGGGCGACGAGAGATCCAGATCGTGAGC 385  
Db GTCCAGCGGCGCTGTATCCGACACAGGAGCTGGGCGACGAGAGATCCAGATCGTGAGC 180  
QY CAGATGTTGAGCTGTGTGAGAAACCCGACGCGGAGCTGGGCGACGAGATCCAGATCGTGAGC 445  
Db CAGATGTTGAGCTGTGTGAGAAACCCGACGCGGAGCTGGGCGACGAGATCCAGATCGTGAGC 240  
QY GAGGCGCAGCAGGAGCTGGGCGACACAGCGGGGCAACAGCGGCAAGGCTGGCGGACAGG 505  
Db GAGGCGCAGCAGGAGCTGGGCGACACAGCGGGGCAACAGCGGCAAGGCTGGCGGACAGG 300  
QY CCAAGAGCGAGCGGCGAGCGGCTGACAGGCTGACAGCCCAACAGAGCGGCTGACAGCGGCGAG 565  
Db CCAAGAGCGGCGAGCGGCTGACAGGCTGACAGCCCAACAGAGCGGCTGACAGCGGCGAG 360  
QY CGCAACAAACGAGAACCGTGAGAACCGGTCCAGCAACAGCGGCAAGGCTGGCGGACAGG 625  
Db CGCAACAAACGAGAACCGGTGAGAACCGGTCCAGCAACAGCGGCAAGGCTGGCGGACAGG 420  
QY GGCAACCCCAAGAGAGAGGCAAGCAAGCTTCCAGAGAGAGGCTTCCAGAGGCAAG 685  
Db GGCAACCCCAAGAGAGAGGCAAGCAAGCTTCCAGAGAGAGGCTTCCAGAGGCAAG 480  
QY GCGGAGCGAGGAGCGCTCCGCGGAGCTCCGCGGAGCTCCGCGGAGCTCCGCGGAGCTCCG 745  
Db GCGGAGCGAGGAGCGCTCCGCGGAGCTCCGCGGAGCTCCGCGGAGCTCCGCGGAGCTCCG 540  
QY CTGTGCAACAGGCTCTCTATGGGAGATGATCGGCTGCGACAAAGAGTGCCCCCATC 805  
Db CTGTGCAACAGGCTCTCTATGGGAGATGATCGGCTGCGACAAAGAGTGCCCCCATC 600  
QY GAGTGGTTCACCTCTCTGCTGGGCTCAATCATAAACCCCAAGGGCAAGT 857  
Db GAGTGGTTCACCTCTCTGCTGGGCTCAATCATAAACCCCAAGGGCAAGT 652

RESULT 5  
US-08-751-230-1  
; Sequence 1, Application US/08751230  
; Patent No. 6117633  
; GENERAL INFORMATION:  
; APPLICANT: Garkavtsev, Igor  
; APPLICANT: Riabowol, Karl  
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR  
; TITLE OF INVENTION: SUPPRESSOR GENE IN1  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/751,230  
; FILING DATE: 15-NOV-1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/569721  
; FILING DATE: 08-DEC-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mool, Leslie A.  
; REGISTRATION NUMBER: 37,047

REFERENCE/DOCKET NUMBER: 028722-144  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-7400  
TELEFAX: 415-854-8275  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1902 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 109..741  
US-08-751-230-1

Query Match 70.7%; Score 605.6; DB 3; Length 1902;  
Best Local Similarity 95.6%; Pred. No. 2.le-124;  
Matches 623; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 206 CTAGGCTGCTGGGAGTGTGCTCCGGCGCGGAAATGGAGATCTCTGAAGAGCTAGACGAG 265  
Db 1 CTGACCCGAGGGTGGGCGCGCGTGGCCGTGAAACAGATCTCTGAAGAGCTAGACGAG 60  
QY 266 TGCTACAGGCGCTTCACTCGCGAGACAGACGGGGCGGAGCGGCGGATGCTGCACTGT 325  
Db 61 TGCTACAGGCGCTTCACTCGCGAGACAGACGGGGCGGAGCGGCGGATGCTGCACTGT 120  
QY 326 GTGCAGCGCGCGCTGATCCGACGACAGGAGCTGGGCGACGAGAGATCCAGATCGTGAGC 385  
Db 121 GTGCAGCGCGCGCTGATCCGACGACAGGAGCTGGGCGACGAGAGATCCAGATCGTGAGC 180  
QY 386 CAGATGTTGAGCTGTGTGAGAAACCCGACGCGGCAAGGCTGGACAGCCAGTGAGTGTTC 445  
Db 181 CAGATGTTGAGCTGTGTGAGAAACCCGACGCGGCAAGGCTGGACAGCCAGTGAGTGTTC 240  
QY 446 GAGGCGCAGCAGGAGCTGGGCGACACAGCGGGGCAACAGCGGCAAGGCTGGCGGACAGG 505  
Db 241 GAGGCGCAGCAGGAGCTGGGCGACACAGTGGGGCAACAGTGGGGCAAGGCTGGCGGACAGG 300  
QY 506 CCCAAAGCGGAGCGGCGAGCGCTGCAAGCCCAACAGAGAGGCTCACCGCGGCGAG 565  
Db 301 CCCAAAGCGGAGCTGGGCTGAGCGCTGCAAGCCCAACAGAGAGGCTCACCGCGGCGAG 360  
QY 566 CGCAACACAGAGACCGTGAGAACCGGTCCAGCAACAGACCCAGCAGCGGCGGCTCG 625  
Db 361 CGCAACACAGAGACCGTGAGAACCGGTCCAGCAACAGACCCAGCAGCGGCGGCTCG 420  
QY 626 GGCACACCCAGAGAGAGGCGGCAAGACCTCCAAGAGAGAGAGGCGCTCCAAGGCGCAAG 685  
Db 421 GGCACACCCAGAGAGAGGCGGCAAGACCTCCAAGAGAGAGAGGCGCTCCAAGGCGCAAG 480  
QY 686 GCGGAGCGAGGCGCTCCCTGCGGAGCTCCCATGAGCCCAACAGACCCAGTACTGT 745  
Db 481 GCGGAGCGAGGCGCTCCCTGCGGAGCTCCCATGAGCCCAACAGACCCAGTACTGT 540  
QY 746 CTGTGCAACAGGCTCTCTATGGGAGATGATCGGCTGCGACAAACAGAGTGGCCCCATC 805  
Db 541 CTGTGCAACAGGCTCTCTATGGGAGATGATCGGCTGCGACAAACAGAGTGGCCCCATC 600  
QY 806 GAGTGGTTCACCTTCTCTGCTGGGCTCAATCATAAACCCCAAGGGCAAGT 857  
Db 601 GAGTGGTTCACCTTCTCTGCTGGGCTCAATCATAAACCCCAAGGGCAAGT 652

RESULT 6  
US-09-499-082-1  
; Sequence 1, Application US/09499082  
; Patent No. 6143522  
; GENERAL INFORMATION:  
; APPLICANT: Helbing, Caren C.  
; APPLICANT: Riabowol, Karl  
; APPLICANT: Johnston, Randall N.



QY 206 CTAGGCTGCTGGAGTGGTGTCCGGCCGCGAATGGAGATCCTGAAGGAGCTAGACGAG 265  
Db 1 CTGACCCGAGGGTGGGGCCGCGGTGGCGGTGGAACAGATCCTGAGAGGAGCTTAGACGAG 60  
QY 266 TGTACAGAGGCTTTCAGTCCGAGACAGACGGGGCGCAGAGCGGCGGATGCTGCATGT 325  
Db 61 TGTACAGAGGCTTTCAGTCCGAGACAGACGGGGCGCAGAGCGGCGGATGCTGCATGT 120  
QY 326 GTCCAGCGGCGCTGATCCGACAGCAGAGAGCTGGGCGCACGAGAACATCCAGATCGTGCAGC 385  
Db 121 GTCCAGCGGCGCTGATCCGACAGCAGAGAGCTGGGCGCACGAGAACATCCAGATCGTGCAGC 180  
QY 386 CAGATGCTGAGCTGTGAGAACCGCAGCGGCGCAGGTGGAAGCAGCAGTGGAGCTGTTTC 445  
Db 181 CAGATGCTGAGCTGTGAGAACCGCAGCGGCGCAGGTGGAAGCAGCAGTGGAGCTGTTTC 240  
QY 446 GAGCGCAGCAGAGAGTGGGCGCACACAGCGGCGCAACAGCGGCAAGGCTGGGCGCGACAGG 505  
Db 241 GAGCGCAGCAGAGAGTGGGCGCACACAGCGGCGCAACAGCGGCAAGGCTGGGCGCGACAGG 300  
QY 506 CCCAAGGCGAGCGGCGCAGGCTGACAGCCCAACAGAACGCTACGCGGCGAG 555  
Db 301 CCCAAGTGGCGATGCGGTAGCGAGTCTGACAGCCCAACAGAACGCTACGCGGCGAG 360  
QY 566 CGCAACACAGAACCGTGGAGAACCGTCCAGCAACACGACCGACCGCGGCGCTCG 625  
Db 361 CGCAACACAGAACCGTGGAGAACCGTCCAGCAACACGACCGACCGCGGCGCTCG 420  
QY 626 GGCACACCCAGAGAGAGAGCCAGACCTCCAGAGAGAGAGAGCGCTCCAGGCGCAAG 685  
Db 421 GGCACACCCAGAGAGAGAGCCAGAGCTCCAGAGAGAGAGAGCGCTCCAGGCGCAAG 480  
QY 686 GCGAGCGAGAGCGCTCCCTCCGACCTCCGACCTCCGACCTCCGACCTCCGACCTCCGACCT 745  
Db 481 GCGAGCGAGAGCGCTCCCTCCGACCTCCGACCTCCGACCTCCGACCTCCGACCTCCGACCT 540  
QY 746 CTGTGCAACAGGTCTCTATGGGAGAGATGATCGGCTCGACAGCAGAGTGCCTCCATC 805  
Db 541 CTGTGCAACAGGTCTCTATGGGAGAGATGATCGGCTCGACAGCAGAGTGCCTCCATC 600  
QY 806 GAGTGTTCACCTTCTGTCGTGGGCTCAATCATATAACCAAGGCGAAGT 857  
Db 601 GAGTGTTCACCTTCTGTCGTGGGCTCAATCATATAACCAAGGCGAAGT 652

## RESULT 8

US-09-258-371-9

; Sequence 9, Application US/09258371

; Patent No. 5986078

; GENERAL INFORMATION:

; APPLICANT: Garkavtsev, Igor

; APPLICANT: Riabowol, Karl

; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR

; TITLE OF INVENTION: SUPPRESSOR GENE INGI

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker &amp; Mathis

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/258,371

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

## RESULT 9

US-08-751-230-9

; Sequence 9, Application US/08751230

; APPLICATION NUMBER: 08/751,230  
; FILING DATE: 08/751,230  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mooi, Leslie A.  
; REGISTRATION NUMBER: 37,047  
; REFERENCE/DOCKET NUMBER: 028722-144  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-854-7400  
; TELEFAX: 415-854-8275  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2061 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 16...900  
; US-09-258-371-9

Query Match 70.7%; Score 605.6; DB 2; Length 2061;  
Best Local Similarity 95.6%; Pred. No. 2.2e-124;  
Matches 623; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 206 CTAGGCTCTCGGAGTGTGTGTCGGCGCGGAATGGAGATCCTGAAGGAGCTAGACGAG 265  
Db 160 CTGACCCGAGGGTGGGGCCGCGGTGGCGGTGGAACAGATCCTGAGAGGAGCTTAGACGAG 219  
QY 266 TGTACAGAGCGCTTTCAGTCCGAGACAGACGGGGCGCAGAGCGGCGGATGCTGCATGT 325  
Db 220 TGTACAGAGCGCTTTCAGTCCGAGACAGACGGGGCGCAGAGCGGCGGATGCTGCATGT 279  
QY 326 GTCCAGCGGCGCTGATCCGACAGCAGAGAGCTGGGCGCACGAGAACATCCAGATCGTGCAGC 385  
Db 280 GTCCAGCGGCGCTGATCCGACAGCAGAGAGCTGGGCGCACGAGAACATCCAGATCGTGCAGC 339  
QY 386 CAGATGCTGAGCTGTGAGAACCGCAGCGGCGCAGGTGGAAGCAGCAGTGGAGCTGTTTC 445  
Db 340 CAGATGCTGAGCTGTGAGAACCGCAGCGGCGCAGGTGGAAGCAGCAGTGGAGCTGTTTC 399  
QY 446 GAGGCGCAGCAGAGAGTGGGCGCACACAGCGGCGCAACAGCGGCGCAAGTGGGCGCGACAGG 505  
Db 400 GAGGCGCAGCAGAGAGTGGGCGCACACAGTGGGCGCAACAGCGGCGCAAGTGGGCGCGACAGG 459  
QY 506 CCCAAGGCGAGGCGGCGCAGCGAGCTGACAGCCCAACAGAACGCTACGCGGCGAG 565  
Db 460 CCCAATGGCGATGCGGTAGCGAGTCTGACAGCCCAACAGAACGCTACGCGGCGAG 519  
QY 566 CGCAACACAGAACCGTGGAGAACCGCTCCAGCAACCCAGCAGCAGCGGCGCTCG 625  
Db 520 CGCAACACAGAACCGTGGAGAACCGCTCCAGCAACCCAGCAGCAGCGGCGCTCG 579  
QY 626 GGCACACCCAGAGAGAGAGCCAGACCTCCAGAGAGAGAGCGCTCCAGAGGCGCAAG 585  
Db 580 GGCACACCCAGAGAGAGAGCCAGACCTCCAGAGAGAGAGCGCTCCAGAGGCGCAAG 639  
QY 686 GCGAGCGAGAGGCGTCCCTCCGACCTCCGACCTCCGACCTCCGACCTCCGACCTCCGACCT 745  
Db 640 GCGAGCGAGAGGCGTCCCTCCGACCTCCGACCTCCGACCTCCGACCTCCGACCTCCGACCT 699  
QY 746 CTGTGCAACAGGTCTCTATGGGAGAGATGATCGGCTCGACAGCAGAGTGCCTCCATC 805  
Db 700 CTGTGCAACAGGTCTCTATGGGAGAGATGATCGGCTCGACAGCAGAGTGCCTCCATC 759  
QY 806 GAGTGTTCACCTTCTGTCGTGGGCTCAATCATATAACCAAGGCGAAGT 857  
Db 760 GAGTGTTCACCTTCTGTCGTGGGCTCAATCATATAACCAAGGCGAAGT 811

## RESULT 9

US-08-751-230-9

; Sequence 9, Application US/08751230

Patent No. 6117633  
GENERAL INFORMATION:  
APPLICANT: Garkavtsev, Igor  
APPLICANT: Riabowol, Karl  
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR  
SUPPRESSOR GENE INGI  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: 699 Prince Street  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/751,230  
FILING DATE: 15-NOV-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/569721  
FILING DATE: 08-DEC-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Mooi, Leslie A.  
REGISTRATION NUMBER: 37,047  
REFERENCE/DOCKET NUMBER: 028722-144  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-7400  
TELEFAX: 415-854-8275  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2061 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
NAME/KEY: CDS  
LOCATION: 16..900  
US-08-751-230-9

Query Match 70.7%; Score 605.6; DB 3; Length 2061;  
Best Local Similarity 95.6%; Pred. No. 2.2e-124;  
Matches 623; Conservative 0; Mismatches 29; Indels 0; Gaps 0;  
Qy 206 CTAGGCTCTGGAGTGTGGTCCGGCGCGGATGAGATCTCTGAAGGAGCTAGACGAG 265  
Db 160 CTGACCCAGGTTGGGCGCGCGTGGCGGTGGAAACAGATCTCTGAAGGAGCTAGACGAG 219  
Qy 266 TGCTACGAGCGCTTCACTGGGAGACAGACCGGGCGGAGAGCGGGCGGATGCTGCACTGT 325  
Db 220 TGCTACGAGCGCTTCACTGGGAGACAGACCGGGCGGAGAGCGGGCGGATGCTGCACTGT 279  
Qy 326 GTGCAGCGCGCTGATCGGAGCAGCAGGAGTGGCGGACGAGATCCAGATCGTGAGC 385  
Db 280 GTGCAGCGCGCTGATCGGAGCAGCAGGAGTGGCGGACGAGATCCAGATCGTGAGC 339  
Qy 386 CAGATGTGGAGCTGGTGGAGAAACCGCAGCGGAGAGTGGAGCAGCCAGCTGGTTC 445  
Db 340 CAGATGTGGAGCTGGTGGAGAAACCGCAGCGGAGAGTGGAGCAGCCAGCTGGTTC 399  
Qy 446 GAGGCGCAGGAGCTGGGCGACACAGCGGCGACAGCGGCGGAGGCTGGCGGACAGG 505  
Db 400 GAGGCGCAGGAGCTGGGCGACACAGTGGGCGACAGCGGCGGAGTGGCGGCGGACAGG 459  
Qy 506 CCCAAAGGCGAGGCGGCGAGCGCTGCAAGCCCAACAGCCGCTACCGCGGAG 565  
Db 460 CCCAATGGCGATGGGTAGCGAGTCTGCAAGCCCAACAGCGGCTACCGCGGAG 519

Qy 566 CGCAACACGAGAACCGTGAGAACCGGTCCAGCAACACGACACGACGAGCGGCGCTCG 625  
Db 520 OGCAACACGAGAACCGTGAGAACCGGTCCAGCAACACGACACGAGCGGCGCTCG 579  
Qy 626 GGCACACCCAGGAGAGAGGCGCAAGACCTCCCAAGAGAGAGCGCTCCAAAGGCCAAG 685  
Db 580 GGCACACCCAGGAGAGAGGCGCAAGACCTCCCAAGAGAGAGCGCTCCAAAGGCCAAG 639  
Qy 686 GCGGAGGAGAGGCGGTCCCTGCGGACCTCCCATCGACCCCAACGACCCACGATCTGT 745  
Db 640 GCGGAGGAGAGGCGGTCCCTGCGGACCTCCCATCGACCCCAACGACCCACGATCTGT 699  
Qy 746 CTGTGCAACGAGGTCTCTATGCGGAGATGATCGGTCGCGACACGAGGTGCCCATC 805  
Db 700 CTGTGCAACGAGGTCTCTATGCGGAGATGATCGGTCGCGACACGAGGTGCCCATC 759  
Qy 806 GAGTGGTTCCACTTCTCGTGGTGGGCTCAATCATAAACCAAGGCAAGT 857  
Db 760 GAGTGGTTCCACTTCTCGTGGTGGGCTCAATCATAAACCAAGGCAAGT 811  
RESULT 10  
US-09-499-082-9  
Sequence 9, Application US/09499082  
Patent No. 6143522  
GENERAL INFORMATION:  
APPLICANT: Helbing, Caren C.  
APPLICANT: Riabowol, Karl  
APPLICANT: Johnston, Randall N.  
APPLICANT: Garkavtsev, Igor  
TITLE OF INVENTION: METHODS OF MODULATING APOPTOSIS  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Burns, Doane, Swecker & Mathis  
STREET: 699 Prince Street  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/499,082  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/828,158  
FILING DATE: 27-MAR-1997  
APPLICATION NUMBER: US 08/751230  
FILING DATE: 15-NOV-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/569721  
FILING DATE: 08-DEC-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Mooi, Leslie A.  
REGISTRATION NUMBER: 37,047  
REFERENCE/DOCKET NUMBER: 028722-148  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-854-7400  
TELEFAX: 650-854-8275  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2061 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
NAME/KEY: CDS  
LOCATION: 16..900

US-09-499-082-9

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Query Match      70.7%; Score 605.6; DB 3; Length 2061;
Best Local Similarity 95.6%; Pred. No. 2.2e-124; Indels 0; Gaps 0;
Matches 623; Conservative 0; Mismatches 29;

QY 206 CTAGGCTGTGGAGTGTGTCGGCCGCGGAGTGGAGATCTCTGAAGGAGCTAGACGAG 265
Db 160 CTGACCCGAGGTGGGGCGCGCTGGCGTGGAAACAGATCTCTGAAGGAGCTAGACGAG 219
QY 266 TGTCTAGACGCTTCAGTCCGAGACAGACGGGGCGAGAGCGCGGATGCTGCACTGT 325
Db 220 TGTCTAGACGCTTCAGTCCGAGACAGACGGGGCGAGAGCGCGGATGCTGCACTGT 279
QY 326 GTGACGCGCGCTGATCCGACGACGAGAGCTGGCGACGAGAGATCCAGATCGTGAGC 385
Db 280 GTGACGCGCGCTGATCCGACGACGAGAGCTGGCGACGAGAGATCCAGATCGTGAGC 339
QY 386 CAGATGTTGGAGTGTGGTGGAGAACCGCACGCGGCGAGGTGGACAGCCAGCTGCTTC 445
Db 340 CAGATGTTGGAGTGTGGTGGAGAACCGCACGCGGCGAGGTGGACAGCCAGCTGCTTC 399
QY 446 GAGGCGCAGAGAGTGGCGACACAGCGGGGACAGCGGCGAGGTGGAGCGGCGAGG 505
Db 400 GAGGCGCAGAGAGTGGCGACACAGCGGGGACAGCGGCGAGGTGGAGCGGCGAGG 459
QY 506 CCCAAGGCGAGGCGCGACGAGCTGACAAAGCCCAACAGCAAGCGCTCACGGCGGCGAG 565
Db 460 CCCAATGGCGATGGGTAGCGAGTCTGACAAAGCCCAACAGCAAGCGCTCACGGCGGCGAG 519
QY 566 CGCAACACGAGACCGTGGAGAGCGGTCCAGCAACACGACGACGACGACGCGCGCTCG 625
Db 520 CGCAACACGAGACCGTGGAGAGCGGTCCAGCAACACGACGACGACGACGCGCGCTCG 579
QY 626 GGCACACCCAGGAGAGAGCCCAAGACCTCCAAAGAGAGAGAGCGCTCCAAAGGCGAG 685
Db 580 GGCACACCCAGGAGAGAGCCCAAGACCTCCAAAGAGAGAGAGCGCTCCAAAGGCGAG 639
QY 686 GCGGAGCGAGGCGCTCCCTGCGGACCTCCGACCTCCGACCCCAAGACGACGAGTACTGT 745
Db 640 GCGGAGCGAGGCGCTCCCTGCGGACCTCCGACCTCCGACCCCAAGACGAGTACTGT 699
QY 746 CTGTGCAACCAAGTCTCTATGGGAGAGTATCGGCTGCGCAACACGAGTGCCTCCATC 805
Db 700 CTGTGCAACCAAGTCTCTATGGGAGAGTATCGGCTGCGCAACACGAGTGCCTCCATC 759
QY 806 GAGTGGTTCACCTTCTGCTGGTGGGCTCAATCATATAACCCAGGCGCAAGT 857
Db 760 GAGTGGTTCACCTTCTGCTGGTGGGCTCAATCATATAACCCAGGCGCAAGT 811

```

## RESULT 11

```

US-09-258-372-9
Sequence 9, Application US/09258372
Patent No. 6238918
GENERAL INFORMATION:
APPLICANT: Garkavtsev, Igor
APPLICANT: Rabinow, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
SUPPRESSOR GENE INGI
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,372
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/751,230
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mooi, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-144
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 16..900
US-09-258-372-9

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Query Match      70.7%; Score 605.6; DB 3; Length 2061;
Best Local Similarity 95.6%; Pred. No. 2.2e-124; Indels 0; Gaps 0;
Matches 623; Conservative 0; Mismatches 29;

QY 206 CTAGGCTGTGGAGTGTGTCGGCCGCGGAGTGGAGATCTCTGAAGGAGCTAGACGAG 265
Db 160 CTGACCCGAGGTGGGGCGCGCTGGCGTGGAAACAGATCTCTGAAGGAGCTAGACGAG 219
QY 266 TGTCTAGACGCTTCAGTCCGAGACAGACGGGGCGAGAGCGCGGATGCTGCACTGT 325
Db 220 TGTCTAGACGCTTCAGTCCGAGACAGACGGGGCGAGAGCGCGGATGCTGCACTGT 279
QY 326 GTGACGCGCGCTGATCCGACGACGAGAGCTGGCGACGAGAGATCCAGATCGTGAGC 385
Db 280 GTGACGCGCGCTGATCCGACGACGAGAGCTGGCGACGAGAGATCCAGATCGTGAGC 339
QY 386 CAGATGTTGGAGTGTGGTGGAGAACCGCACGCGGCGAGGTGGACAGCCAGCTGCTTC 445
Db 340 CAGATGTTGGAGTGTGGTGGAGAACCGCACGCGGCGAGGTGGACAGCCAGCTGCTTC 399
QY 446 GAGGCGCAGAGAGTGGCGACACAGCGGGGACAGCGGCGAGGTGGAGCGGCGAGG 505
Db 400 GAGGCGCAGAGAGTGGCGACACAGCGGGGACAGCGGCGAGGTGGAGCGGCGAGG 459
QY 506 CCCAAGGCGAGGCGCGACGAGCTGACAAAGCCCAACAGCAAGCGCTCACGGCGGCGAG 565
Db 460 CCCAATGGCGATGGGTAGCGAGTCTGACAAAGCCCAACAGCAAGCGCTCACGGCGGCGAG 519
QY 566 CGCAACACGAGACCGTGGAGAGCGGTCCAGCAACACGACGACGACGACGCGCGCTCG 625
Db 520 CGCAACACGAGACCGTGGAGAGCGGTCCAGCAACACGACGACGACGACGCGCGCTCG 579
QY 626 GGCACACCCAGGAGAGAGCCCAAGACCTCCAAAGAGAGAGAGCGCTCCAAAGGCGAG 685
Db 580 GGCACACCCAGGAGAGAGCCCAAGACCTCCAAAGAGAGAGAGCGCTCCAAAGGCGAG 639
QY 686 GCGGAGCGAGGCGCTCCCTGCGGACCTCCGACCTCCGACCCCAAGACGAGTACTGT 745
Db 640 GCGGAGCGAGGCGCTCCCTGCGGACCTCCGACCTCCGACCCCAAGACGAGTACTGT 699
QY 746 CTGTGCAACCAAGTCTCTATGGGAGAGTATCGGCTGCGCAACACGAGTGCCTCCATC 805
Db 700 CTGTGCAACCAAGTCTCTATGGGAGAGTATCGGCTGCGCAACACGAGTGCCTCCATC 759
QY 806 GAGTGGTTCACCTTCTGCTGGTGGGCTCAATCATATAACCCAGGCGCAAGT 857
Db 760 GAGTGGTTCACCTTCTGCTGGTGGGCTCAATCATATAACCCAGGCGCAAGT 811

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## RESULT 12

US-09-006-783A-2  
; Sequence 2, Application US/09006783A  
; Patent No. 6297366  
; GENERAL INFORMATION:  
; APPLICANT: Gudkov, Andrey V  
; APPLICANT: Garkavetev, Igor  
; APPLICANT: Riabowol, Karl  
; TITLE OF INVENTION: p53/ING1 as a Mediator of p53 Signaling  
; TITLE OF INVENTION: Pathway  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
; STREET: 300 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/006,783A  
; FILING DATE: 15-JAN-1998  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6297366nan, Kevin E  
; REGISTRATION NUMBER: 35,303  
; REFERENCE/DOCKET NUMBER: 97,837  
; TELEPHONE: 312-913-0001  
; TELEFAX: 312-913-0002  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2061 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 16...897  
US-09-006-783A-2

Query Match 70.5%; Score 604; DB 3; Length 2061;  
Best Local Similarity 95.4%; Pred. No. 4.9e-124;  
Matches 622; Conservative 0; Mismatches 30; Indels 0; Gaps 0;  
QY 206 CTAGGCTCTGGAGTGGTGTCCGCGCGGAATGGAGATCCTGAAGGAGCTAGACGAG 265  
DB 160 CTGACCCGAGGTGGGCGCGGTGGCCGTGGAAACAGATCCTGAAGCGCTAGACGAG 219  
QY 266 TGCTACGAGCGCTTCAGTCCGAGACAGACGGGGCGCAGAAAGCGCGGATGCTGCACTGT 325  
DB 220 TGCTACGAGCGCTTCAGTCCGAGACAGACGGGGCGCAGAAAGCGCGGATGCTGCACTGT 279  
QY 326 GTGACGCGCGGCTGATCCGAGCAGGAGCTGGGCGACGAGATCCAGATCGTGAGC 385  
DB 280 GTGACGCGCGGCTGATCCGAGCAGGAGCTGGGCGACGAGATCCAGATCGTGAGC 339  
QY 386 CAGATGTTGGAGCTGGTGGAGAACCGCAGCGGCGAGGTGGACGACCTGGAGCTGTTTC 445  
DB 340 CAGATGTTGGAGCTGGTGGAGAACCGCAGCGGCGAGGTGGACGACCTGGAGCTGTTTC 399  
QY 446 GAGGCGCAGCAGGAGCTGGGCGACACAGGGGCGAAGCGGCGAGGCTGGGCGCGACAGG 505  
DB 400 GAGGCGCAGCAGGAGCTGGGCGACACAGTGGGCGAAGCGGCGAGGTTGGGCGCGACAGG 459  
QY 506 CCAAAAGGCGGCGGCGAGCTGACAAAGCCCAACAGCAAGCGCTCACGCGCGGAG 565

DB 460 CCCAATGGCGATGCGGTAGCGCAGTCTGCAAGACCCCAAGAGCGCTCACGCGGCAG 519  
QY 566 CGCAACACGAGAACCGTGGAGAACCGCTCCAGCAACACACGACGACGAGCGGCGCTCG 625  
DB 520 CGCAACACGAGAACCGTGGAGAACCGCTCCAGCAACACACGACGACGAGCGGCGCTCG 579  
QY 626 GGCACACCCAAAGGAGAGAGCGGCAAGACTTCCAGAGAGAGAGCGCTCCAGGCGCAAG 685  
DB 580 GGCACACCCAAAGGAGAGAGCGGCAAGACTTCCAGAGAGAGAGCGCTCCAGGCGCAAG 639  
QY 686 GCGAGCGAGAGGCGTCCCTGCGGAGCTCCCATCGACCCCGACGACGACGACGACTACTGT 745  
DB 640 GCGAGCGAGAGGCGTCCCTGCGGAGCTCCCATCGACCCCGACGACGACGACTACTGT 699  
QY 746 CTGTGCAACACGAGTCTCTATGCGGAGATGATCGGCTCGGACAGAGAGTGGCCATC 805  
DB 700 CTGTGCAACACGAGTCTCTATGCGGAGATGATCGGCTCGGACAGAGAGTGGCCATC 759  
QY 806 GAGTGGTTCACACTTCTGTCGTCGGGCTCAATATAACCCCAAGGCGCAAGT 857  
DB 760 GAGTGGTTCACACTTCTGTCGTCGGGCTCAATATAACCCCAAGGCGCAAGT 811

## RESULT 13

US-09-159-871-1  
; Sequence 1, Application US/09159871A  
; Patent No. 6420136  
; GENERAL INFORMATION:  
; APPLICANT: RIABOWOL, Karl T.  
; TITLE OF INVENTION: METHOD OF MODULATING P53 ACTIVITY  
; FILE REFERENCE: 028722-181  
; CURRENT APPLICATION NUMBER: US/09/159,871A  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: US 60/060,138  
; PRIOR FILING DATE: 1997-09-26  
; PRIOR APPLICATION NUMBER: US 09/006,783  
; PRIOR FILING DATE: 1998-01-14  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 1  
; LENGTH: 2061  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (16)...(897)  
US-09-159-871-1

Query Match 70.3%; Score 602.4; DB 4; Length 2061;  
Best Local Similarity 95.2%; Pred. No. 1.1e-123;  
Matches 621; Conservative 0; Mismatches 31; Indels 0; Gaps 0;  
QY 206 CTAGGCTCTGGAGTGGTGTCCGCGCGGAATGGAGATCCTGAAGGAGCTAGACGAG 265  
DB 160 CTGACCCGAGGTGGGCGCGGTGGCCGTGGAAACAGATCCTGAAGGAGCTAGACGAG 219  
QY 266 TGCTACGAGCGCTTCAGTCCGAGACAGACGGGGCGCAGAAAGCGGATGCTGCACTGT 325  
DB 220 TGCTACGAGCGCTTCAGTCCGAGACAGACGGGGCGCAGAAAGCGGATGCTGCACTGT 279  
QY 326 GTGACGCGCGGCTGATCCGAGCAGGAGCTGGGCGACGAGATCCAGATCGTGAGC 385  
DB 280 GTGACGCGCGGCTGATCCGAGCAGGAGCTGGGCGACGAGATCCAGATCGTGAGC 339  
QY 386 CAGATGTTGGAGCTGGTGGAGAACCGCAGCGGCGAGGTGGACGACCTGGAGCTGTTTC 445  
DB 340 CAGATGTTGGAGCTGGTGGAGAACCGCAGCGGCGAGGTGGACGACCTGGAGCTGTTTC 399  
QY 446 GAGGCGCAGCAGGAGCTGGGCGACACAGGGGCGAAGCGGCGAGGCTGGGCGCGACAGG 505  
DB 400 GAGGCGCAGCAGGAGCTGGGCGACACAGTGGGCGAAGCGGCGAGGTTGGGCGCGACAGG 459



506	QY	CCCAAGGCGAGGCGGCGACGCGCTGACAAGCCCAACAGCAAGCGCTCAACGCGCGACG	566
460	DB	CCCAATGCGGATGCGGTGACGCGCTGACAAGCCCAACAGCAAGCGCTCAACGCGCGACG	519
566	QY	CGCAACACAGAGAACCGTGAGAACCGTCCACGACCAACAGCAGCAGCGCGCGCTCG	625
520	DB	CGCAACACAGAGAACCGTGAGAACCGCTCCAGCAACCAACGACGAGCGCGCGCTCG	579
626	QY	GGCACACCAAGGAGAGAGGCGCAGACCTCCAGAGAAAGAGCGCTCCAGAGGCGACG	685
580	DB	GGCACACCAAGGAGAGAGGCGCAGACCTCCAGAGAGAGAGCGCTCCAGAGGCGACG	639
686	QY	GGGAGCGAGAGGCGTCCCTCGCGACCTCCGCCATCGACCCCAACCAACCGACTACTGT	745
640	DB	GGGAGCGAGAGGCGTCCCTCGCGACCTCCGCCATCGACCCCAACCAACCGACTACTGT	699
746	QY	CTGTGCAACCAAGGTCCTATGGGGAGATGATCGCTGCGACCAACGAGTGCCTCCATC	805
700	DB	CTGTGCAACCAAGGTCCTATGGGGAGATGATCGCTGCGACCAACGAGTGCCTCCATC	759
806	QY	GAGTCGTTCCACTTCTCGTGGGTGGGTCTCAATCATAAACCCCAAGGCGCAAGT	857
760	DB	GAGTCGTTCCACTTCTCGTGGGTGGGTCTCAATCATAAACCCCAAGGCGCAAGT	811

RESIST 14

US-09-006-783A-6  
; Sequence 6, Application US/09006783A

Patent No. 6257366  
GENERAL INFORMATION:  
APPLICANT: Guckov, Andrey V  
APPLICANT: Garkavstev, Igor  
APPLICANT: Rishowol, Karl  
TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling  
TITLE OF INVENTION: Pathway  
NUMBER OF SEQUENCES: 7

;  
CORRESPONDENCE ADDRESS:  
;  
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff

STREET: 300 South

Query Match 62.4%; Score 534.4; DB 3; Length 633;  
Best Local Similarity 98.9%; Pred. No. 7.5e-109;

Matches	538;	Conservative	0;	Mismatches	6;	Indels	0;	Gaps	0;
Qy	314	ATGTCACCTGTGTGCAGCGCGTGTATCCGACGCCAGGAGCTGGCGCAGAGAAGATC	373						
Db	1	ATGTCACCTGTGTGCAGCGCGTGTATCCGACGCCAGGAGCTGGCGCAGAGAAGATC	60						
Qy	374	CAGATCTGAGCCAGATGTTGAGCTGTGTGAGAAACCGCACGCGCGCAGGTGGACAGCGAC	433						
Db	61	CAGATCTGAGCCAGATGTTGAGCTGTGTGAGAAACCGCACGCGCGCAGGTGGACAGCGAC	120						
Qy	434	GTGAGCTGTTTGAGCGCGCAGCAGAGACTTGGCGGCAACAGCGGGCAACAGCGGCAAGGCT	493						
Db	121	GTGAGCTGTTTGAGCGCGCAGCAGAGACTTGGCGGCAACAGCGGGCAACAGCGGCAAGGTT	180						
Qy	494	GGCGCGCAGACAGCGCCCAAAGCGCAGCGCGCAGCGCAAGCGCTGACAAGCCCCAACAGCAAGCGC	553						
Db	181	GGCGCGCAGACAGCGCCCAAAGCGCAGCGCGCAGCGCAAGCGCTGACAAGCCCCAACAGCAAGCGC	240						
Qy	554	TCAAGCGCGCAGCGCAACAAAGAGAACCGTGAGAACCGTCCAGCAACCAGCACCGAC	613						
Db	241	TCAAGCGCGCAGCGCAACAAAGAGAACCGTGAGAACCGTCCAGCAACCAGCACCGAC	300						
Qy	614	CACGGCGCTTCGGGCAACCCCAAGGAGAGAGGCCCAGACCTCCAAGAAGAAGAGCGC	673						
Db	301	CACGGCGCTTCGGGCAACCCCAAGGAGAGAGGCCCAGACCTCCAAGAAGAAGAGCGC	360						
Qy	674	TCCAAGCGCAAGCGGAGAGCGCTCCCTCGCGACCTCCCGCATCGACCCCAAGCA	733						
Db	361	TCCAAGCGCAAGCGGAGAGCGCTCCCTCGCGACCTCCCGCATCGACCCCAAGCA	420						
Qy	734	CCCACGTACTCTGTGTGCAACCAAGCTCTCTATTGGGAGATGATCGGCTGCGAACAACGAC	793						
Db	421	CCCACGTACTCTGTGTGCAACCAAGCTCTCTATTGGGAGATGATCGGCTGCGAACAACGAC	480						
Qy	794	GAGTCCCGCATCGAGTGGTTCACACTCTCTGTCGTCGTCGGGCTCAATCATTAACCCCAAGGGC	853						
Db	481	GAGTCCCGCATCGAGTGGTTCACACTCTCTGTCGTCGTCGGGCTCAATCATTAACCCCAAGGGC	540						
Qy	854	AAGT 857							
Db	541	AAGT 544							
 RESULT 15 US-09-370-838-146 ; Sequence 146, Application US/09370838 ; Patent No. 6444425 ; GENERAL INFORMATION: ; APPLICANT: Reed, Steven G. ; APPLICANT: Lodes, Michael J. ; APPLICANT: Mohamath, Roadoh ; APPLICANT: Secrist, Heather ; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF ; FILE REFERENCE: 210121.475C1 ; CURRENT APPLICATION NUMBER: US/09/370,838 ; CURRENT FILING DATE: 1999-08-09 ; EARLIER APPLICATION NUMBER: US 09/285,323 ; EARLIER FILING DATE: 1999-04-02 ; NUMBER OF SEQ ID NOS: 289 ; SOFTWARE: FastSeq for Windows Version 3.0 ; SEQ ID NO 146 ; LENGTH: 451 ; TYPE: DNA ; ORGANISM: Homo sapien US-09-370-838-146									

DEPT. T 15

RESULT IS  
US-09-370-838-146  
: Sequence 146. Application US/093370838

Patent No. 6444325  
GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
APPLICANT: Lodes, Michael J.  
APPLICANT: Mohamath, Roadoh  
APPLICANT: Secrist, Heather  
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF  
LUNG CANCER AND METHODS FOR THEIR USE  
FILE REFERENCE: 210121.47501  
CURRENT APPLICATION NUMBER: US/09/370.838

Query Match 41.4%; Score 355; DB 4; Length 451;  
Best Local Similarity 99.7%; Pred. No. 1.9e-69;  
Matches 366; Conservative 0; Mismatches 0; Indels

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Search completed: May 6, 2004, 11:51:27  
Job time : 84.0178 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 6, 2004, 06:20:28 ; Search time 422.45 Seconds  
(without alignments)  
8618.076 Million cell updates/sec

Title: US-09-451-739H-4  
Perfect score: 857  
Sequence: 1 cctccgagaacggtgcat.....tcataaacccagggcaagt 857

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : N Geneseq 29Jan04.\*
- 1: geneseq1980s.\*
  - 2: geneseq1990s.\*
  - 3: geneseq2000s.\*
  - 4: geneseq2001as.\*
  - 5: geneseq2001bs.\*
  - 6: geneseq2002s.\*
  - 7: geneseq2003as.\*
  - 8: geneseq2003bs.\*
  - 9: geneseq2003cs.\*
  - 10: geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	857	100.0	857	4	Aah28481 Nucleotid
2	616.4	71.9	2886	6	Abk86976 Human inh
3	616	71.9	742	4	Aah28480 Nucleotid
4	616	71.9	1533	4	Aah28478 Nucleotid
5	616	71.9	1905	6	Aad46126 Human tum
6	616	71.9	2897	6	Abk86977 Human inh
7	616	71.9	8487	4	Aal37089 Human mus
8	616	71.9	8487	7	Abx60077 cDNA enco
9	616	71.9	163350	6	Aad46127 Human tum
10	606.4	70.8	911	3	Aas3792 Human p37
11	605.6	70.7	1143	4	Aah28479 Nucleotid
12	605.6	70.7	1302	2	Aat69651 Tumour su
13	605.6	70.7	1902	2	Aav62285 Partial I
14	605.6	70.7	2061	2	Aat69652 Tumour su
15	605.6	70.7	2061	2	Aav62292 Human ING
16	602.4	70.3	2061	2	Aax28688 Nucleotid
17	446.4	52.1	2817	3	Aas3790 Murine p3
18	445.4	52.0	1835	3	Aas3789 Murine in
19	414.8	48.4	693	6	Abq50058 Oligonucl
20	414.8	48.4	693	6	Abq50059 Oligonucl
21	377.2	44.0	683	6	Abq47312 Oligonucl
22	377.2	44.0	683	6	Abq47313 Oligonucl
23	375	43.8	693	6	Abq50060 Oligonucl

24	375	43.8	693	6	Abq50061 Oligonucl
25	355	41.4	451	2	Aaz07188 Human lun
26	355	41.4	451	3	Aac79140 Human lun
27	355	41.4	451	4	Aad23215 Human lun
28	355	41.4	451	9	AAD266454 Human lun
29	355	41.4	451	9	ADe87708 Human lun
30	331	38.6	683	6	Abq47310 Oligonucl
31	331	38.6	683	6	Abq47311 Oligonucl
32	262	30.6	303	6	Abk92991 cDNA enco
33	203.4	23.7	313	3	AAc23407 Human sec
34	175.4	20.5	772	4	AAH28482 Nucleotid
35	156.8	18.3	8370	4	AAH28482 Nucleotid
36	142.6	16.6	840	2	Aaz08595 Human ING
37	142.6	16.6	1078	2	Aaz08595 Human ING
38	142.6	16.6	1080	4	Ad12783 Tumour su
39	142	16.6	1153	3	Aaz47473 Human tum
40	140.4	16.4	1154	6	Abk70424 Human bon
41	140.4	16.4	222	6	Abn26558 Human ORF
42	140.2	16.4	481	9	ADb51204 Primary r
43	131.4	15.3	8370	4	AAH28482 Nucleotid
44	110.2	12.9	421	8	ACH49821 Human leu
45	99.8	11.6	540	5	AAH74005 DNA enco

ALIGNMENTS

RESULT 1  
AAH28481  
ID AAH28481 standard; DNA; 857 BP.  
XX  
AC AAH28481;  
XX  
DT 17-SEP-2001. (first entry)  
XX  
DE Nucleotide sequence of a human cancer associated antigen.  
XX  
KW Cancer associated antigen; INGI; tumour suppressor; cancer; vaccine; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200147959-A2.  
XX  
PD 05-JUL-2001.  
XX  
PF 29-NOV-2000; 2000WO-US042334.  
XX  
PR 30-NOV-1999; 99US-00451739.  
XX  
PR 24-OCT-2000; 2000US-00602362.  
XX  
XX (LUDW.) LUDWIG INST CANCER RES.  
XX (SLOK ) SLOAN KETTERING INST CANCER RES.  
XX (CORR ) CORNELL RES FOUND INC.  
XX Jager D, Stockert E, Scanlan M, Knuth A, Old L, Gure A, Chen Y;  
XX WPI; 2001-441706/47.  
XX Isolated cancer associated nucleic acid molecule identified by SEREX  
XX (serological identification of antigens by recombinant expression  
XX cloning) technique, useful in nucleic acid based therapies to treat  
XX cancer.  
XX Claim 1; Page 45; 62pp; English.  
XX The present sequence encodes a human cancer associated antigen. The  
XX sequence is a variant of the INGI gene, which is a tumour suppressor gene  
XX candidate. The cancer associated antigen polynucleotides and polypeptides  
XX are useful for screening for the possible presence of a pathological  
XX condition in a subject such as cancer. The cancer associated antigen  
XX polypeptides are useful for producing vaccines  
XX  
SQ Sequence 857 BP; 200 A; 256 C; 297 G; 104 T; 0 U; 0 Other;

XX	DE	XX	Human inhibitor of growth 1 (ING1) isoform, p47ING1a, cDNA.
XX	Human; gene; ss; monoclonal antibody; epitope; inhibitor of growth 1;	XX	Human; gene; ss; monoclonal antibody; epitope; inhibitor of growth 1;
KW	ING1; tumour suppressor; cell cycle; breast tumour; lymphoid malignancy;	KW	ING1; tumour suppressor; cell cycle; breast tumour; lymphoid malignancy;
KW	cell growth; anti-ING1; CAB; isoform; diagnosis; tumour; antigen;	KW	cell growth; anti-ING1; CAB; isoform; diagnosis; tumour; antigen;
XX	p47ING1a.	XX	p47ING1a.
OS	Homo sapiens.	OS	Homo sapiens.
XX	Key	XX	Location/Qualifiers
FT	CDS	FT	433..1701
FT	/*tag= a	FT	/product= "p47ING1a"
FT	US2002039735-A1.	FT	US2002039735-A1.
XX	PD	XX	04-APR-2002.
XX	PP	XX	04-JUN-2001; 2001US-00874347.
XX	PR	XX	08-DEC-1995; 95US-00569721.
PR	15-NOV-1996; 96US-00751230.	PR	15-NOV-1996; 96US-00751230.
PR	26-FEB-1999; 99US-00258372.	PR	26-FEB-1999; 99US-00258372.
PR	22-MAR-2000; 2000US-00532868.	PR	22-MAR-2000; 2000US-00532868.
PR	02-JUN-2000; 2000US-0208829P.	PR	02-JUN-2000; 2000US-0208829P.
XX	(RIAB/) RIABOWOL K T.	XX	(RIAB/) RIABOWOL K T.
PA	(BOLA/) BOLAND D.	PA	(BOLA/) BOLAND D.
XX	Riabowol KT, Boland D;	XX	Riabowol KT, Boland D;
PI	WPI; 2002-526652/56.	PI	WPI; 2002-526652/56.
DR	P-PSDB; AAU79586.	DR	P-PSDB; AAU79586.
XX	Novel monoclonal antibody which specifically recognizes epitope of ING1,	XX	Novel monoclonal antibody which specifically recognizes epitope of ING1,
PT	inhibitor of growth 1 protein, and designated CAB1-10, useful for	PT	inhibitor of growth 1 protein, and designated CAB1-10, useful for
PT	detecting two different isoforms of ING1 and diagnosing a medical	PT	detecting two different isoforms of ING1 and diagnosing a medical
XX	condition.	XX	condition.
PS	Disclosure; Page 7-9; 15pp; English.	PS	Disclosure; Page 7-9; 15pp; English.
XX	The invention discloses monoclonal antibodies which can be used, in	XX	The invention discloses monoclonal antibodies which can be used, in
CC	combination, to specifically recognise epitopes of ING1 (inhibitor of	CC	combination, to specifically recognise epitopes of ING1 (inhibitor of
CC	growth 1) protein isoforms. ING1 is a tumour suppressor gene and its	CC	growth 1) protein isoforms. ING1 is a tumour suppressor gene and its
CC	expression is regulated through the cell cycle, peaking in the S phase.	CC	expression is regulated through the cell cycle, peaking in the S phase.
CC	Expression of ING1 is down regulated in breast tumours and lymphoid	CC	Expression of ING1 is down regulated in breast tumours and lymphoid
CC	malignancies. Overexpression of a construct containing the ING1 gene is	CC	malignancies. Overexpression of a construct containing the ING1 gene is
CC	able to inhibit cell growth by reducing the fraction of cells which enter	CC	able to inhibit cell growth by reducing the fraction of cells which enter
CC	into the S phase. The monoclonal antibodies are useful for detecting an	CC	into the S phase. The monoclonal antibodies are useful for detecting an
CC	ING1 protein in a cell, which involves selecting a cell that ectopically	CC	ING1 protein in a cell, which involves selecting a cell that ectopically
CC	or endogenously expresses ING1 protein. The anti-ING1 monoclonal antibody	CC	or endogenously expresses ING1 protein. The anti-ING1 monoclonal antibody
CC	combination consists of two or more antibodies of CAB1-CAB10 (not	CC	combination consists of two or more antibodies of CAB1-CAB10 (not
CC	defined), preferably a mixture of CAB1-CAB4, which can detect at least	CC	defined), preferably a mixture of CAB1-CAB4, which can detect at least
CC	two different isoforms of ING1. The antibodies are also useful for	CC	two different isoforms of ING1. The antibodies are also useful for
CC	diagnosing a disease e.g. tumour or medical condition in an animal	CC	diagnosing a disease e.g. tumour or medical condition in an animal
CC	(preferably, human) associated with aberrant levels of an ING1 protein.	CC	(preferably, human) associated with aberrant levels of an ING1 protein.
CC	The sequence presented is the human inhibitor of growth 1 (ING1) isoform,	CC	The sequence presented is the human inhibitor of growth 1 (ING1) isoform,
CC	p47ING1a, cDNA, isolated from a human cDNA library, which encodes a	CC	p47ING1a, cDNA, isolated from a human cDNA library, which encodes a
CC	protein used to raise antibodies	CC	protein used to raise antibodies
XX	Sequence 2886 BP; 741 A; 649 C; 789 G; 707 T; 0 U; 0 Other;	XX	Sequence 2886 BP; 741 A; 649 C; 789 G; 707 T; 0 U; 0 Other;
XX	Query Match	XX	Query Match
XX	Best Local Similarity 71.9%; Score 616.4; DB 6; Length 2886;	XX	Best Local Similarity 71.9%; Score 616.4; DB 6; Length 2886;
XX	Matches 686; Conservative 0; Mismatches 116; Indels 0; Gaps 0;	XX	Matches 686; Conservative 0; Mismatches 116; Indels 0; Gaps 0;
Qy	56 CGCCCTTCGGCTATCCACCTCTTCGGGGCTCGCAGTACGAGCAGCTCCCTCTCA 115	Qy	56 CGCCCTTCGGCTATCCACCTCTTCGGGGCTCGCAGTACGAGCAGCTCCCTCTCA 115
Db	811 CTCTCCCGCTCAGCCCGGCACTTCGGGGCGGGATTTATAGCATGATGATCCCG 870	Db	811 CTCTCCCGCTCAGCCCGGCACTTCGGGGCGGGATTTATAGCATGATGATCCCG 870
Qy	116 GGCCCTTTCTCTCCAAAGCGGTTCCAAAGTACCGGGAGACGACACAAAGGGAGGC 175	Qy	116 GGCCCTTTCTCTCCAAAGCGGTTCCAAAGTACCGGGAGACGACACAAAGGGAGGC 175

RESULT 2

ABX86976  
ID ABX86976 standard; cDNA; 2886 BP.  
XX  
AC ABX86976;  
XX  
DT 24-SEP-2002 (first entry)

871	GGCCTGTGGCTCGGGGCGGGGGCTCGAGTTCGGACCGCTCCCGGACCCGCGGGGGCGG	930
176	GGTGACGGATGGCGCAGCGCGCGGAGCCGCTAGGTGCTGGGAGTGGTGGTCCGGCCGC	235
931	GCTCGGAGACAGTTTCAGGCGGCATCTTTGCTGACCCGAGGGTGGGCGCGCGTGGCGG	990
236	GGATGGAGATCCTGAAGAGGCTAGACGAGTGTCTACGAGCGTTTCACTCCGAGACAGAC	295
991	TGGAAAACAGATCTGAAGGAGCTAGACGAGTGTCTACGAGCGTTCACTCCGAGACAGAC	1050
296	GGGCGCGAGAAAGCGGGGATGCTGCATGTGTGCAGCGCGCGTGTATCCCGACGACGAG	355
1051	GGGGCGCAGAAAGCGGCGGATGCTGCATGTGTGCAGCGCGCGTGTATCCCGACGACGAG	1110
356	CTGGGCGACAGAAAGATCCAGATCTGAGCCAGATGTTGAGTGTGGAGAGACCGCACG	415
1111	CTGGGCGACAGAAAGATCCAGATCTGAGCCAGATGTTGAGTGTGGAGAGACCGCACG	1170
416	CGGCAGGTGCACAGCCACGCTGGAGCTCTTCGAGGCGCAGCAGGAGCTGGGCGCACAGCG	475
1171	CGGCAGGTGCACAGCCACGCTGGAGCTCTTCGAGGCGCAGCAGGAGCTGGGCGCACAGCG	1230
476	GGCAACAGCGGCAAGGCTGGCGCGGACAGCGCCAAAGCGAGCGCGGACGCGAGGCTGAC	535
1231	GGCAACAGCGGCAAGGCTGGCGCGGACAGCGCCAAAGCGAGCGCGGACGCGAGGCTGAC	1290
536	AAGCCCAACAGCAAGCGCTACGGCGGCGAGCGCAACCAAGAGAACCGTGAGAACCGCTCC	595
1291	AAGCCCAACAGCAAGCGCTACGGCGGCGAGCGGCAACCAAGAGAACCGTGAGAACCGCTCC	1350
596	AGCAACCAAGCAACGACGAGCGCGCTCTGGGCGACACCCAGGAGAGAGAGGCCAAGACC	655
1351	AGCAACCAAGCAACGACGAGCGCGCTCTGGGCGACACCCAGGAGAGAGAGGCCAAGACC	1410
656	TCCAAAGAGAGAAAGCGCTCCCAAGGCCAAAGCGGAGCGAGAGGCGTCCCTCGCGACCTC	715
1411	TCCAAAGAGAGAAAGCGCTCCAAAGGCCAAAGCGGAGCGAGAGGCGTCCCTCGCGACCTC	1470
716	CCCATCGACCCCAACGAAACCACTACTGTGTGTGAAACAGAGTCTCTTATGGGGAATG	775
1471	CCCATCGACCCCAACGAAACCACTACTGTGTGTGAAACAGAGTCTCTTATGGGGAATG	1530
776	ATCGGCTCGCAACACGACGAGTGCCCATCGAGTGGTTTCCACTTCTCGTGGTGGGGCTC	835
1531	ATCGGCTCGCAACACGACGAGTGCCCATCGAGTGGTTTCCACTTCTCGTGGTGGGGCTC	1590
836	AATCATAAACCCAAAGGCAAGT	857
1591	AATCATAAACCCAAAGGCAAGT	1612

DECLASSIFIED

RESULI.3	
AAH28480	
ID	AAH28480 standard; DNA; 742 BP.
XX	
XX	
XX	AAH28480;
XX	
DT	17-SEP-2001 (first entry)
XX	
XX	
DE	Nucleotide sequence of a human cancer associated antigen.
XX	
KW	Cancer associated antigen; INGI; tumour suppressor; cancer; vaccine; ss.
XX	
XX	
OS	Homo sapiens.
XX	
PN	WO200147959-A2.
XX	
XX	
PD	05-JUL-2001.
XX	
PF	29-NOV-2000; 2000WO-US042334.
XX	
XX	
PR	30-NOV-1999; 99US-00451739.
PR	24-OCT-2000; 2000US-00602362.
PR	

XX (LUDW-) LUDWIG INST CANCER RES.  
PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
PA (CORR ) CORNELL RES FOUND INC.  
XX  
XX Jager D, Stockert E, Scanlan M, Knuth A, Old L, Gure A, Chen Y;  
XX WFI; 2001-441706/47.  
DR  
XX Isolated cancer associated nucleic acid molecule identified by SEREX  
PT (serological identification of antigens by recombinant expression  
PT cloning) technique, useful in nucleic acid based therapies to treat  
PT cancer.  
XX  
XX Claim 1; Page 44-45; 62pp; English.  
XX  
XX The present sequence encodes a human cancer associated antigen. The  
CC sequence is a variant of the INGI gene, which is a tumour suppressor gene  
CC candidate. The cancer associated antigen polynucleotides and polypeptides  
CC are useful for screening for the possible presence of a pathological  
CC condition in a subject such as cancer. The cancer associated antigen  
CC polypeptides are useful for producing vaccines  
XX  
XX Sequence 742 BP; 174 A; 243 C; 247 G; 78 T; 0 U; 0 Other;  
SQ

Query Match	71.9%;	Score 616;	DB 4;	Length 742;
Best Local Similarity	100.0%;	Pred. No. 2.le-110;		
Matches 616;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	242	GAGATCTCTGAAGGAGCTAGACGAGTGTCTACGAGCGCTTCAGTCTCGGAGACAGACAGCGGGCG	301	
DB	127	GAGATCTCTGAAGGAGCTAGACGAGTGTCTACGAGCGCTTCAGTCTCGGAGACAGACAGCGGGCG	186	
QY	302	CAGAAGCGGCGGATGTCTGCACTGTGTGCGAGCGCGCGCTGATCCGCGAGCAGGAGCTGGGC	361	
DB	187	CAGAAGCGGCGGATGTCTGCACTGTGTGCGAGCGCGCGCTGATCCGCGAGCAGGAGCTGGGC	246	
QY	362	GACGAGAAGATCCAGATCTGTGAGCCAGATGCTGGAGCTGTGTGGAGAACCGCACGCGGCGAG	421	
DB	247	GACGAGAAGATCCAGATCTGTGAGCCAGATGCTGTGGAGTGTGTGGAGAACCGCACGCGGCGAG	306	
QY	422	GTGACACGCGCATGTGGAGCTGTTTCGAGGCGGAGCAGGAGAGCTGGGCGACACAGCGGGCAAC	481	
DB	307	GTGACACGCGCATGTGGAGCTGTTTCGAGGCGGAGCAGGAGAGCTGGGCGACACAGCGGGCAAC	366	
QY	482	AGCGGCAAGGCTGTGCGGGGACAGAGCCCAAAGCGGAGCGGAGCGGAGCTGTGCAAGGCC	541	
DB	367	AGCGGCAAGGCTGTGCGGGGACAGAGCCCAAAGCGGAGCGGAGCGGAGCTGTGCAAGGCC	426	
QY	542	AACAGCAAGCGCTCACGCGCGCAGCGCAACAAACAGAGAACCGTGTGAGAACCGTCTCAGCAAC	601	
DB	427	AACAGCAAGCGCTCACGCGCGCAGCGCAACAAACAGAGAACCGTGTGAGAACCGTCTCAGCAAC	486	
QY	602	CACGACCAAGCAGCAGCGGCGCTCGGGGCACACCCAAAGGAGAGAGAGGCCCAAGACCTCCCAAG	661	
DB	487	CACGACCAAGCAGCAGCGGCGCTCGGGGCACACCCAAAGGAGAGAGAGGCCCAAGACCTCCCAAG	546	
QY	662	AAGAGAGACGCGTCTCAAGGGCCAAAGCGGAGCGGAGAGGCGTCCCTGTGCGAGCTCCCTCCCATC	721	
DB	547	AAGAGAGACGCGTCTCAAGGGCCAAAGCGGAGCGGAGAGGCGTCCCTGTGCGAGCTCCCTCCCATC	606	
QY	722	GACCCCAACGACCAAGTACTGTGTGTGCAACAGGCTCTCTATGTGGGAGATGATCGCG	781	
DB	607	GACCCCAACGACCAAGTACTGTGTGTGCAACAGGCTCTCTATGTGGGAGATGATCGCG	666	
QY	782	TGCGAACACGACGAGTGCCCATCGAGTGGTTCACCTTCTCGTGTGGTGGGGCTCAATCAT	841	
DB	667	TGCGAACACGACGAGTGCCCATCGAGTGGTTCACCTTCTCGTGTGGTGGGGCTCAATCAT	726	
QY	842	AAACCCAAAGGGCAAGT	857	
DB	727	AAACCCAAAGGGCAAGT	742	

## RESULT 4

```

AAH28478
ID AAH28478 standard; DNA; 1533 BP.
XX
AC AAH28478;
XX
DT 17-SEP-2001 (first entry)
DE Nucleotide sequence of a human cancer associated antigen.
XX
KW Cancer associated antigen; INGI; tumour suppressor; cancer; vaccine; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 451..1290
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FT /transl_except= (pos: 859..861, aa: Asp)
FT /transl_except= (pos: 865..867, aa: Val)
FT /transl_except= (pos: 874..876, aa: Ser)
FT /product= cancer associated antigen
XX
XX WO200147959-A2.
XX
XX 05-JUL-2001.
XX
XX 29-NOV-2000; 2000WO-US042334.
XX
XX 30-NOV-1999; 99US-00451739.
XX
XX 24-OCT-2000; 2000US-00602362.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX (SLOK) SLOAN KETTERING INST CANCER RES.
XX
XX (CORR) CORNELL RES FOUND INC.
XX
XX Jager D, Stockert E, Scanlan M, Knuth A, Old L, Gure A, Chen Y;
XX
XX WPI; 2001-441706/47.
XX
XX P-PSDB; AAB84698.
XX
XX Isolated cancer associated nucleic acid molecule identified by SREX
XX (serological identification of antigens by recombinant expression
XX cloning) technique, useful in nucleic acid based therapies to treat
XX cancer.
XX
XX Claim 1; Page 43-44; 62pp; English.
XX
XX The present sequence encodes a human cancer associated antigen. The
XX sequence is a variant of the INGI gene, which is a tumour suppressor gene
XX candidate. The cancer associated antigen polynucleotides and polypeptides
XX are useful for screening for the possible presence of a pathological
XX condition in a subject such as cancer. The cancer associated antigen
XX polypeptides are useful for producing vaccines
XX
XX Query Match 71.9%; Score 616; DB 4; Length 1533;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-110;
XX Matches 616; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 242 GAGATCTTGAGGAGCTAGACAGAGTCTACGAGCGCTTCAGTCGCGACACAGCGGGCG 301
XX
XX 586 GAGATCTTGAGGAGCTAGACAGAGTCTACGAGCGCTTCAGTCGCGACACAGCGGGCG 645
XX
XX 302 CAGAGCGCGGATGCTGACCTGTGTGCGAGCGCGCTGATCCGCGAGCCAGGAGCTGGGC 361
XX
XX 646 CAGAGCGCGGATGCTGACCTGTGTGCGAGCGCGCTGATCCGCGAGCCAGGAGCTGGGC 705
XX
XX 362 GACGAGAGATCCAGATCTGAGCCAGATGTTGGAGCTGTGGAGAACCGCACCGCGCAG 421

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Db 706 GACGAGAGATCCAGATCGTAGCCAGATGGTGGAGTGGTGGAGAAACCGCAGCGGCAG 765
Qy 422 GTGGACAGCCACCTGAGAGCTGTTCGAGCGCGACGAGGCTGGCGACACAGCGGCAAC 481
Db 766 GTGGACAGCCACCTGAGAGCTGTTCGAGCGCGACGAGGCTGGCGACACAGCGGCAAC 825
Qy 482 AGCGGCAAGGCTGGCGCGACAGCGCCCAAGAGCGAGCGCGCAGCGAGCTGACAAAGCCC 541
Db 826 AGCGGCAAGGCTGGCGCGACAGCGCCCAAGAGCGAGCGCGCAGCGAGCTGACAAAGCCC 885
Qy 542 AACAGCAAGCGCTCAGCGGCGACGCGCAACAGCAACCGTGAGAACCGCTCCAGCAAC 601
Db 886 AACAGCAAGCGCTCAGCGGCGACGCGCAACAGCAACCGTGAGAACCGCTCCAGCAAC 945
Qy 602 CACGACCACGACGAGCGCGCTCGGGCACACACCCCAAGAGAGAGAGCCCAAGAGCTCCAAG 661
Db 946 CACGACCACGAGCGCGCTCGGGCACACACCCCAAGAGAGAGAGCCCAAGAGCTCCAAG 1005
Qy 662 AAGAGAGCGCTTCAAGCGCGAGCGGCGAGAGCGCTCCCTCCGACCTCCCATC 721
Db 1006 AAGAGAGCGCTTCAAGCGCGAGCGGCGAGAGCGCTCCCTCCGACCTCCCATC 1065
Qy 722 GACCCCAAGCAACCGCTACTGTCTGTGCAACCAAGCTCTCTTATGGGAGATGATCGGC 781
Db 1066 GACCCCAAGCAACCGCTACTGTCTGTGCAACCAAGCTCTCTTATGGGAGATGATCGGC 1125
Qy 782 TCGACACAGCAGAGTCCCGCATCGAGTGTTCATCTTCGTGCGTGGGCTCAATCAT 841
Db 1126 TCGACACAGCAGAGTCCCGCATCGAGTGTTCATCTTCGTGCGTGGGCTCAATCAT 1185
Qy 842 AAACCCAGGCGAAGT 857
Db 1186 AAACCCAGGCGAAGT 1201
XX
XX RESULT 5
XX AAD46126
XX ID AAD46126 standard; cDNA; 1905 BP.
XX AC AAD46126;
XX
XX 27-DEC-2002 (first entry)
XX
XX Human tumour suppressor protein encoding cDNA.
XX
XX Human; tumour suppressor protein; cell proliferative disorder; vaccine;
XX inflammation; brain cancer; adenocarcinoma; cervix cancer; bone cancer;
XX apoptosis; leukaemia; lymphoma; melanoma; therapy; chromosome 13; gene;
XX ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX 5'UTR 1..160
XX /tag= a
XX CDS 161..1036
XX /tag= b
XX /product= "Human tumour suppressor protein"
XX 3'UTR 1037..1905
XX /tag= c
XX
XX WO200268468-A2.
XX
XX 06-SEP-2002.
XX
XX 05-FEB-2002; 2002WO-US003235.
XX
XX 27-FEB-2001; 2001US-00793706.
XX (PEKE ) PE CORP NY.
XX
XX Gong F, Yan C;

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XX WPI; 2002-698658/75.  
DR P-PSDB; AAE28633.  
XX  
XX New human tumor suppressor proteins, useful for developing human  
PT therapeutic agents, or preventing or treating inflammation, or disorders  
PT associated with cell proliferation, e.g. bone cancer, brain cancer,  
PT leukemia or lymphoma.  
XX  
XX Claim 4; Fig 1; 200pp; English.  
XX  
XX The invention relates to human tumor suppressor polypeptides and  
CC polynucleotides. Sequences of the invention are useful for diagnosing,  
CC preventing or treating inflammation, or disorders associated with cell  
CC proliferation and apoptosis e.g. bone cancer, brain cancer, cervix  
CC cancer, adenocarcinoma, leukemia, lymphoma or melanoma. They are  
CC particularly useful as models for developing human therapeutic targets,  
CC identifying therapeutic proteins, or serving as targets for the  
CC development of human therapeutic agents that modulate tumor suppressor  
CC protein activity in cells and tissues that express the tumor suppressor  
CC protein. Polypeptides of the invention are used for identifying agents  
CC that modulate their activity. They are useful for raising antibodies or  
CC eliciting an immune response; as a reagent in assays designed to  
CC quantitatively determine levels of the protein (or its binding partner or  
CC ligand) in biological fluids; or as markers for tissues in which the  
CC corresponding protein is preferentially expressed. The invention is also  
CC used as vaccines. The present sequence is human tumor suppressor protein  
CC encoding cDNA. The tumor suppressor gene is located on chromosome 13  
XX  
XX Sequence 1905 BP; 532 A; 428 C; 528 G; 417 T; 0 U; 0 Other;  
S0  
Query Match 71.9%; Score 616; DB 6; Length 1905;  
Best Local Similarity 100.0%; Pred. No. 2.3e-110;  
Matches 616; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 392 CAGAGCGGGCGATGCTGCACTGTGTGAGCGCGCGCTGTATCGCAGCCAGGAGCTGGC 451  
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DB 452 GACGAGAGATCCAGATGCTGAGCGAGATGCTGAGCTGTGGAGACCGCAGCGCGCAG 511  
QY 422 GTGACACGCCACGCTGGAGCTGTTCGAGCGCAGCAGGAGCTGGCGGACACAGCGGGCAAC 481  
DB 512 GTGACACGCCACGCTGGAGCTGTTCGAGCGCAGCAGGAGCTGGCGGACACAGCGGGCAAC 571  
QY 482 AGCGGCAAGGCTGGCGGAGCAGCGCCCAAGCGCAGCGCGCAGCGAGGCTGACAGCCC 541  
DB 572 AGCGGCAAGGCTGGCGGAGCAGCGCCCAAGCGCAGCGCGCAGCGAGGCTGACAGCCC 631  
QY 542 AACGACAGCGCTCAGCGCGCGCAGCGCAACACAGAGAACCGTGAGAACGGCTCCAGCAAC 601  
DB 632 AACGACAGCGCTCAGCGCGCGCAGCGCAACACAGAGAACCGTGAGAACGGCTCCAGCAAC 691  
QY 602 CAGACACAGCAGCGCGCGCTCGGCGCACCCAGAGAGAGAGAGCGCAGACCTCCAG 661  
DB 692 CAGACACAGCAGCGCGCGCTCGGCGCACCCAGAGAGAGAGAGCGCAGACCTCCAG 751  
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DB 752 AAGAGAGAGCGCTCCAGGCGCAAGCGCGAGGAGGCGTCCCTGCGGAGCTCCCGATC 811  
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DB 812 GACCCCAACGACCCACCTACTGTGTGTGCAACAGAGTCTCTATGGGGAGATGATCGG 871  
QY 782 TCGACACAGCAGGAGTGGCCCATCGAGTGGTTCACCTTCGTCGGTGGGCTCAATCAT 841

Db 872 TGCACAAACGACGAGTGGCCCATCGAGTGGTTCACCTTCGTCGGTGGGCTCAATCAT 931  
QY 842 AAACCCAAAGGCAAGT 857  
Db 932 AAACCCAAAGGCAAGT 947  
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XX ABR6977;  
XX  
XX 24-SEP-2002 (first entry)  
XX Human inhibitor of growth 1 (ING1) isoform, p33ING1b, cDNA.  
XX Human; gene; ss; monoclonal antibody; epitope; inhibitor of growth 1;  
KW ING1; tumour suppressor; cell cycle; breast tumour; lymphoid malignancy;  
KW cell growth; anti-ING1; CAB; isoform; diagnosis; tumour; antigen;  
KW p33ING1b.  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
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FT /\*tag= a  
FT /product= "p33ING1b"  
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XX US2002039735-A1.  
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XX 04-APR-2002.  
XX  
XX 04-JUN-2001; 2001US-00874347.  
XX  
XX 08-DEC-1995; 95US-00569721.  
XX 15-NOV-1995; 95US-00751230.  
XX 26-FEB-1995; 99US-00258372.  
XX 22-MAR-2000; 2000US-00532868.  
XX 02-JUN-2000; 2000US-02088299.  
XX (RIAB/) RIABOWOL K T.  
XX (BOLA/) BOLAND D.  
XX  
XX Riabowol KT, Boland D;  
XX  
XX WPI; 2002-526652/56.  
XX P-PSDB; AAU79587.  
XX  
XX Novel monoclonal antibody which specifically recognizes epitope of ING1,  
PT inhibitor of growth 1 protein, and designated Cabi-10, useful for  
PT detecting two different isoforms of ING1 and diagnosing a medical  
PT condition.  
XX  
XX Disclosure; Page 10-12; 15pp; English.  
XX  
XX The invention discloses monoclonal antibodies which can be used, in  
CC combination, to specifically recognise epitopes of ING1 (inhibitor of  
CC growth 1) protein isoforms. ING1 is a tumour suppressor gene and its  
CC expression is regulated through the cell cycle, peaking in the S phase.  
CC Expression of ING1 is down regulated in breast tumours and lymphoid  
CC malignancies. Overexpression of a construct containing the ING1 gene is  
CC able to inhibit cell growth by reducing the fraction of cells which enter  
CC into the S phase. The monoclonal antibodies are useful for detecting an  
CC ING1 protein in a cell, which involves selecting a cell that ectopically  
CC or endogenously expresses ING1 protein. The anti-ING1 monoclonal antibody  
CC combination consists of two or more antibodies of Cabi-Cab10 (not  
CC defined), preferably a mixture of Cabi-Cab4, which can detect at least  
CC two different isoforms of ING1. The antibodies are also useful for  
CC diagnosing a disease e.g. tumour or medical condition in an animal  
CC (preferably, human) associated with aberrant levels of an ING1 protein.  
CC The sequence presented is the human inhibitor of growth 1 (ING1) isoform,  
CC p33ING1b, cDNA, isolated from a human cDNA library, which encodes a



Fri May 7 09:17:27 2004

us-09-451-739h-4.rng

CC protein used to raise antibodies

XX Sequence 2897 BP; 733 A; 710 C; 819 G; 635 T; 0 U; 0 Other;

Query Match 71.9%; Score 616; DB 6; Length 2897;  
Best Local Similarity 100.0%; Pred. No. 2.3e-110;  
Matches 616; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 GAGATCCTGAAGAGCTAGACGAGTCTACGAGCGTTTACGTCGCGAGACACAGCGGGCG 301  
Db 1008 GAGATCCTGAAGAGCTAGACGAGTCTACGAGCGTTTACGTCGCGAGACACAGCGGGCG 1067

QY 302 CAGAGCGCGGAGTCTGCTACTGTGTCAGCGCGCTGATCCGACGCGAGAGTGGGC 361  
Db 1068 CAGAGCGCGGAGTCTGCTACTGTGTCAGCGCGCTGATCCGACGCGAGAGTGGGC 1127

QY 362 GAGGAGAAGATCCAGATCTGTGACCGAGTGTGAGAACCGCGACGCGGCAG 421  
Db 1128 GAGGAGAAGATCCAGATCTGTGACCGAGTGTGAGAACCGCGACGCGGCAG 1187

QY 422 GTGGACAGCCACGTGGAGCTGTTTCGAGCGCAGCAGAGTGGCGGACACAGCGGGCAAC 481  
Db 1188 GTGGACAGCCACGTGGAGCTGTTTCGAGCGCAGCAGAGTGGCGGACACAGCGGGCAAC 1247

QY 482 AGCGGCAAGGCTGGCGCGGACAGCGCCCAAGGCGAGCGCGCAGCGCTGACAAAGCCG 541  
Db 1248 AGCGGCAAGGCTGGCGCGGACAGCGCCCAAGGCGAGCGCGCAGCGCTGACAAAGCCG 1307

QY 542 AACAGCAAGCGCTCAGCGCGGACGCGCAACACAGAACCGTGACGCGTCCAGCAAC 601  
Db 1308 AACAGCAAGCGCTCAGCGCGGACGCGCAACACAGAACCGTGACGCGTCCAGCAAC 1367

QY 602 CAGCACCACGACGAGCGGCTCGGCGACACCCCAAGGAGAGAGGCGCAAGACTCCAAG 661  
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QY 662 AAGAAAGCGCTCAAGCGCCAGCGGAGCGGAGCGGCTCCCTCGGACCTCCCATC 721  
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QY 722 GACCCCAAGCAACCCACTGCTGTGCAACCCAGCTCTCTATGGGAGATGATCGGC 781  
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QY 782 TGCGAACACGACGAGTGGCCCATCGAGTGTTCACCTTCGTCGTCGGGCTCAATCAT 841  
Db 1548 TGCGAACACGACGAGTGGCCCATCGAGTGTTCACCTTCGTCGTCGGGCTCAATCAT 1607

QY 842 AAACCCAGGGCAAGT 857  
Db 1608 AAACCCAGGGCAAGT 1623

RESULT 7

AAL37089

ID AAL37089 standard; DNA; 8487 BP.

XX AAL37089;

XX AAL37089;

DT 08-JAN-2002 (first entry)

DE Human musculoskeletal system related polynucleotide SEQ ID NO 3454.

XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;  
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;  
KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;  
KW cardiac; gene therapy; cancer; immune disorder; cardiovascular disorder;  
KW neurological disease; infection; human; secreted protein;  
XX musculoskeletal system; ds.

OS Homo sapiens.

XX WO20015367-A1.

FN

XX 02-AUG-2001.  
PD 17-JAN-2001; 2001WO-US001338.  
XX 31-JAN-2000; 2000US-0179065P.  
XX 04-FEB-2000; 2000US-0180628P.  
PR 24-FEB-2000; 2000US-0184664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
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PR 19-MAY-2000; 2000US-0205515P.  
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PR 30-JUN-2000; 2000US-0215135P.  
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PR 14-AUG-2000; 2000US-0224518P.  
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PR 14-AUG-2000; 2000US-0225214P.  
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PR 22-AUG-2000; 2000US-0226681P.  
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PR 30-AUG-2000; 2000US-0228924P.  
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PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
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PR 06-SEP-2000; 2000US-0230438P.  
PR 08-SEP-2000; 2000US-0231242P.  
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PR 12-SEP-2000; 2000US-0231968P.  
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PR 26-SEP-2000; 2000US-0235484P.  
PR 27-SEP-2000; 2000US-0235834P.  
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PR 29-SEP-2000; 2000US-0236327P.

PR	29-SEP-2000;	2000US-0236367P.	DR	WPI; 2001-451937/48.
PR	29-SEP-2000;	2000US-0236368P.	XX	Isolated polypeptide for treating, preventing and/or prognosing
PR	29-SEP-2000;	2000US-0236369P.	PT	disorders related to the musculoskeletal system including musculoskeletal
PR	29-SEP-2000;	2000US-0236370P.	PT	cancers and also for testing and detection e.g. diagnosis.
PR	02-OCT-2000;	2000US-0236802P.	XX	Example 2; SEQ ID NO 3454; 781pp + Sequence Listing; English.
PR	02-OCT-2000;	2000US-0237037P.	PS	
PR	02-OCT-2000;	2000US-0237038P.	XX	The invention relates to novel genes (AAL34669-AAL37666) and proteins
PR	02-OCT-2000;	2000US-0237039P.	CC	(AB03087-AB04109) associated with the musculoskeletal system useful for
PR	02-OCT-2000;	2000US-0237040P.	CC	preventing, treating or ameliorating medical conditions e.g. by protein
PR	13-OCT-2000;	2000US-0239935P.	CC	or gene therapy. The genes are isolated from a range of human tissues
PR	13-OCT-2000;	2000US-0239937P.	CC	disclosed in the specification. The nucleic acids, proteins, antibodies
PR	20-OCT-2000;	2000US-0240960P.	CC	and (ant)agonists are useful in the diagnosis, treatment and prevention
PR	20-OCT-2000;	2000US-0241212P.	CC	of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the
PR	20-OCT-2000;	2000US-0241785P.	CC	adrenal gland, bone marrow, breast, gastrointestinal tract, liver,
PR	20-OCT-2000;	2000US-0241787P.	CC	lung, or urogenital; (b) immune disorders e.g. Addison's disease,
PR	20-OCT-2000;	2000US-0241808P.	CC	allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
PR	20-OCT-2000;	2000US-0241809P.	CC	diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
PR	20-OCT-2000;	2000US-0241846P.	CC	arthritis and ulcerative colitis; (c) cardiovascular disorders such as
PR	01-NOV-2000;	2000US-0244617P.	CC	myocardial ischaemia; (d) wound healing; (e) neurological diseases e.g.
PR	08-NOV-2000;	2000US-0246474P.	CC	cerebral anoxia and epilepsy; and (f) infectious diseases such as viral,
PR	08-NOV-2000;	2000US-0246475P.	CC	bacterial, fungal and parasitic infections. Note: The sequence data for
PR	08-NOV-2000;	2000US-0246476P.	CC	this patent did not form part of the printed specification, but was
PR	08-NOV-2000;	2000US-0246477P.	CC	obtained in electronic format directly from WIPO at
PR	08-NOV-2000;	2000US-0246478P.	CC	ftp.wipo.int/pub/published_pct_sequences
PR	08-NOV-2000;	2000US-0246523P.	XX	Sequence 8487 BP; 1948 A; 1987 C; 2408 G; 2144 T; 0 U; 0 Other;
PR	08-NOV-2000;	2000US-0246524P.	SQ	
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PR	08-NOV-2000;	2000US-0246528P.		
PR	08-NOV-2000;	2000US-0246529P.		
PR	08-NOV-2000;	2000US-0246530P.		
PR	08-NOV-2000;	2000US-0246531P.		
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PR	08-NOV-2000;	2000US-0246607P.		
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PR	08-NOV-2000;	2000US-0246612P.		
PR	08-NOV-2000;	2000US-0246613P.		
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PR	08-NOV-2000;	2000US-0246615P.		
PR	08-NOV-2000;	2000US-0246616P.		
PR	08-NOV-2000;	2000US-0246617P.		
PR	08-NOV-2000;	2000US-0246618P.		
PR	08-NOV-2000;	2000US-0246619P.		
PR	08-NOV-2000;	2000US-0246620P.		
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PR	08-NOV-2000;	2000US-0246640P.		
PR	08-NOV-2000;	2000US-0246641P.		
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PR	08-NOV-2000;	2000US-0246646P.		
PR	08-NOV-2000;	2000US-0246647P.		
PR	08-NOV-2000;	2000US-0246648P.		
PR	08-NOV-2000;	2000US-0246649P.		
PR	08-NOV-2000;	2000US-0246650P.		
PR	08-NOV-2000;	2000US-0246651P.		
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PR	08-NOV-2000;	2000US-0246658P.		
PR	08-NOV-2000;	2000US-0246659P.		
PR	08-NOV-2000;	2000US-0246660P.		
PR	08-NOV-2000;	2000US-0246661P.		
PR	08-NOV-2000;	2000US-0246662P.		
PR	08-NOV-2000;	2000US-0246663P.		
PR	08-NOV-2000;	2000US-0246664P.		
PR	08-NOV-2000;	2000US-0246665P.		
PR	08-NOV-2000;	2000US-0246666P.		
PR	08-NOV-2000;	2000US-0246667P.		
PR	08-NOV-2000;	2000US-0246668P.		
PR	08-NOV-2000;	2000US-0246669P.		
PR	08-NOV-2000;	2000US-0246670P.		
PR	08-NOV-2000;	2000US-0246671P.		
PR	08-NOV-2000;	2000US-0246672P.		
PR	08-NOV-2000;	2000US-0246673P.		
PR	08-NOV-2000;	2000US-0246674P.		
PR	08-NOV-2000;	2000US-0246675P.		
PR	08-NOV-2000;	2000US-0246676P.		
PR	08-NOV-2000;	2000US-0246677P.		
PR	08-NOV-2000;	2000US-0246678P.		
PR	08-NOV-2000;	2000US-0246679P.		
PR	08-NOV-2000;	2000US-0246680P.		
PR	08-NOV-2000;	2000US-0246681P.		
PR	08-NOV-2000;	2000US-0246682P.		
PR	08-NOV-2000;	2000US-0246683P.		
PR	08-NOV-2000;	2000US-0246684P.		
PR	08-NOV-2000;	2000US-0246685P.		
PR	08-NOV-2000;	2000US-0246686P.		
PR	08-NOV-2000;	2000US-0246687P.		
PR	08-NOV-2000;	2000US-0246688P.		
PR	08-NOV-2000;	2000US-0246689P.		
PR	08-NOV-2000;	2000US-0246690P.		
PR	08-NOV-2000;	2000US-0246691P.		
PR	08-NOV-2000;	2000US-0246692P.		
PR	08-NOV-2000;	2000US-0246693P.		
PR	08-NOV-2000;	2000US-0246694P.		
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PR	08-NOV-2000;	2000US-0246696P.		
PR	08-NOV-2000;	2000US-0246697P.		
PR	08-NOV-2000;	2000US-0246698P.		
PR	08-NOV-2000;	2000US-0246699P.		
PR	08-NOV-2000;	2000US-0246700P.		
PR	08-NOV-2000;	2000US-0246701P.		
PR	08-NOV-2000;	2000US-0246702P.		
PR	08-NOV-2000;	2000US-0246703P.		
PR	08-NOV-2000;	2000US-0246704P.		
PR	08-NOV-2000;	2000US-0246705P.		
PR	08-NOV-2000;	2000US-0246706P.		
PR	08-NOV-2000;	2000US-0246707P.		
PR	08-NOV-2000;	2000US-0246708P.		
PR	08-NOV-2000;	2000US-0246709P.		
PR	08-NOV-2000;	2000US-0246710P.		
PR	08-NOV-2000;	2000US-0246711P.		
PR	08-NOV-2000;	2000US-0246712P.		
PR	08-NOV-2000;	2000US-0246713P.		
PR	08-NOV-2000;	2000US-0246714P.		
PR	08-NOV-2000;	2000US-0246715P.		
PR	08-NOV-2000;	2000US-0246716P.		
PR	08-NOV-2000;	2000US-0246717P.		
PR	08-NOV-2000;	2000US-0246718P.		
PR	08-NOV-2000;	2000US-0246719P.		
PR	08-NOV-2000;	2000US-0246720P.		
PR	08-NOV-2000;	2000US-0246721P.		
PR	08-NOV-2000;	2000US-0246722P.		
PR	08-NOV-2000;	2000US-0246723P.		
PR	08-NOV-2000;	2000US-0246724P.		
PR	08-NOV-2000;	2000US-0246725P.		
PR	08-NOV-2000;	2000US-0246726P.</		

Fri May 7 09:17:27 2004

us-09-451-739h-4.rng

QY 842 AAACCAAGGCAACT 857  
D5 6832 AAACCAAGGCAACT 6847  
RESULT 8  
ID ABX60077 standard; cDNA; 8487 BP.  
XX AC ABX60077;  
XX DT 26-FEB-2003 (first entry)  
XX DE cDNA encoding novel human musculoskeletal system antigen #2421.  
XX KW Gene; ss; musculoskeletal system antigen; cancer; metastasis;  
KW re-vascularisation; thrombosis; arteriosclerosis; mineral content;  
KW cardiovascular condition; wound; injury; burn; angiogenesis; ulcer;  
KW post-operative tissue repair; limb regeneration; neuronal growth;  
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;  
KW AIDS-related complex; chondrocyte growth; bone regeneration;  
KW periodontal regeneration; tissue transport; bone graft; skin aging;  
KW keratinocyte growth; hair loss; melanocyte growth; cell proliferation;  
KW cell growth; organ transplant; cell differentiation; body height; weight;  
KW hair colour; eye colour; skin; percentage of adipose tissue;  
KW pigmentation; cosmetic surgery; metabolism; biorhythm; cardiac rhythm;  
KW depression; tendency for violence; pain; reproductive capability;  
KW hormone level; endocrine level; appetite; libido; memory; stress;  
KW storage capability; fat content; lipid content; protein content;  
KW carbohydrate content; vitamin content; cofactor content;  
KW nutritional component.  
XX OS Homo sapiens.  
XX PN US2002147140-A1.  
XX PD 10-OCT-2002.  
XX PF 17-JAN-2001; 2001US-00764877.  
XX PR 31-JAN-2000; 2000US-0179065P.  
XX PR 04-FEB-2000; 2000US-0180628P.  
XX PR 28-JUN-2000; 2000US-0214886P.  
XX PR 07-JUL-2000; 2000US-0216647P.  
XX PR 07-JUL-2000; 2000US-0216880P.  
XX PR 11-JUL-2000; 2000US-0217487P.  
XX PR 11-JUL-2000; 2000US-0217486P.  
XX PR 14-JUL-2000; 2000US-0218290P.  
XX PR 26-JUL-2000; 2000US-0220963P.  
XX PR 14-AUG-2000; 2000US-0224518P.  
XX PR 14-AUG-2000; 2000US-0224519P.  
XX PR 14-AUG-2000; 2000US-0225267P.  
XX PR 14-AUG-2000; 2000US-0225268P.  
XX PR 14-AUG-2000; 2000US-0225270P.  
XX PR 14-AUG-2000; 2000US-0225447P.  
XX PR 14-AUG-2000; 2000US-0225757P.  
XX PR 14-AUG-2000; 2000US-0225758P.  
XX PR 22-AUG-2000; 2000US-0226868P.  
XX PR 30-AUG-2000; 2000US-0228924P.  
XX PR 01-SEP-2000; 2000US-0229287P.  
XX PR 01-SEP-2000; 2000US-0229343P.  
XX PR 01-SEP-2000; 2000US-0229344P.  
XX PR 01-SEP-2000; 2000US-0229345P.  
XX PR 05-SEP-2000; 2000US-0229509P.  
XX PR 05-SEP-2000; 2000US-0229513P.  
XX PR 08-SEP-2000; 2000US-0231413P.  
XX PR 21-SEP-2000; 2000US-0234223P.  
XX PR 21-SEP-2000; 2000US-0234274P.  
XX PR 25-SEP-2000; 2000US-0234997P.  
XX PR 27-SEP-2000; 2000US-0235834P.  
XX PR 29-SEP-2000; 2000US-0236327P.  
XX PR 29-SEP-2000; 2000US-0236367P.

29-SEP-2000; 2000US-0236368P.  
29-SEP-2000; 2000US-0236369P.  
29-SEP-2000; 2000US-0236370P.  
02-OCT-2000; 2000US-0236802P.  
02-OCT-2000; 2000US-0237037P.  
02-OCT-2000; 2000US-0237038P.  
02-OCT-2000; 2000US-0237039P.  
02-OCT-2000; 2000US-0237040P.  
13-OCT-2000; 2000US-0239935P.  
20-OCT-2000; 2000US-0240960P.  
20-OCT-2000; 2000US-0241785P.  
20-OCT-2000; 2000US-0241809P.  
01-NOV-2000; 2000US-0244617P.  
17-NOV-2000; 2000US-0249299P.  
08-DEC-2000; 2000US-0251356P.  
08-DEC-2000; 2000US-0251868P.  
08-DEC-2000; 2000US-0251869P.  
(ROSE/) ROSEN C A.  
(RUBE/) RUBEN S M.  
(BARA/) BARASH S C.  
Rosen CA, Ruben SM, Barash SC;  
WPI; 2003-128199/12.  
Isolated nucleic acid molecules encoding musculoskeletal system associated polypeptides, useful for detecting disorders, e.g. cancer.  
Disclosure; SEQ ID NO 3454; 321pp; English.  
The invention describes an isolated nucleic acid molecule comprising a sequence encoding musculoskeletal system associated polypeptides useful for detecting disorders, e.g., cancer or cancer metastases, in animals or humans. The nucleic acid: stimulates re-vascularisation of ischaemic tissues associated with conditions such as thrombosis, arteriosclerosis, and other cardiovascular conditions; treats wounds due to injuries, burns, post-operative tissue repair, and ulcers; stimulates angiogenesis and limb regeneration; stimulates neuronal growth; can treat and prevent neuronal damage occurring in certain disorders or neurodegenerative conditions, such as, Alzheimer's disease, Parkinson's disease, and AIDS-related complex; stimulates chondrocyte growth, thus they can be used to enhance bone and periodontal regeneration and aid in tissue transports or bone grafts; prevents skin aging due to sunburn by stimulating keratinocyte growth; prevents hair loss, since FGF family members activate hair-forming cells and promotes melanocyte growth; stimulates growth and differentiation of hematopoietic cells and bone marrow cells when used in combination with other cytokines; maintains organs before transplantation or for supporting cell culture of primary tissues; induces tissue of mesodermal origin to differentiate in early embryos; increases or decreases the differentiation or proliferation of embryonic stem cells, besides, haematopoietic lineage; modulates mammalian characteristics, such as, body height, weight, hair colour, eye colour, skin, percentage of adipose tissue, pigmentation, size, and shape (e.g., cosmetic surgery); modulates mammalian metabolism; changes mammal's metal state or physical state by influencing biorhythms, cardiac rhythms, depression, tendency for violence, tolerance for pain, reproductive capabilities, hormonal or endocrine levels, appetite, libido, memory, or stress; increases or decreases storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors, or other nutritional components. This sequence encodes a novel human musculoskeletal system antigen. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at ftp.seqdata.uspto.gov/sequence.html?DocID=20020147140  
Sequence 8487 BP; 1948 A; 1987 C; 2408 G; 2144 T; 0 U; 0 Other;

Query Match 71.9%; Score 616; DB 7; Length 8487;  
Best Local Similarity 100.0%; Pred. No. 2.5e-110;  
Matches 616; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
242 GAGATCTCGAAGGAGCTAGACGAGTCTACGAGCGCTTCAGTCGCGAGACACGCGGCG 301

[illegible]

Matches	616:	Conservative	0:	Mismatches	0:	Indels	0:	Gaps	0:
QY	242	GAGATCTCTGAAGGAGCTACACGAGTGCTTACGAGCGCTTCAGTCCGCGAGACAGACGGGGCG	301						
Db	159807	GAGATCTCTGAAGGAGCTACACGAGTGCTTACGAGCGCTTCAGTCCGCGAGACAGACGGGGCG	159866						
QY	302	CAGAAGCGCGGAGTGTGCATCTGTGTGACGCGCGCTGTATCCGACGCCAGGAGCTGGGC	361						
Db	159867	CAGAAGCGCGGAGTGTGCATCTGTGTGACGCGCGCTGTATCCGACGCCAGGAGCTGGGC	159926						
QY	362	GACGAGAGATCCAGATCGTGAGCCAGATCGTGAGCTGTGTGAGAACCCGACGCGGCAG	421						
Db	159927	GACGAGAGATCCAGATCGTGAGCCAGATCGTGAGCTGTGTGAGAACCCGACGCGGCAG	159986						
QY	422	GTGGACAGCCACCTGGAGGCTGTTCGAGCGCGACGAGGAGCTGGGCGGCACACAGCGGGCAAC	481						
Db	159987	GTGGACAGCCACCTGGAGGCTGTTCGAGCGCGACGAGGAGCTGGGCGGCACACAGCGGGCNAC	160046						
QY	482	AGCGGCAAGGCTGGCGCGGACAGGCCAAAGCGGAGCGCGGACGCGCTGTGACAGCCC	541						
Db	160047	AGCGGCAAGGCTGGCGCGGACAGGCCAAAGCGGAGCGCGGACGCGCTGTGACAGCCC	160106						
QY	542	ACAGCAAGCGCTCACGGCGGACGCGCAACACGAGAACCGTGAGACGGCTCCACGCAAC	601						
Db	160107	ACAGCAAGCGCTCACGGCGGACGCGCAACACGAGAACCGTGAGACGGCTCCACGCAAC	160166						
QY	602	CACGACCACGACGACGCGCCTCTGGGCGCACCCCAAGGAGAGAGGCGCAAGACCTCCAAG	661						
Db	160167	CACGACCACGACGACGCGCCTCTGGGCGCACCCCAAGGAGAGAGGCGCAAGACCTCCAAG	160226						

QY 662 AAGAAGACGCTCCCAAGCCAGGCGGAGGAGGCGTCCCTGCCGACCTCCCATC 721  
 Db 160227 AAGAAGACGCTCCCAAGCCAGGCGGAGGAGGCGTCCCTGCCGACCTCCCATC 160286  
 QY 722 GACCCCAACGACCCACGCTACTCTGTGCAACACAGGCTCTCTATGGGAGATGATCGGC 781  
 Db 160287 GACCCCAACGACCCACGCTACTCTGTGCAACACAGGCTCTCTATGGGAGATGATCGGC 160346  
 QY 782 TGGGACACGACGATGCCCATCGATGCTTCCACTTCTCTGCTGGGCTCAATCAT 841  
 Db 160347 TGGGACACGACGATGCCCATCGATGCTTCCACTTCTCTGCTGGGCTCAATCAT 160406  
 QY 842 AAACCCCAAGGGCAAGT 857  
 Db 160407 AAACCCCAAGGGCAAGT 160422

RESULT 10  
 ID AA53792  
 AC AA53792  
 AC AA53792  
 XX AA53792;  
 DT 19-DEC-2000 (first entry)  
 XX Human P37ING1 coding sequence.  
 DE p53; tumour; cancer; detection; antibody; hybridisation; exon 1b; INGI1;  
 KW ing1; p37ING1; oncogene; gene therapy; diagnosis;  
 KW proliferation disorder; transformation; transformed cell; human; ds.  
 XX Homo sapiens.  
 OS  
 XX WO200046370-A1.  
 FN  
 XX 10-AUG-2000.  
 PD  
 XX 04-FEB-2000; 2000WO-US002959.  
 PF  
 XX 04-FEB-1999; 99US-0118941P.  
 FR  
 XX (UNII ) UNIV ILLINOIS FOUND.  
 PA  
 XX Gudkov A, Zeremski M, Gurova KV, Grigorian IA;  
 PI  
 XX WPI; 2000-491278/43.  
 DR  
 XX P-PSDB; AAY97244.  
 XX  
 PT Detecting nucleic acid encoding exon 1b of ing1, useful for diagnosing  
 PT and treating cancer, comprises contacting sample with isolated nucleic  
 PT acid comprising sequence of exon 1b and detecting hybridized products.  
 XX  
 PS Disclosure; Page 122-123; 134pp; English.  
 CC Mutations in or loss of the p53 gene occur in more than 50% of human  
 CC tumours and tumour cell lines, but functional inactivation of the p53  
 CC pathway occurs in a much larger proportion of tumours. In many cases the  
 CC mechanism of functional inactivation of the p53 gene remains unknown but  
 CC p53 has been found to act in cooperation with INGI1. Functional  
 CC cooperation between INGI1 and p53 suggested that INGI1 encoded a tumour  
 CC suppressor protein that functioned within the p53 pathway. This data  
 CC suggested a possible role for INGI1 in head and neck cancers and  
 CC chromosomal location of the INGI1 placed it within a region that is  
 CC frequently rearranged in head and neck cancers. Large scale analysis of  
 CC tumours involving INGI1 has not revealed mutations in INGI1 nor significant  
 CC variations in its expression suggesting that INGI1 was not a useful gene  
 CC to study in cancer etiology. However, alternative initiation exons of the  
 CC ing1 gene, each having their own promoter have been discovered.  
 CC Expression of one promoter (1a) produces a protein identical to INGI1.  
 CC Expression of a second promoter (1b) produces a protein having an  
 CC identical C-terminal fragment to INGI1 but an additional 104 N-terminal  
 CC amino acids. The newly discovered protein has been designated p37ING1  
 CC (Wild type: p37ING1). p37ING1 has the characteristics of an oncogene.

CC When overexpressed in cells (even those expressing wild type p53) p37ING1  
 CC is able to cause proliferation or transformation of those cells. Thus  
 CC detecting a nucleic acid encoding exon 1b of ing1 by hybridisation with  
 CC an isolated nucleic acid having the sequence of exon 1b of ing1 or its  
 CC antisense sequence can identify individuals expressing the oncogenic form  
 CC of ing1. Novel peptide sequences taken from the 104 N-terminal peptide of  
 CC p37ING1 can also be used to raise antibodies that can also be used in  
 CC detection methods for the p37ING1 variant. The polypeptides may be useful  
 CC in gene therapy for treatment of cell proliferation disorders, especially  
 CC cancers and for diagnosing and studying cancers  
 XX  
 SQ Sequence 911 BP; 228 A; 255 C; 305 G; 123 T; 0 U; 0 Other;

Query Match 70.8%; Score 606.4; DB 3; Length 911;  
 Best Local Similarity 99.0%; Pred. No. 1.6e-108;  
 Matches 610; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 242 GAGATCCTGAGGAGCTAGACGAGTGTACGAGCGTTTCAGTCCGAGACAGACGGGCG 301  
 Db 180 GAGATCCTGAGGAGCTAGACGAGTGTACGAGCGTTTCAGTCCGAGACAGACGGGCG 239  
 QY 302 CAGAAAGCGGCGGATGCTGCACTGTGTGACGCGCGCTGTATCCGACAGCCAGGAGTGGC 361  
 Db 240 CAGAAAGCGGCGGATGCTGCACTGTGTGACGCGCGCTGTATCCGACAGCCAGGAGTGGC 299  
 QY 362 GACGAGAGATCCAGATCGTGTGAGCCAGATGTTGGAGTGTGGAGAACCCGACGCGCAG 421  
 Db 300 GACGAGAGATCCAGATCGTGTGAGCCAGATGTTGGAGTGTGGAGAACCCGACGCGCAG 359  
 QY 422 GTGACACGACCGTGGAGCTTTCGAGCGGCGACGAGAGTGTGGCGGACACAGCGGGCAAC 481  
 Db 360 GTGACACGACCGTGGAGCTTTCGAGCGGCGACGAGAGTGTGGCGGACACAGCGGGCAAC 419  
 QY 482 AGCGCAAGGCTGGCGGCGGACGAGCCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 541  
 Db 420 AGCGCAAGGCTGGCGGCGGACGAGCCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 479  
 QY 542 AACAGCAAGCGCTCACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 601  
 Db 480 AACAGCAAGCGCTCACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 539  
 QY 602 CACGACCAAGCGCTCACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 661  
 Db 540 CACGACCAAGCGCTCACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 599  
 QY 662 AAGAAGAGCGCTCCCAAGGCGGAGGCGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 721  
 Db 600 AAGAAGAGCGCTCCCAAGGCGGAGGCGGAGGCGGCGGAGGCGGCGGCGGCGGCGGCGGCGG 659  
 QY 722 GACCCCAACGACCCACGCTACTGTGTGCAACACAGGCTCTCTATGGGAGATGATCGGC 781  
 Db 660 GACCCCAACGACCCACGCTACTGTGTGCAACACAGGCTCTCTATGGGAGATGATCGGC 719  
 QY 782 TCGGACACGACGAGTGGCCCATCGAGTGTTCACACTTCTCGTGGTGGGCTCAATCAT 841  
 Db 720 TCGGACACGACGAGTGGCCCATCGAGTGTTCACACTTCTCGTGGTGGGCTCAATCAT 779  
 QY 842 AAACCCCAAGGGCAAGT 857  
 Db 780 AAACCCCAAGGGCAAGT 795

RESULT 11  
 ID AAH28479  
 ID AAH28479 standard; DNA; 1143 BP.  
 XX  
 AC AAH28479;  
 XX  
 DT 17-SEP-2001 (first entry)  
 XX  
 DE Nucleotide sequence of a human cancer associated antigen.  
 XX  
 KW Cancer associated antigen; INGI1; tumour suppressor; cancer; vaccine; ss.



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XX SQ Sequence 1902 BP; 574 A; 391 C; 461 G; 476 T; 0 U; 0 Other;
Query Match 70.7%; Score 605.6; DB 2; Length 1902;
Best Local Similarity 95.6%; Pred. No. 2.3e-108;
Matches 623; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 206 CTAGGCTGCTGGAGTGTGTGTCGCGCCCGGGAATGGAGATCCTGAAGAGCTAGACGAG 265
Db 1 CTGACCCGAGGTTGGGGCGCGCGTGTGGCGTGAACACAGATCCTGAAGAGCTAGACGAG 60

QY 266 TGTCTAGGAGCGCTTCAGTCCGAGACAGACAGCGGGCGGAGAGCGCGGATGCTGCACTGT 325
Db 61 TGCTACGAGCGCTTCAGTCCGAGACAGACAGCGGGCGGAGAGCGCGGATGCTGCACTGT 120

QY 326 GTTCAGCGCGCGCTGATCCGCGACGAGAGCTGGCGGAGAGAGATCCAGATCGTGAGC 385
Db 121 GTTCAGCGCGCGCTGATCCGCGACGAGAGCTGGCGGAGAGAGATCCAGATCGTGAGC 180

QY 386 CAGATGGTGGAGCTGTGCTGAGAACCGCAGCGCGGAGTGGACAGCCAGCTGGAGCTGTC 445
Db 181 CAGATGGTGGAGCTGTGCTGAGAACCGCAGCGCGGAGTGGACAGCCAGCTGGAGCTGTC 240

QY 446 GAGCGCAGCAGAGCTGGCGGAGACCGCAGCGCGGAGTGGACAGCCAGCTGGAGCTGTC 505
Db 241 GAGCGCAGCAGAGCTGGCGGAGACCGCAGCGCGGAGTGGACAGCCAGCTGGAGCTGTC 300

QY 506 CCCAAGCGGAGCGCGGAGCGGAGCTGACAGAGCCCAACAGCAGCGCTCACGCGCGGAG 565
Db 301 CCCAAGCGGAGCGCGGAGCGGAGCTGACAGAGCCCAACAGCAGCGCTCACGCGCGGAG 360

QY 566 CGCAACAGCAGAGCGTGGAGAGCGGCTGACAGAGCCCAACAGCAGCGCTCACGCGCGGAG 625
Db 361 CGCAACAGCAGAGCGTGGAGAGCGGCTGACAGAGCCCAACAGCAGCGCTCACGCGCGGAG 420

QY 626 GGCACACCCCAAGAGAGGCGGAGCGGAGCTGACAGAGCCCAACAGCAGCGCTCACGCGCGGAG 685
Db 421 GGCACACCCCAAGAGAGGCGGAGCGGAGCTGACAGAGCCCAACAGCAGCGCTCACGCGCGGAG 480

QY 686 GCGGAGCGGAGCGGCTGCGGAGCGGCTGCGGAGCGGCTGCGGAGCGGCTGCGGAGCGGCTG 745
Db 481 GCGGAGCGGAGCGGCTGCGGAGCGGCTGCGGAGCGGCTGCGGAGCGGCTGCGGAGCGGCTG 540

QY 746 CTGTGCAACAGAGCTCTCTATGGGAGAGATGATCGGCTGCGGAGCGGCTGCGGAGCGGCTG 805
Db 541 CTGTGCAACAGAGCTCTCTATGGGAGAGATGATCGGCTGCGGAGCGGCTGCGGAGCGGCTG 600

QY 806 GAGTGTGCTCCACTTCGCTGCGTGGGCTCATGATTAACCCAGAGCGGAGCT 857
Db 601 GAGTGTGCTCCACTTCGCTGCGTGGGCTCATGATTAACCCAGAGCGGAGCT 552

RESULT 13
AAV62285
ID AAV62285 standard; cDNA; 1902 BP.
XX AC AAV62285;
XX KW 18-JAN-1999 (first entry)
XX DE Partial INGI partial cDNA sequence.
XX INGI gene; p33ING1; human; apoptosis; cell death; breast cancer;
XX brain tumour; gene therapy; tumour suppressor; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX CDS 109..742
XX FT /*tag= a
XX PN WO9844102-A2.
XX

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PD XX 08-OCT-1998.
PF XX 26-MAR-1998; 98WO-CA000277.
PR XX 27-MAR-1997; 97US-00828158.
XX PA (UYTB-) UNIV TECHNOLOGIES INT INC.
XX PI Helbing CC, Riabowol K, Johnston RN, Garkavtsev I;
XX DR WPI; 1998-542700/46.
XX DR P-PSDB; AAV79674.
XX PT Modulating eukaryotic apoptosis by increasing p33ING1 activity - using
PT p33ING1 derivatives, to induce apoptosis in cancer cells, and in the
PT investigation of apoptotic pathways.
XX Example 2; Fig 2; 66pp; English.
XX This is the nucleotide sequence of a human INGI (Inhibitor of Growth)
CC partial cDNA clone that codes for a p33ING1 polypeptide (see AAV79674);
CC a novel inhibitor of cell growth and a candidate tumour suppressor. INGI
CC is a new gene that is expressed in normal mammary epithelial cells, but
CC which is expressed only at lower levels in several cancerous mammary
CC epithelial cell lines and is not expressed in many primary brain tumours.
CC To isolate INGI, a subtractive hybridisation of breast cancer cell line
CC cDNAs was performed with cDNA from normal mammary epithelial cells, and
CC subcloned into INCI. An INGI fragment was obtained by PCR (see AAV62290-
CC 91) and subcloned into INCI. A normal human fibroblast and HeLa cell cDNA libraries
CC were screened to obtain the partial INGI sequence. The complete cDNA
CC sequence (see AAV62292) was obtained by RACE. A claimed method to
CC potentiate apoptosis in a eukaryotic cell involves administering an
CC active p33ING1 peptide or an oligonucleotide encoding such as a peptide.
CC A claimed method for inhibiting apoptosis in a eukaryotic cell involves
CC administering an antisense oligonucleotide. Also claimed are a method for
CC determining the apoptotic characteristics of a eukaryotic cell, an assay
CC for determining the level of p33ING1 activity in a eukaryotic cell, and
CC an isolated eukaryotic cell substantially free of p33ING1 biological
CC activity. The invention discloses INGI derivatives or variants that may
CC be used to induce apoptosis in eukaryotic cancer cells
XX
XX Sequence 1902 BP; 574 A; 390 C; 462 G; 476 T; 0 U; 0 Other;
Query Match 70.7%; Score 605.6; DB 2; Length 1902;
Best Local Similarity 95.6%; Pred. No. 2.3e-108;
Matches 623; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 206 CTAGGCTGCTGGAGTGTGTGTCGCGCCCGGGAATGGAGATCCTGAAGAGCTAGACGAG 265
Db 1 CTGACCCGAGGTTGGGGCGCGCGTGTGGCGTGAACACAGATCCTGAAGAGCTAGACGAG 60

QY 266 TGTCTAGGAGCGCTTCAGTCCGAGACAGACAGCGGGCGGAGAGCGCGGATGCTGCACTGT 325
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QY 326 GTTCAGCGCGCGCTGATCCGCGACGAGAGCTGGCGGAGAGAGATCCAGATCGTGAGC 385
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Db 421 GGCACACCCAGGAGAGAGAGCGGCAACACCTCCAAAGAGAGAGCGCTCCAAAGGCCAAG 480
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Db 481 GCGAGCGAGAGCGCTCCCTGCGGAGCTCCCAATCCCAATCCCAATCCCAATCCCAATCCCAAT 540
Qy 746 CTGTGCAACACAGGCTCTCTATGGGAGATGATCGCTGCGACACAGAGTGCCCATC 805
Db 541 CTGTGCAACACAGGCTCTCTATGGGAGATGATCGCTGCGACACAGAGTGCCCATC 600
Qy 806 GAGTGGTTTCCACTTCTCGTGGGGGCTCAATCATATAAACCAAGGGCAAGT 857
Db 601 GAGTGGTTTCCACTTCTCGTGGGGGCTCAATCATATAAACCAAGGGCAAGT 652

RESULT 14
ID AAT69652
XX AAT69652 standard; cDNA; 2061 BP.
AC AAT69652;
XX

27-AUG-1997 (first entry)
Tumour suppressor gene INGI full-length cDNA.
Tumour suppressor gene; INGI; p33ING1; breast cancer; brain cancer;
diagnosis; gene therapy; ss.
XX Homo sapiens.
XX

Key Location/Qualifiers
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FT primer_bind /tag= a
FT primer_bind /tag= b
FT primer_bind /note= "direct primer 1"
FT primer_bind /note= "direct primer 2"
FT primer_bind /tag= d
FT primer_bind /note= "reverse primer 3"
FT primer_bind /tag= e
FT primer_bind /note= "reverse primer 4"
XX
XX WO9721809-A1.
XX
XX 19-JUN-1997.
XX
XX 06-DEC-1996; 96WO-CA000819.
XX
XX 08-DEC-1995; 95US-00569721.
XX
XX 15-NOV-1996; 96US-00751230.
XX
XX (UYTE-) UNIV TECHNOLOGIES INT INC.
XX
XX Garkavstev I, Riabowol K;
XX
XX WPI; 1997-332781/30.
XX
XX P-PSDB; AAW18119.
XX
XX Isolated tumour suppressor gene, INGI - useful to develop products for
XX inhibiting or increasing cell proliferation, in particular for treatment
XX or diagnosis of cancer.

```

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XX Claim 11; Fig 3; 63pp; English.
XX
XX A full-length cDNA clone (AAT69652), designated INGI, codes for a novel
XX 33 kDa tumour suppressor protein p33ING1 (AAW19119), formerly p33ING1,
XX that is a potent inhibitor of cell growth. A partial clone (AAT69651) was
XX isolated by subtractive hybridisation between normal mammary and
XX transformed epithelial cDNAs, isolation of an antisense INGI cDNA insert
XX that caused increased cell proliferation, and use of the insert to screen
XX normal human fibroblast and HeLa cDNA libraries. The complete INGI
XX sequence was then obt'd. by 5'RACE. INGI is localised to the 13q33-34
XX chromosome region, to which a number of human cancers have been mapped.
XX INGI nucleic acids can be used in the diagnosis of breast cancer; a
XX decreased level of INGI mRNA indicates cancerous cells. They can also be
XX used in gene therapy methods to block the proliferation of cancer cells
XX
XX Sequence 2061 BP; 602 A; 439 C; 515 G; 505 T; 0 U; 0 Other;
XX
Query Match 70.7%; Score 605.6; DB 2; Length 2061;
Best Local Similarity 95.6%; Pred. No. 2.4e-108;
Matches 623; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
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Qy 326 GTGCGAGCGCGCTGATCCGAGCCAGGAGCTGGCGGACAGAGATCCAGATCTGTGAGC 385
Db 280 GTGCGAGCGCGCTGATCCGAGCCAGGAGCTGGCGGACAGAGATCCAGATCTGTGAGC 339
Qy 386 CAGATGCTGGAGCTGTGTGGAGAACCGGACCGCGCGGAGTGGACAGCAGCGTGTGCTTTC 445
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Qy 806 GAGTGGTTTCCACTTCTCGTGGGGGCTCAATCATATAAACCAAGGGCAAGT 857
Db 760 GAGTGGTTTCCACTTCTCGTGGGGGCTCAATCATATAAACCAAGGGCAAGT 811

RESULT 15
AAV62292
ID AAV62292 standard; cDNA; 2061 BP.
XX
XX AAV62292;
XX

```

DT 18-JAN-1999 (first entry)  
XX Human INGI1 full-length cDNA sequence.  
DE  
XX INGI1 gene; p33INGI; human; apoptosis; cell death; breast cancer;  
KW brain tumour; gene therapy; tumour suppressor; ss.  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
PH 16 900  
FT CDS /\*tag= a  
XX  
XX WO9844102-A2.  
XX  
XX 08-OCT-1998.  
XX  
XX 26-MAR-1998; 98WO-CA000277.  
XX  
XX 27-MAR-1997; 97US-00828158.  
XX (UYTE-) UNIV TECHNOLOGIES INT INC.  
XX  
XX Helbing CC, Riabowol K, Johnston RN, Garkavtsev I;  
XX  
XX WPI; 1998-542700/46.  
XX P-PSDB; AAW79675.  
XX  
XX Modulating eukaryotic apoptosis by increasing p33INGI activity - using  
XX p33INGI derivatives, to induce apoptosis in cancer cells, and in the  
XX investigation of apoptotic pathways.  
XX  
XX Claim 7; Fig 3; 66pp; English.  
XX  
XX This is the nucleotide sequence of a human INGI1 (Inhibitor of Growth)  
XX that codes for a p33INGI polypeptide (see AAW79675), a novel inhibitor  
XX of cell growth and a candidate tumour suppressor. INGI1 is a new gene that  
XX is expressed in normal mammary epithelial cells, but which is expressed  
XX only at lower levels in several cancerous mammary epithelial cell lines  
XX and is not expressed in many primary brain tumours. To isolate INGI1, a  
XX subtractive hybridisation of breast cancer cell line cDNAs was performed  
XX with cDNA from normal mammary epithelial cells, and subcloned cDNAs were  
XX cloned into retrovirus vector pLNCX. Following passage through a  
XX packaging line, normal mouse mammary epithelial cells were infected, and  
XX infected cells were injected into nude mice. Putative transforming  
XX fragments from tumours were isolated by PCR (see AAW62280-91) and  
XX subcloned into LNCX. An INGI1 fragment was obtained and used to screen  
XX normal human fibroblast and HeLa cell cDNA libraries. 2 Clones were  
XX sequenced to obtain a partial INGI1 sequence (see AAW62285). The complete  
XX cDNA sequence was then obtained by RACE. A claimed method to potentiate  
XX apoptosis in a eukaryotic cell involves administering an active p33INGI  
XX peptide or an oligonucleotide encoding such as a peptide. A claimed  
XX method for inhibiting apoptosis in a eukaryotic cell involves  
XX administering an antisense oligonucleotide. Also claimed are a method for  
XX determining the apoptotic characteristics of a eukaryotic cell, an assay  
XX for determining the level of p33INGI activity in a eukaryotic cell, and  
XX an isolated eukaryotic cell substantially free of p33INGI biological  
XX activity. The invention discloses INGI1 derivatives or variants that may  
XX be used to induce apoptosis in eukaryotic cancer cells  
XX  
XX Sequence 2061 BP; 602 A; 439 C; 515 G; 505 T; 0 U; 0 Other;  
XX  
XX Query Match 70.7%; Score 605.6; DB 2; Length 2061;  
XX Best Local Similarity 95.6%; Pred. No. 2.4e-105;  
XX Matches 623; Conservative 0; Mismatches 23; Indels 0; Gaps 0;  
XX  
XX 206 CTAGGCTGTGGAGTGGTGGTTCGGCGCGCGGAGTGGAGATCCTGAAGAGCTAGACGAG 265  
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QY 326 GTGAGCGCGCGCTGATCCGACGACGAGAGCTGGGCGACGAGAGATCCAGATCGTGAGC 385  
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QY 446 GAGCGCAGCAGAGCTGGGCGGACACAGCGGGCAAACAGCGGCAAGGCTGGCGGACAGG 505  
DB 400 GAGCGCAGCAGAGCTGGGCGGACACAGTGGGCAAACAGCGGCAAGGCTGGCGGACAGG 459  
QY 506 CCCAAAGCGCAGCGCGCAGCGCTGACAGCCCAAACAGCAAGCGCTCACCGCGGCGAG 565  
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DB 580 GGCACACCCAAAGAGAGAGAGGCCCAAGACCTCCAAAGAGAGAGCGCTCCAAAGGCCAAG 639  
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DB 640 GCGAGCGAGAGCGCTCCCTGCGGACCTCCCGCATCGACCCCAACCAAGCAAGCAAGTACTGT 699  
QY 746 CTGTGCAACCAAGGCTCTCTATGCGGAGATGATCGGCTGCGACACAGCAGTGCCTCCATC 805  
DB 700 CTGTGCAACCAAGGCTCTCTATGCGGAGATGATCGGCTGCGACACAGCAGTGCCTCCATC 759  
QY 806 GAGTGGTTCCACTTCTCTGCTGGGCTCAATCATATAACCCAAAGGCGAAGT 857  
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Search completed: May 6, 2004, 08:19:34  
Job time : 426.45 secs

GenCore version 5.1.6  
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OM'nucleic - nucleic search, using sw model

Run on: May 6, 2004, 06:25:29 ; Search time 3731.55 Seconds  
(without alignments)  
9954.293 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: gb\_hg.\*
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- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pri.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
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- 28: em\_un.\*
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- 30: em\_hg\_hum.\*
- 31: em\_hg\_inv.\*
- 32: em\_hg\_other.\*
- 33: em\_hg\_mus.\*
- 34: em\_hg\_pln.\*
- 35: em\_hg\_rod.\*
- 36: em\_hg\_mam.\*
- 37: em\_hg\_vrt.\*
- 38: em\_sy.\*
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- 40: em\_hgo\_mus.\*
- 41: em\_hgo\_other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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10	616	71.9	1905	6	AX839842 Sequence
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12	616	71.9	2552	9	AF167551 Homo sapi
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23	606.4	70.8	1533	9	AF149721 Homo sapi
24	606.4	70.8	1980	9	AB024404 Homo sapi
25	606.4	70.8	2444	9	AB024401 Homo sapi
26	606.4	70.8	2891	9	AB024402 Homo sapi
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ACCESSION AX367045  
VERSION AX367045.1 GI:18855270  
KEYWORDS  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS Jager,D., Stockert,E., Scanlan,M., Knuth,A., Old,L., Gure,A. and Chen,Y.T.  
TITLE Isolated nucleic acid molecules encoding cancer associated

Pred. No. is the number of results predicted by chance to have a

antigens, the antigens per se, and uses thereof  
 Patent: WO 0147959-A 4 05-JUL-2001;  
 LUDWIG INSTITUTE FOR CANCER RESEARCH (US) ; MEMORIAL  
 SLOAN-KETTERING CANCER CENTER (US) ; Coriell Research Foundation  
 (US)

FEATURES

source

ORIGIN

Query Match 100.0%; Score 857; DB 6; Length 857;  
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Db 781 CTGGACAAACAGCAGTGTCCCATCGAGTGTGTTCCACTTCTGTCGTGGGGTCAATCA 840  
Qy 841 TAAACCCAGGCGCAAGT 857  
Db 841 TAAACCCAGGCGCAAGT 857

RESULT 3  
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DEFINITION BC018348  
ACCESSION BC018348  
VERSION BC018348.1 GI:22450777  
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 2296)  
Strausberg, R.  
Direct Submission  
Submitted (03-DEC-2001) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: DCTD/Drp  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Baylor College of Medicine Human Genome  
Sequencing Center  
Center code: BCM-HGSC  
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,  
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,  
Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
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Qy 116 GGCCTCTTGTCTCCAGCGCTTCCAACTGATACCGGAGACGACAAAGGAGGCG 175  
Db 306 GGCCTGTGGGCTCGGGCGCGGCTGCGAGTTCGGACCCCTCCCGGACCCCGGGCGG 365  
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DEFINITION AB037594
ACCESSION AB037594.2 GI:27263168
VERSION INGI isoform.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Gunduz, M., Ouchida, M., Fukushima, K., Hanafusa, H., Etani, T.,
Nishio, S., Nishizaki, K. and Shimizu, K.
TITLE Genomic structure of the human INGI gene and tumor-specific
mutations detected in head and neck squamous cell carcinomas
JOURNAL Cancer Res. 60 (12), 3143-3146 (2000)
MEDLINE 20322670
PubMed 10866301
REFERENCE 2 (bases 1 to 888)
AUTHORS Ouchida, M. and Hanafusa, H.
TITLE Direct Submission
JOURNAL Submitted (25-JAN-2000) Mamoru Ouchida, Okayama University Medical
School, Department of Molecular Genetics; Shikata-cho, 2-5-1,
Okayama 700-8558, Japan (E-mail:ouchida@med.okayama-u.ac.jp,
Tel:81-86-235-7379, Fax:81-86-235-7383)
COMMENT On Dec 19, 2002 this sequence version replaced gi:12231169.
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ACCESSION AF181849
VERSION AF181849.1 GI:6409277
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2886)
AUTHORS Ma, D., Lawless, D. and Riabowol, K.
TITLE Sequence conservation of INGI1 splicing isoforms in divergent
species
JOURNAL Nat. Genet. 23, 373 (1999)
REFERENCE 2 (bases 1 to 2886)
AUTHORS Ma, D., Lawless, D. and Riabowol, K.
TITLE Direct Submission
JOURNAL Submitted (30-AUG-1999) Department of Biochemistry and Molecular
Biology, University of Calgary, 3330 Hospital Drive N.W., Calgary,
Alberta T2N 4N1, Canada
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DEFINITION	AX367044	Sequence 3 from Patent WO0147959.	
ACCESSION	AX367044	GI:18855269	
VERSION	AX367044.1	GI:18855269	
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Jager,D., Stockert,E., Scanlan,M., Knuth,A., Old,L., Gure,A. and Chen,Y.T.		
TITLE	Isolated nucleic acid molecules encoding cancer associated antigens, the antigens per se, and uses thereof		
JOURNAL	Patent: WO 0147959-A 3 05-JUL-2001;		
	LUDWIG INSTITUTE FOR CANCER RESEARCH (US); MEMORIAL SLOAN-KETTERING CANCER CENTER (US); Cornell Research Foundation (US)		
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RESULT 7
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LOCUS Homo sapiens p33ING1 (ING1) mRNA, complete cds. PRI 15-AUG-2001
DEFINITION Homo sapiens p33ING1 (ING1) mRNA, complete cds.
ACCESSION AF078835
VERSION AF078835.1 GI:10039544
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 840)
AUTHORS Nagashima,M., Shieski,M., Miura,K., Hagiwara,K., Linke,S.P.,
Pedoux,R., Wang,X.W., Yokota,J., Riabowol,K. and Harris,C.C.
TITLE DNA damage-inducible gene p33ING2 negatively regulates cell
proliferation through acetylation of p53
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9671-9676 (2001)
MEDLINE 21396501
PUBMED 11481424
REFERENCE 2 (bases 1 to 840)
AUTHORS Nagashima,M., Hagiwara,K., Hancock,A.R. and Harris,C.C.
TITLE Direct Submission
JOURNAL National Cancer Institute, National Institutes of Health, 37
Convent Dr., Bldg. 37, Rm. 2C01, Bethesda, MD 20892, USA
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Matches 616; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 6
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DEFINITION Homo sapiens mRNA for p33ING1b (ING1b gene).
ACCESSION AJ310392
VERSION AJ310392.1 GI:13992538
KEYWORDS ING1b; p33ING1b.
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Numan,G.S., Anderson,J.J., Angus,B. and Lunec,J.
TITLE Supplement:Sequencing of ING1 tumour suppressor gene cDNAs
generated from mRNA recovered from normal and neoplastic cell lines
J. Pathol. 192, 266-266 (2000)
JOURNAL
REFERENCE 2
AUTHORS Numan,G.S., Angus,B., Lunec,J., Lodge,A.J. and Anderson,J.J.
TITLE Comparative Assessment of ING1 Expression in Normal and Neoplastic
Tissues
Unpublished
REFERENCE 3 (bases 1 to 845)
AUTHORS Numan,G.S.
TITLE Direct Submission
JOURNAL Submitted (24-APR-2001) Numan G.S., Pathology Department, Royal
Victoria Infirmary, Faculty of Medicine, University of Newcastle
upon Tyne, Department of Pathology, Royal Victoria Infirmary,
Newcastle upon Tyne, NE3 4PH, UNITED KINGDOM
COMMENT Identical sequence found in:
Newborn Foreskin Fibroblast HS-68
Epithelial Lung Carcinoma line: A549
Breast Carcinoma Cell lines: ZR75, T47D, MCF-7
Neuroblastoma lines: SK-N-SH, SKN-BE, SKN-BE-2C
Cervical Carcinoma line: HeLa.
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YNR"

ORIGIN
Query Match 71.9%; Score 616; DB 9; Length 845;
Best Local Similarity 100.0%; Pred. No. 2.9e-82; Indels 0; Gaps 0;
Matches 616; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 CAGATCCTGAAGGAGCTAGACAGTGTCTACGAGCGCTTCAGTCGCGAGACAGACGCGGCG 301
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QY 302 CAGAACGCGCGGATGCTGCACTGTGTGAGCGCGCGTGTATCCGAGCAGGAGCTGGGC 361
DB 201 CAGAACGCGCGGATGCTGCACTGTGTGAGCGCGCGTGTATCCGAGCAGGAGCTGGGC 260
QY 362 GACGAGAGATCCAGATCGTGAGCGAGATGTGTGAGCTGTGTGAGAGACCGCAGCGCGAG 421
DB 261 GACGAGAGATCCAGATCGTGAGCGAGATGTGTGAGCTGTGTGAGAGACCGCAGCGCGAG 320
QY 422 GTGACAGCAGCTGTGTGAGCGAGCTGTGTGAGCGAGCAGGAGCTGGGCGACACAGCGGCAAC 481
DB 321 GTGACAGCAGCTGTGTGAGCGAGCTGTGTGAGCGAGCAGGAGCTGGGCGACACAGCGGCAAC 380
QY 482 AGCGCAAGGCTGGCGGAGCAGCGCCCAAGCGGAGCGGAGCGGAGCTGACAGCGCC 541
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DB 441 AACAGCAAGCGCTCAAGCGGCGAGCGCCCAAGCGGAGCGGAGCTGACAGCGCC 500
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DB 501 CACGACCAAGCGCTCAAGCGGCGAGCGCCCAAGCGGAGCGGAGCTGACAGCGCC 560
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DB 621 GACCCCAAGCGCTCAAGCGGCGAGCGCCCAAGCGGAGCGGAGCTGACAGCGCC 680
QY 782 TGCAGCAAGCGAGTGGCCCATCGAGTGGTTCACCTTCTCGTGGGGGCTCAATCAT 841
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DB 741 AACCCCAAGGCGCAAGT 756

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RESULT 9  
AX367042

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LOCUS AX367042 1533 bp DNA linear PAT 16-FEB-2002
DEFINITION Sequence 1 from Patent WO0147959.
ACCESSION AX367042
VERSION AX367042.1 GI:18855267
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE Jager,D., Stockert,E., Scanlan,M., Knuth,A., Old,L., Gure,A. and
AUTHORS Chen,Y.T.
TITLE Isolated nucleic acid molecules encoding cancer associated
antigens, the antigens per se, and uses thereof
JOURNAL Patent: WO 0147959-A 1 05-JUL-2001;
LUDWIG INSTITUTE FOR CANCER RESEARCH (US); MEMORIAL
SLOAN-KETTERING CANCER CENTER (US); Cornell Research Foundation
(US)
FEATURES
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ORIGIN
Query Match 71.9%; Score 616; DB 6; Length 1533;
Best Local Similarity 100.0%; Pred. No. 2.5e-82; Indels 0; Gaps 0;
Matches 616; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 646 CAGAACGCGCGGATGCTGCACTGTGTGAGCGCGCGTGTATCCGAGCAGGAGCTGGGC 705
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DB 706 GACGAGAGATCCAGATCGTGAGCGAGCTGTGTGAGAGCTGTGTGAGAGACCGCAGCGGCGAG 765
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QY 482 AGCGCAAGGCTGGCGGAGCAGCGCCCAAGCGGAGCGGAGCTGACAGCGCC 541
DB 826 AGCGCAAGGCTGGCGGAGCAGCGCCCAAGCGGAGCGGAGCTGACAGCGCC 885
QY 542 AACAGCAAGCGCTCAAGCGGCGAGCGCCCAAGCGGAGCGGAGCTGACAGCGCC 601
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DB 1126 TGCAGCAAGCGAGTGGCCCATCGAGTGGTTCACCTTCTCGTGGGGGCTCAATCAT 1185
QY 842 AACCCCAAGGCGCAAGT 857
DB 1186 AACCCCAAGGCGCAAGT 1201

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RESULT 10
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LOCUS
DEFINITION
Sequence 1 from Patent WO2068468.
ACCESSION
AX839842
VERSION
AX839842.1 GI:39978381
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
REFERENCE
1
AUTHORS
Isolated human tumor suppressor proteins, nucleic acid molecules
TITLE
encoding these human tumor suppressor proteins, and uses thereof
JOURNAL
Patent: WO 02068468-A 1 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.3e-82;
Matches 616; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 GAGATCTCTGAAGGAGCTAGACGAGTCTACGAGCGCTTCAGTCCGCGAGACAGACGGGGCG 301
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QY 302 CAGAGCGGGGAGTCTGACACTGTGTGACGCGCGCTGATCCGACGACGAGAGTGGGC 361
DB 392 CAGAGCGGGGAGTCTGACACTGTGTGACGCGCGCTGATCCGACGACGAGAGTGGGC 451
QY 362 GACGAGAGATCCAGATCTGTGACCCAGATCTGTGAGAGTCTGTGGAGAACCGCACGCGGAG 421
DB 452 GACGAGAGATCCAGATCTGTGACCCAGATCTGTGAGAGTCTGTGGAGAACCGCACGCGGAG 511
QY 422 GTGACAGCCAGCTGAGAGTCTGTGAGGCGAGCGAGAGTCTGGCGACACAGCGGGCAAC 481
DB 512 GTGACAGCCAGCTGAGAGTCTGTGAGGCGAGCGAGAGTCTGGCGACACAGCGGGCAAC 571
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QY 782 TGGCACAACGAGTCCCGCATCTGAGTGGTTCCTCTCTCTGCGTGGGGTCAATCAT 841
DB 872 TGGCACAACGAGTCCCGCATCTGAGTGGTTCCTCTCTCTGCGTGGGGTCAATCAT 931
QY 842 AAACCCCAAGGCGAGT 857
DB 932 AAACCCCAAGGCGAGT 947

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RESULT 11
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LOCUS
DEFINITION
Homo sapiens p33ING1 (ING1) gene, exon 2 and complete cds.
ACCESSION
AF078837
VERSION
AF078837.1 GI:10039548
KEYWORDS
2 of 2
SEGMENT
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
REFERENCE
1
AUTHORS
Nagashima,M., Hagiwara,K. and Harris,C.C.
TITLE
Direct Submission
JOURNAL
Submitted (18-JUL-1998) Laboratory of Human Carcinogenesis,
National Cancer Institute, National Institutes of Health, 37
Convent Dr., Bldg. 37, Rm. 2C01, Bethesda, MD 20892, USA
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Location/Qualifiers
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polyA_signal

ORIGIN
Query Match 71.9%; Score 616; DB 9; Length 2096;
Best Local Similarity 100.0%; Pred. No. 2.3e-82;
Matches 616; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 205 CAGAGCGGCGAGTCTGCACTGTGTGACGCGCGCTGATCCGACGACGAGAGTGGGC 264
QY 362 GACGAGAGATCCAGATCTGTGAGCGAAGTGTGTGAGTCTGTGAGAACCCGACCGCGCAG 421
DB 265 GACGAGAGATCCAGATCTGTGAGCGAAGTGTGTGAGTCTGTGAGAACCCGACCGCGCAG 324
QY 422 GTGGACAGCCAGCTCGAGCTCTGTGAGCGCGAGCGAGTCTGGGCGGACACAGCGGGCAAC 481
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QY 482 AGCGGCAAGGCTGGCGGAGCAGGCCCAAGCGGCGGAGCGGAGTCTGACAAAGCCC 541
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QY 602 CAGACCAACGACGCGCGCTCGGCGCACACCAACGAGAGAGAGAGGCGCAAGCTCCAG 661  
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Db 685 TGGGACCAACGACGAGTGCCTCCATCGAGTGGTTCCACTTCTCGTGGGCGCTCAATCAT 744  
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Db 745 AATCCCAAGGCGCAAGT 760

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DEFINITION Homo sapiens growth inhibitory protein ING1 (ING1) gene, exon 2 and partial and complete cds.  
ACCESSION AF167551  
VERSION AF167551.1 GI:9944279  
KEYWORDS  
SEGMENT  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 2552)  
Baranova, A.V., Ivanov, D.V., Makeeva, N.V., Corcoran, M., Nikitin, E.A., Poltarau, A.B., Glinshikova, O., Soudarikov, A.B., Oscier, D. and Yankovsky, N.K.  
Genomic organization of the ING1 tumor suppressor gene  
FEBS Lett. (1999) In press  
REFERENCE 2 (bases 1 to 2552)  
Baranova, A.V., Ivanov, D.V., Makeeva, N.V., Corcoran, M., Poltarau, A.B., Borodina, I.A. and Tyazelova, I.A.  
Direct Submission  
Submitted (12-JUL-1999) Genome Analysis Lab, Vavilov Institute of General Genetics, Gubkina, 3, Moscow 117809 GSP-1, Russia  
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Best Local Similarity 100.0%; Pred. No. 2.2e-82;  
Matches 616; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 289 GACGAGAGATCCAGATCGTGAAGCAAGTGTGAGTGTGTGAGAACCCGACGCGGCGAG 348  
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QY 542 AACACGACGCTACGCGCGGCGAGCAACACGAGACCGTGAGACCGCTCCAGCAAC 601  
Db 469 AACACGACGCTACGCGCGGCGAGCGGCAACACGAGACCGTGAGACCGCTCCAGCAAC 528  
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QY 662 AAGAGAGCGCTCCAGAGCGGAGGAGGCGCTCCCTCGCGACCTCCCGCATC 721  
Db 589 AAGAGAGCGCTCCAGAGCGGAGGAGGCGCTCCCTCGCGACCTCCCGCATC 648  
QY 722 GACCCCAACGAGAACCCACGTACTGTGTGTGCAACCGAGCTCTCTATGGGAGATGATCGGC 781

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QY	542	RACAGCAGCGCTCAGCGCGGCGACGCACACAGCAGGAGACCGTGTAGAACCGTCCAGCAAC	601
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QY	602	CACGACACACGACGAGCGCGCTCGGGCACACACCAAGAGAGAGAGGCGCAGGCTCCCAAG	661
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Df	1428	AGAAGAAGCGCTCAGCGCGGCGACGAGGCGGAGGAGGCGTCCCTGCGGAGCTCCCCCATC	1487
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<b>LOCUS</b>			
<b>DEFINITION</b> Homo sapiens INGI gene for p33INGlb, p47INGla, p24INGlc, complete cds and exon 2.			
<b>ACCESSION</b> ABO37387			
<b>VERSION</b> ABO37387.1 GI:9712187			
<b>KEYWORDS</b> p47INGla; p33INGlb; ING1; p24INGlc.			
<b>SEGMENT</b> 2 of 2			
<b>SOURCE</b> Homo sapiens (human)			
<b>ORGANISM</b> Homo sapiens			
<b>REFERENCE</b> Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
<b>AUTHORS</b> Gunduz M., Ouchida M., Fukushima K., Hanafusa H., Etani T., Nishio S., Nishizaki K. and Shimizu K.			
<b>TITLE</b> Genomic structure of the human INGI gene and tumor-specific mutations detected in head and neck squamous cell carcinomas			
<b>JOURNAL MEDLINE</b> Cancer Res. 60 (12), 3143-3146 (2000)			
<b>PUBMED</b> 20322670			
<b>REFERENCE</b> 1. (bases 1 to 2925) 2. Ouchida, M., Mehmet G. and Shimizu, K.			
<b>AUTHORS</b> Direct Submission			
<b>TITLE</b> Submitted (21-JUN-2000) Mamoru Ouchida, Okayama University Medical School, Department of Molecular Genetics, Shikata-cho, 2-5-1,			
<b>JOURNAL</b> Okayama 700-8558, Japan [E-mail:ouchidamed@okayama-u.ac.jp, Tel:81-86-235-7379, Fax:81-86-235-7383]			
<b>FEATURES</b> Location/Qualifiers 1..2925 organism="Homo sapiens" /mol type="genomic DNA"			
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Center clone name: 133\_E\_17

NOTE: This record contains 88 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.

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Qy	662	AGAGAGAGCGCTCCAGGCCCAAGCGCGAGGAGCGGTCCCTGCGGACCTCCCCATC	721	
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